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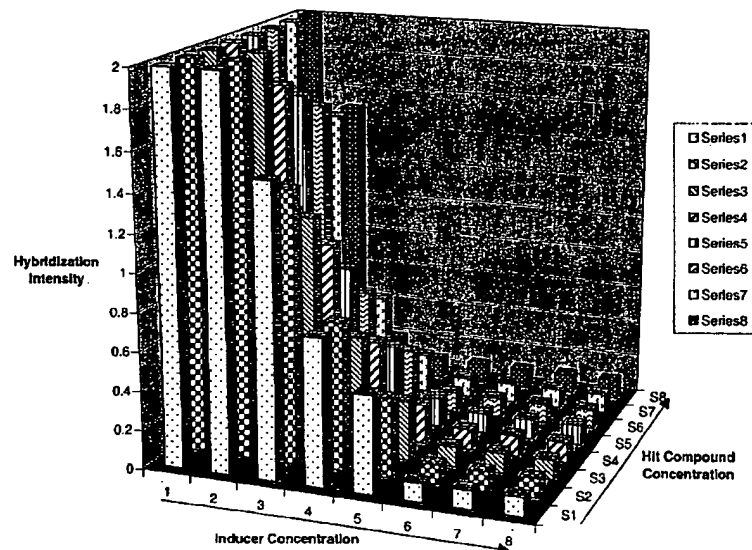
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(54) Title: METHODS FOR IDENTIFYING THE TARGET OF A COMPOUND WHICH INHIBITS CELLULAR PROLIFERATION

Hypothetical 3 D Matrix Hybridization Results for A Specific Clone



(57) Abstract: The present invention relates to cultures or collections of strains which overexpress or underexpress gene products required for the proliferation of an organism. The present invention also includes methods for identifying the target on which a compound which inhibits the proliferation of an organisms acts and methods for identifying the extent to which a strain is present in a culture or collection of strains.

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METHODS FOR IDENTIFYING THE TARGET OF A COMPOUND WHICH INHIBITS CELLULAR PROLIFERATION

Background of the Invention

5 Many important therapeutic compounds act by reducing or eliminating the activity or level of a gene product required for cellular proliferation. For example, most antibiotic compounds act by reducing or eliminating the activity or level of gene products which are required for the proliferation of a pathogenic organism. Similarly, compounds used to treat or ameliorate cancer also reduce or inhibit the activity or
10 level of a gene product required for cellular proliferation.

 Current drug discovery methods involve screening large number of prospective therapeutic compounds to identify those that are effective therapeutic agents or that can be optimized to provide an effective therapeutic agents. For example, the compounds to be evaluated for therapeutic activity may be members of a
15 library of compounds generated by combinatorial chemistry or members of a library of natural products.

 Unfortunately, current methods are laborious and time consuming and may yield compounds which have already been identified or which act on gene products which are already targeted by an existing therapeutic agent. Accordingly, there is a
20 need for rapid screening techniques which yield novel compounds or compounds which act on novel targets.

 In addition, a large number of compounds have been identified which have antimicrobial activity but which cannot be administered to individuals suffering from infection due to the fact that their targets are unknown. Accordingly, there is a need
25 for methods which permit the identification of the target on which a compound with antimicrobial activity acts.

Field of the Invention

 The present invention provides reagents and methods for identifying the target
30 of a compound which reduces the activity or level of gene products required for

cellular proliferation. In addition, the present invention provides reagents and methods for identifying novel therapeutic compounds or compounds which act on novel targets.

Sequence Listing

5 The present application is being filed along with 4 copies of a CD-ROM marked "Copy 1," "Copy 2," "Copy3" and "CRF" containing a Sequence Listing in electronic format. The copies of the CD-ROM each contain a file entitled 028vpc-final.txt created on February 8, 2002 which is 36,220,587 bytes in size. The information on these duplicate CD-ROMs is incorporated herein by reference in its
10 entirety.

Definitions

As used herein, the terminology "proliferation-required" or "required for proliferation" encompasses instances where the absence or substantial reduction of a gene transcript and/or gene product completely eliminates cell growth as well as
15 instances where the absence of a gene transcript and/or gene product merely reduces cell growth.

By "E. coli or Escherichia coli" is meant Escherichia coli or any organism previously categorized as a species of Shigella including Shigella boydii, Shigella flexneri, Shigella dysenteriae, Shigella sonnei, Shigella 2A.

20 By "homologous coding nucleic acid" is meant a nucleic acid homologous to a nucleic acid encoding a gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795 or a portion thereof. In some embodiments, the homologous coding nucleic acid may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide
25 sequence identity to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. In other embodiments the homologous coding
30 nucleic acids may have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 70% , at least 60%, at least 50%, or at least 40% nucleotide sequence

identity to a nucleotide sequence selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOs.: 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Identity may be measured using BLASTN version 2.0 with the default parameters or tBLASTX with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety) Alternatively a "homologous coding nucleic acid" could be identified by membership of the gene of interest to a functional orthologue cluster. All other members of that orthologue cluster would be considered homologues. Such a library of functional orthologue clusters can be found at <http://www.ncbi.nlm.nih.gov/COG>. A gene can be classified into a cluster of orthologous groups or COG by using the COGNITOR program available at the above web site, or by direct BLASTP comparison of the gene of interest to the members of the COGs and analysis of these results as described by Tatusov, R.L., Galperin, M.Y., Natale, D. A. and Koonin, E.V. (2000) The COG database: a tool for genome-scale analysis of protein functions and evolution. Nucleic Acids Research v. 28 n. 1, pp. 33-36.

The term "homologous coding nucleic acid" also includes nucleic acids comprising nucleotide sequences which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the amino acid sequence of one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 or to a polypeptide whose expression is inhibited by a nucleic acid comprising a nucleotide sequence of one of SEQ ID NOs: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, TBLASTN with the default parameters, or tBLASTX with the

default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, *Nucleic Acid Res.* 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

The term "homologous coding nucleic acid" also includes coding nucleic acids which hybridize under stringent conditions to a nucleic acid selected from the group consisting of the nucleotide sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and coding nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944. As used herein, "stringent conditions" means hybridization to filter-bound nucleic acid in 6xSSC at about 45°C followed by one or more washes in 0.1xSSC/0.2% SDS at about 68°C. Other exemplary stringent conditions may refer, e.g., to washing in 6xSSC/0.05% sodium pyrophosphate at 37°C, 48°C, 55°C, and 60°C as appropriate for the particular probe being used.

The term "homologous coding nucleic acid" also includes coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and coding nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequences complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944. As used herein, "moderate conditions" means hybridization to filter-bound DNA in 6x sodium chloride/sodium citrate (SSC) at about 45°C followed by one, preferably 3-5 washes in 0.2xSSC/0.1% SDS at about 42-65°C.

The term "homologous coding nucleic acids" also includes nucleic acids comprising nucleotide sequences which encode a gene product whose activity may be

complemented by a gene encoding a gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 8-3795. In some embodiments, the homologous coding nucleic acids may encode a gene product whose activity is complemented by the gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944. In other embodiments, the homologous coding nucleic acids may comprise nucleotide sequences which encode a gene product whose activity is complemented by one of the polypeptides of SEQ ID NOS. 3801-3805, 4861-5915, 10013-14110 and 14945-15778.

The term "homologous antisense nucleic acid" includes nucleic acids comprising a nucleotide sequence having at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, or at least 40% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Homologous antisense nucleic acids may also comprising nucleotide sequences which have at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, or at least 40% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of the sequences complementary to one of sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof. Nucleic acid identity may be determined as described above.

The term "homologous antisense nucleic acid" also includes antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence complementary to one of SEQ ID NOS.: 8-3795 and antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to

one of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and antisense
5 nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944.

The term "homologous antisense nucleic acid" also includes antisense nucleic
10 acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence complementary to one of SEQ ID NOs.: 8-3795 and antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one
15 of SEQ ID NOs. 8-3795. Homologous antisense nucleic acids also include antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and antisense nucleic acids which comprising nucleotide sequences hybridize under moderate conditions to
20 a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944.

By "homologous polypeptide" is meant a polypeptide homologous to a polypeptide whose activity or level is inhibited by a nucleic acid comprising a
25 nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 or by a homologous antisense nucleic acid. The term "homologous polypeptide" includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide whose activity or level is inhibited by a nucleic acid
30 selected from the group consisting of SEQ ID NOs: 8-3795 or by a homologous

antisense nucleic acid, or polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOs: 8-3795 or by a homologous antisense nucleic acid. Identity or similarity may be determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

The term homologous polypeptide also includes polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a fragment comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778.

The term, *Salmonella*, is the generic name for a large group of gram-negative enteric bacteria that are closely related to *Escherichia coli*. The diseases caused by *Salmonella* are often due to contamination of foodstuffs or the water supply and affect millions of people each year. Traditional methods of *Salmonella* taxonomy were based on assigning a separate species name to each serologically distinguishable strain (Kauffmann, F 1966 The bacteriology of the *Enterobacteriaceae*. Munksgaard, Copenhagen). Serology of *Salmonella* is based on surface antigens (O [somatic] and

H [flagellar]). Over 2,400 serotypes or serovars of *Salmonella* are known (Popoff, et al. 2000 Res. Microbiol. 151:63-65). Therefore, each serotype was considered to be a separate species and often given names, accordingly (e.g. *S. paratyphi*, *S. typhimurium*, *S. typhi*, *S. enteritidis*, etc.).

5 However, by the 1970s and 1980s it was recognized that this system was not only cumbersome, but also inaccurate. Then, many *Salmonella* species were lumped into a single species (all serotypes and subgenera I, II, and IV and all serotypes of *Arizona*) with a second subspecies, *S. bongorii* also recognized (Crosa, et al., 1973, J. Bacteriol. 115:307-315). Though species designations are based on the highly
10 variable surface antigens, the *Salmonella* are very similar otherwise with a major exception being pathogenicity determinants.

 There has been some debate on the correct name for the *Salmonella* species. Currently (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467), the accepted name is *Salmonella enterica*. *S. enterica* is divided into six subspecies (I, *S. enterica* subsp.
15 *enterica*; II, *S. enterica*, subsp. *salamae*; IIIa, *S. enterica* subsp. *arizonae*; IIIb, *S. enterica* subsp. *diarizonae*; IV, *S. enterica* subsp. *houstenae*; and VI, *S. enterica* subsp. *indica*). Within subspecies I, serotypes are used to distinguish each of the serotypes or serovars (e.g. *S. enterica* serotype Enteritidis, *S. enterica* serotype Typhimurium, *S. enterica* serotype Typhi, and *S. enterica* serotype Choleraesuis, etc.). Current
20 convention is to spell this out on first usage (*Salmonella enterica* ser. Typhimurium) and then use an abbreviated form (*Salmonella* Typhimurium or *S. Typhimurium*). Note, the genus and species names (*Salmonella enterica*) are italicized but not the serotype/serovar name (Typhimurium). Because the taxonomic committees have yet to officially approve of the actual species name, this latter system is what is employed
25 by the CDC (Brenner, et al. 2000 J. Clin. Microbiol. 38:2465-2467). Due to the concerns of both taxonomic priority and medical importance, some of these serotypes might ultimately receive full species designations (*S. typhi* would be the most notable).

 Therefore, as used herein "*Salmonella enterica* or *S. enterica*" includes serovars Typhi, Typhimurium, Paratyphi, Choleraesuis, etc." However, appeals of the
30 "official" name are in process and the taxonomic designations may change (*S.*

choleraesuis is the species name that could replace *S. enterica* based solely on priority).

By "inducer" is meant an agent or solution which, when placed in contact with a cell or microorganism, increases transcription, or inhibitor and/or promoter clearance/fidelity, from a desired promoter.

As used herein, "nucleic acid" means DNA, RNA, or modified nucleic acids. Thus, the terminology "the nucleic acid of SEQ ID NO: X" or "the nucleic acid comprising the nucleotide sequence" includes both the DNA sequence of SEQ ID NO: X and an RNA sequence in which the thymidines in the DNA sequence have been substituted with uridines in the RNA sequence and in which the deoxyribose backbone of the DNA sequence has been substituted with a ribose backbone in the RNA sequence. Modified nucleic acids are nucleic acids having nucleotides or structures which do not occur in nature, such as nucleic acids in which the internucleotide phosphate residues with methylphosphonates, phosphorothioates, phosphoramidates, and phosphate esters. Nonphosphate internucleotide analogs such as siloxane bridges, carbonate bridges, thioester bridges, as well as many others known in the art may also be used in modified nucleic acids.

Modified nucleic acids may also comprise, α -anomeric nucleotide units and modified nucleotides such as 1,2-dideoxy-d-ribofuranose, 1,2-dideoxy-1-phenylribofuranose, and N^4 , N^4 -ethano-5-methyl-cytosine are contemplated for use in the present invention. Modified nucleic acids may also be peptide nucleic acids in which the entire deoxyribose-phosphate backbone has been exchanged with a chemically completely different, but structurally homologous, polyamide (peptide) backbone containing 2-aminoethyl glycine units.

As used herein, the terminology "overexpress" refers to strains which possess either a level of the gene product which is higher than the level possessed by wild type cells or an affinity for a test compound which is lower than the affinity of a wild type gene product, while the terminology "underexpress" refers to strains which possess a level of the gene product which is lower than the level possessed by wild

type cells or an affinity for a test compound which is higher than the affinity of a wild type gene product.

Summary of the Invention

5 Some aspects of the present invention are described in the following numbered paragraphs:

1. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

10 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism;

15 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

20 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

2. The method of Paragraph 1, wherein said culture includes at least one strain which does not overexpresses a gene product which is essential for proliferation of said organism.

25 3. The method of Paragraph 1, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

4. The method of Paragraph 1, wherein said strains which overexpress said gene products a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

5. The method of Paragraph 1, wherein said identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said culture.

6. The method of Paragraph 1, wherein said identification step comprises
5 performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

7. The method of Paragraph 6, wherein the products of said amplification reaction are labeled with a detectable dye.

8. The method of Paragraph 1, wherein said identification step comprises
10 performing a hybridization procedure.

9. The method of Paragraph 1, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

10. The method of Paragraph 1, wherein said organism is selected from the
15 group consisting of bacteria, fungi, and protozoa.

11. The method of Paragraph 1, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called
20 *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
25 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*,
30 *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*,

Salmonella enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

12. The method of Paragraph 1, wherein said compound is obtained from a library of natural compounds.

13. The method of Paragraph 1, wherein said compound is obtained from a library of synthetic compounds.

14. The method of Paragraph 1, wherein said compound is present in a crude or partially purified state.

15. The method of Paragraph 1, further comprising determining whether said gene product in said strain which proliferated more rapidly in said culture has a counterpart in at least one other organism.

16. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

17. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed;

10 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

15 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

18. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

20 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

25 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

30

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

19. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain
in said culture overexpresses a different gene product which is essential for
proliferation of said organism, wherein said culture comprises a strain in which
a gene product selected from the group consisting of a gene product having at
least 70% nucleotide sequence identity as determined using BLASTN version
10 2.0 with the default parameters to a gene product whose expression is inhibited
by an antisense nucleic acid comprising a nucleotide sequence selected from
the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a
nucleic acid having at least 70% nucleotide sequence identity as determined
using BLASTN version 2.0 with the default parameters to a nucleic acid
15 encoding a gene product whose expression is inhibited by an antisense nucleic
acid comprising a nucleotide sequence selected from the group consisting of
SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity
as determined using FASTA version 3.0t78 with the default parameters to a
gene product whose expression is inhibited by an antisense nucleic acid
20 comprising a nucleotide sequence selected from the group consisting of SEQ
ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes
to a nucleic acid comprising a nucleotide sequence selected from the group
consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product
encoded by a nucleic acid which hybridizes to a nucleic acid comprising a
25 nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-
3795 under moderate conditions, and a gene product whose activity may be
complemented by the gene product whose activity is inhibited by a nucleic
acid comprising a nucleotide sequence selected from the group consisting of
SEQ ID NOs.: 8-3795 is overexpressed;

5 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

10 20. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence
15 selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide
20 sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944
25 under moderate conditions is overexpressed;

 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate

more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

5 21. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which
10 a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected
15 from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains
20 which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

25 22. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining an array of strains on a solid growth medium wherein each strain in overexpresses a different gene product which is essential for proliferation of said organism

contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

23. The method of Paragraph 21, wherein at least one strain in said array does not overexpresses a gene product which is essential for proliferation of said organism.

24. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism;

contacting each of said cultures with a different concentration of said compound ; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

25. The method of Paragraph 23, wherein at least one strain in said plurality of cultures does not overexpress a gene product which is essential for proliferation of said organism.

26. A method of profiling a compound's activity comprising

performing the method of Paragraph 1 on a first culture using a first compound;

performing the method of Paragraph 1 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

27. A method of profiling a first compound's activity comprising

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

28. The method of any one of Paragraphs 26 and 27, wherein said first compound is present in a crude or partially purified state.

29. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

30. The method of Paragraph 29, wherein at least one strain in said culture does not underexpresses a gene product which is essential for proliferation of said organism.

31. The method of Paragraph 29, wherein said strains which underexpresses said gene products comprise a nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

32. The method of Paragraph 29, wherein said strains which underexpress said gene products express an antisense nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism, wherein expression of said antisense nucleic acid reduces expression of said gene product in said strain.

33. The method of Paragraph 29, wherein said identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in said strain which proliferated more slowly.

34. The method of Paragraph 29, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more slowly.

35. The method of Paragraph 34, wherein the products of said amplification reaction are labeled with a detectable dye.

36. The method of Paragraph 29, wherein said identification step comprises performing a hybridization procedure.

37. The method of Paragraph 29, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more slowly.

38. The method of Paragraph 29, wherein said organism is selected from the group consisting of bacteria, fungi, protozoa.

39. The method of Paragraph 29, wherein said compound is obtained from a library of natural compounds.

40. The method of Paragraph 29, wherein said compound is obtained from a library of synthetic compounds.

41. The method of Paragraph 29, wherein said compound is present in a crude or partially purified state.

42. The method of Paragraph 29, further comprising determining whether said gene product in said strain which proliferated more slowly in said culture has a counterpart in at least one other organism.

43. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed;

10 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

15 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

44. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

20 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is underexpressed;

25 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

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identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

45. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

10 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

15 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

46. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

20 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid

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encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

47. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least

70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

48. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

49. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism; and

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

50. A method of profiling a compound's activity comprising

performing the method of Paragraph 29 on a first culture using a first compound;

performing the method of Paragraph 29 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

51. A method of profiling a first compound's activity comprising

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of

an organism and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

5 52. The method of any one of Paragraphs 49 and 50, wherein said first compound is present in a crude or partially purified state.

53. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

10 obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism ; and

15 identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

54. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism.

20 55. The culture of Paragraph 54, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

25 56. The culture of Paragraph 54, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

30 57. The culture of Paragraph 54, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida*

guilliermondii, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
 5 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus*
 10 *vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.
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58. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence
 20 selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed.

59. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of
 25 SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed.

60. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising

an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed.

5 61. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a
10 gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as
15 determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent
20 conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
25 8-3795 is overexpressed.

62. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by
a nucleic acid comprising a nucleotide sequence selected from the group consisting of
30 a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence

identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed.

63. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed.

64. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism.

65. The culture of Paragraph 64, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

66. The culture of Paragraph 64, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

67. The culture of Paragraph 64, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia*

cepacia, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called
Torulopsis glabrata), *Candida tropicalis*, *Candida parapsilosis*, *Candida*
guilliermondii, *Candida krusei*, *Candida kefyr* (also called *Candida*
pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia*
 5 *trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
Coccidioides immitis, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
Enterobacter cloacae, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*,
Haemophilus influenzae, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella*
pneumoniae, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium*
 10 *tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*,
Pasteurella haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus*
vulgaris, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*,
Salmonella enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
typhimurium, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella*
 15 *dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
Streptococcus pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia*
enterocolitica, and *Yersinia pestis*.

68. A culture comprising a plurality of strains wherein each strain
 underexpresses a different gene product which is essential for proliferation of said
 20 organism, wherein said culture comprises a strain in which a gene product whose
 activity or level is inhibited by a nucleic acid comprising a nucleotide sequence
 selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

69. A culture comprising a plurality of strains wherein each strain
 underexpresses a different gene product which is essential for proliferation of said
 25 organism, wherein said culture comprises a strain in which a gene product encoded by
 a nucleic acid comprising a nucleotide sequence selected from the group consisting of
 SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is
 underexpressed.

70. A culture comprising a plurality of strains wherein each strain
 30 underexpresses a different gene product which is essential for proliferation of said

organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed.

5 71. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a
10 gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense
15 nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product
20 encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid
25 comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

72. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by
30 a nucleic acid comprising a nucleotide sequence selected from the group consisting of

5 a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed.

10 73. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed.

20 74. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

25 obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes;

30 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains

which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

5 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

75. The method of Paragraph 74, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate overexpression of said
10 gene products.

76. The method of Paragraph 74, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates overexpression of said gene products.

15 77. The method of Paragraph 76, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

20 78. The method of Paragraph 74, wherein the step of identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

25 79. The method of Paragraph 75, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

80. The method of Paragraph 75, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of
30 promoters selected to give a desired expression level for each gene product.

81. The method of Paragraph 75, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

82. The method of Paragraph 75, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

5 83. The method of Paragraph 74, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

84. The method of Paragraph 74, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
 10 *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*,
 15 *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
 20 *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

85. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain
 30 overexpresses a different gene product which is essential for proliferation of

said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

86. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains

which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

5 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

87. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

10 obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene
15 product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

20 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

25 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

88. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

30 obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of

said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate

more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

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89. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes;

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contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

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identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

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90. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene

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product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed.

91. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

92. The method of Paragraph 91, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate underexpression of said gene products.

93. The method of Paragraph 91, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates underexpression of said gene products.

94. The method of Paragraph 93, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

95. The method of Paragraph 91, wherein the step of identifying the gene product which is underexpressed in a strain which proliferated more slowly in said

culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

5 96. The method of Paragraph 92, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

97. The method of Paragraph 92, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

10 98. The method of Paragraph 92, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

99. The method of Paragraph 92, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

15 100. The method of Paragraph 91, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

101. The method of Paragraph 91, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called
20 *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
25 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*,
30 *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*,

Salmonella enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

102. The method of Paragraph 91, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

103. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes and wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

104. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

10 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

15 identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

20 105. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

25 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 30 70% nucleotide sequence identity as determined using BLASTN version 2.0

with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

106. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 10 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 15 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed;

20 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

25 identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

107. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a
10 polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-
15 14110 and 14945-15778 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts
20 proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

25 108. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a
30 different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

109. The method of Paragraph 108, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

110. The method of Paragraph 108 wherein:

said nucleic acid sample is divided into N aliquots;

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

111. The method of Paragraph 109, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

112. The method of Paragraph 108, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

113. The method of Paragraph 111, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

114. The method of Paragraph 111, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

5 115. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism
10 wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which
15 are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or
20 collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

25 116. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism ,
30 wherein said culture comprises a strain in which a gene product encoded by a

nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed;

5 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide
10 sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

117. A method for determining the extent to which each of a plurality of
15 strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism,
20 wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which
25 are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide

sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

5 118. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a
10 different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense
15 nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid
20 comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-
25 3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under
30 moderate conditions, and a gene product whose activity may be complemented

by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 8-3795 is overexpressed or underexpressed;

5 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or
10 collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

119. A method for determining the extent to which each of a plurality of
15 strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism ,
20 wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a
25 sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a
30 nucleotide sequence selected from the group consisting of SEQ ID NOS.:

3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed;

5 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or
10 collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

120. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

15 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least
20 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of
25 SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer
30 pairs are designed such that each primer pair would yield an amplification

product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

5 determining the lengths of the amplification products obtained in said amplification reaction.

121. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

10 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

15 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

20 performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length
25 distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

30 performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products.

122. The method of Paragraph 121, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

123. The method of Paragraph 121, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

124. The method of Paragraph 121, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

125. The method of Paragraph 121, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

126. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

127. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

5 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

10 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

15 performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other
20 primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

25 and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification
30 product is the target of said compound if said culture or strain overexpresses

said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

128. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

5 and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses
10 said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains
15 comprise a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

129. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

20 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been
25 contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with
30 said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is

inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is overexpressed or underexpressed.

130. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide

sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence

selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

5 131. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been
10 contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with
15 said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;
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performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;
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and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification
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product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second culture or collection of strains comprise a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

132. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

133. The method of Paragraph 132, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

5 134. The method of Paragraph 132 wherein:

said nucleic acid sample is divided into N aliquots;

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

10 135. The method of Paragraph 134, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

15 136. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

20 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

25 determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene

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product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

5 137. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

10 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the
15 nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene
20 product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

138. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

25 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which
30 are complementary to nucleotide sequences within or adjacent to the nucleic

acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

139. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by

an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

140. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the

amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

5 determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

141. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

20 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

25 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the

nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

5 determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

10 142. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

15 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

20 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

25 identifying the amplification products obtained in said amplification reaction.

30 143. The method of Paragraph 142, wherein said primer pairs are divided into at least two sets, each primer pair comprises a primer which is labeled with a

distinguishable dye, and the distinguishable dye used to label each set of primer pairs is distinguishable from the dye used to label the other sets of primer pairs.

144. The method of Paragraph 142 wherein:

said nucleic acid sample is divided into N aliquots;

5 said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

10 145. The method of Paragraph 144, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

146. The method of Paragraph 142, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

147. The method of Paragraph 146, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

20 148. The method of Paragraph 146, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

149. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

25 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

30 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that

each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

150. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the

group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

151. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

10 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both
15 length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product
20 comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

152. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

25 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

 performing an amplification reaction using primer pairs which are
30 complementary to nucleotide sequences within or adjacent to the genes which

5 encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

10 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a
15 nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity
20 as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a
25 nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic

acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is overexpressed or underexpressed.

153. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

10 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both
15 length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product
20 encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-
25 14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.:

3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

154. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

10 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both
15 length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product
20 comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the
25 group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

Brief Description of the Drawings

30 Figures 1A and 1B illustrate one method for identifying amplification products which are underrepresented or overrepresented in a culture.

Figures 2A and 2B illustrate another method for identifying amplification products which are underrepresented or overrepresented in a culture.

Figure 3 illustrates the results of a hybridization analysis where the antisense nucleic acid expressed by a strain in the culture is not complementary to all or a portion of the gene encoding the target of the compound (i.e. a nonspecific strain).

Figure 4 illustrates the results of a hybridization analysis where the antisense nucleic acid expressed by a strain in the culture is complementary to all or a portion of the gene encoding the target of the compound, the hybridization intensity for that strain will be intimately correlated with the concentration of the compound (i.e. a specific strain).

Figure 5A illustrates a method for replacing a promoter using a promoter replacement cassette comprising a 5' region homologous to the sequence which is 5' of the natural promoter in the chromosome, the promoter which is to replace the chromosomal promoter and a 3' region which is homologous to sequences 3' of the natural promoter in the chromosome.

Figure 5B illustrates a method for replacing a promoter using a promoter replacement cassette comprising a nucleic acid encoding an identifiable or selectable marker disposed between the 5' region which is homologous to the sequence 5' of the natural promoter and the promoter which is to replace the chromosomal promoter and a transcriptional terminator 3' of the gene encoding an identifiable or selectable marker.

Figures 6A and 6B depict the GRACE method for constructing a gene disruption of one allele of a gene (*CaKRE9*), and promoter replacement of the second allele of the target gene, placing the second allele under conditional, regulated control by a heterologous promoter.

Figure 7A depicts growth of a wild-type strain and a *CaHIS3* heterozygote strain as compared with a *CaHIS3* GRACE strain constitutively expressing the tetracycline promoter-regulated imidazoleglycerol phosphate dehydratase, in the presence of inhibitory levels of 3-aminotriazole.

Figure 7B depicts growth of a wild-type strain, a haploinsufficient *CaHIS3* heterozygote strain, and a *CaHIS3* GRACE strain constitutively expressing the tetracycline promoter-regulated imidazoleglycerol phosphate dehydratase, in the presence of an intermediate level of 3-aminotriazole.

5 Figure 7C depicts growth of a wild-type strain, a haploinsufficient *CaHIS3* heterozygote strain, and a *CaHIS3* GRACE strain minimally expressing the tetracycline promoter-regulated imidazoleglycerol phosphate dehydratase, in the presence of an intermediate level of 3-aminotriazole.

10 Figure 7D demonstrates the hypersensitivity of the *CaHIS3* GRACE strain minimally expressing the tetracycline promoter-regulated imidazoleglycerol phosphate dehydratase, in the presence of an intermediate level of 3-aminotriazole.

Figure 8 presents a Northern Blot Analysis of *CaHIS3*, *CaALR1*, *CaCDC24* and *CaKRE9* mRNA isolated from GRACE strains to illustrate elevated expression under non-repressing conditions.

15 Figure 9 presents conditional gene expression, using GRACE technology, with *KRE1*, *KRE5*, *KRE6* and *KRE9*.

Figure 10 presents conditional gene expression using GRACE technology with *CaKRE1*, *CaTUB1*, *CaALG7*, *CaAUR1*, *CaFKS1* and *CaSAT2*.

20 Figure 11 illustrates an oligonucleotide comprising a lac operator flanked on each side by 40 nucleotides homologous to the promoter is the promoter which drives expression of the *yabB yabC ftsL ftsI murE* genes in an operon for use in inserting the lac operator into the promoter.

Figure 12 illustrates a microtitration plate which contains antibiotic and inducer at gradient concentrations in a matrix format in 10 times excess quantity.

25 Figure 13 illustrates the results of an experiment demonstrating that at appropriate concentrations of inducer, cells which overexpress the *defB* gene product were able to grow at elevated concentrations of the antibiotic actinonin

Figure 14 illustrates the results of an experiment demonstrating that at appropriate concentrations of inducer cells which overexpress the *folA* gene product
30 were able to grow at elevated concentrations of the antibiotic trimethoprim.

Figure 15 illustrates the results of an experiment demonstrating that overexpression of the *fabI* gene confers resistance to triclosan, which acts on the gene product of the *fabI* gene, but does not confer resistance to cerulenin, trimethoprim, or actinonin, each of which act on other gene products.

5 Figure 16 illustrates the results of an experiment demonstrating that overexpression of the *folA* gene confers resistance to trimethoprim, which acts on the gene product of the *folA* gene but does not confer resistance to triclosan, cerulenin, or actinonin, each of which act on other gene products.

10 Figure 17 illustrates the results of an experiment demonstrating that overexpression of the *defB* gene conferred resistance to actinonin, which acts on the gene product of the *defB* gene but does not confer resistance to cerulenin, trimethoprim, or triclosan, each of which act on other gene products.

15 Figure 18 illustrates the results of an experiment demonstrating that overexpression of the *fabB* gene conferred resistance to cerulenin, which acts on the gene product of the *fabB* gene, β keto-acyl carrier protein synthase but does not confer resistance to triclosan, trimethoprim, or actinonin, each of which act on other gene products.

20 Figure 19 illustrates the results of experiments in which a mixture of nine strains was grown wells in a 96 well plate in medium containing various concentrations of inducer and a sufficient concentration of actinonin, cerulenin, triclosan or trimethoprim to inhibit the growth of strains which do not overexpress the targets of these antibiotics.

Detailed Description of the Preferred Embodiment

25 The present invention utilizes collections or cultures of strains comprising strains which either overexpress a different gene product which is required for cellular proliferation or underexpress a different gene product which is required for cellular proliferation (i.e. at least some of the strains in the culture overexpress or underexpress a gene product required for cellular proliferation). In some
30 embodiments, the present invention uses collections or cultures of strains comprising

both strains which overexpress gene products required for cellular proliferation and strains which underexpress the same gene products required for cellular proliferation. Preferably, each of the strains present in the culture or collection either overexpresses or underexpresses a different gene product which is required for cellular proliferation (i.e. all of the strains in the culture overexpress or underexpress a gene product required for cellular proliferation). The gene product which is overexpressed or underexpressed in each strain may be any gene product which is required for cellular proliferation. The gene product may be a nucleic acid or a polypeptide. As used herein the term "culture" refers to a plurality of strains growing in a single aliquot of a liquid growth medium and the term "collection" refers to a plurality of strains each of which is growing in a separate aliquot of liquid growth medium or a different location on a solid growth medium.

In some embodiments, if desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product which is required for cellular proliferation. In this embodiment, the gene products which are overexpressed or underexpressed in one or more of the strains may be functionally related or functionally unrelated. This may facilitate the identification of compounds when two or more gene products share similar functions in the cell or where the cell has multiple biochemical pathways which lead to a particular end product.

Alternatively, if the gene product to be overexpressed or underexpressed is encoded by a gene which is part of an operon containing a plurality of genes, the desired gene may be overexpressed or underexpressed while the remaining genes in the operon are expressed at levels where they do not impact the ability of the cell to grow in the presence of a particular compound. For example, the desired gene may be placed under the control of a regulatable promoter, a transcriptional terminator may be placed 3' of the desired gene and a promoter, preferably a constitutive promoter, may be placed 3' of the transcriptional terminator and 5' of the remaining genes in the operon.

In some embodiments, the culture or collection of strains may comprise a strain which overexpresses or underexpresses a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795. In some embodiments, the culture or collection of strains may comprise strains which in aggregate overexpress or underexpress at least two gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 10 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 20 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 30 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 50 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 100 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, at least 300 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795 or more than 300 gene products whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS. 8-3795. Alternatively, if desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product whose activity or level is inhibited by a nucleic acid selected from the group consisting of SEQ ID NOS. 8-3795.

In other embodiments, the culture or collection of strains may comprise a strain which overexpresses or underexpresses a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944. In some embodiments, the culture or collection of strains may comprise strains which in aggregate

overexpress or underexpress at least two gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 10 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 20 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 30 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 50 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 100 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, at least 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ IN NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 or more than 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs. 3796-3800, 3806-4860, 5916-10012, and 14111-14944, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NOs. 3796-3800, 3806-4860, 5916-10012, and 14111-14944. Alternatively, if desired, one or more strains in the culture or collection of strains may overexpress or underexpress more than one gene product encoded by a nucleic acid selected from the group consisting of SEQ ID NOs. 3796-3800, 3806-4860, 5916-10012, and 14111-14944.

In some embodiments the culture or collection of strains comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed. In some embodiments, the culture or collection of

strains may comprise strains which in aggregate overexpress or underexpress at least two gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 10 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 20 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 30 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 50 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 100 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, at least 300 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 or more than 300 gene products comprising an amino acid sequence selected from the group consisting of SEQ IN NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, wherein each strain in the culture or collection of strains overexpresses or underexpresses a single gene product selected from the group consisting of SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110 and 14945-15778. Alternatively, if desired one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product selected from the group consisting of SEQ ID NOs. 3801-3805, 4861-5915, 10013-14110 and 14945-15778.

In other embodiments, the culture or collection of strains comprises a strain in which at least one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300 or more than 300 gene products encoded by a homologous coding nucleic acid as defined above is overexpressed or underexpressed. If desired the culture or collection of strains may comprise one or more strains which overexpress or underexpress more than one gene product encoded by a homologous coding nucleic acid. In further embodiments, the culture or collection of strains comprises a strain in which at least

one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300 or more than 300 homologous polypeptides as defined above is overexpressed or underexpressed. If desired the culture or collection of strains may comprise one or more strains which overexpress or underexpress more than one homologous polypeptide.

For example, in some embodiments, the culture or collection of strains comprises a strain or a group of strains in which in aggregate at least one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300, or more than 300 gene products selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795.

In further embodiments, the culture or collection of strains comprises a strain or a group of strains in which in aggregate at least one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300, or more than 300 gene products encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide

sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800,
5 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one gene product encoded by a nucleic acid
10 comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence
15 which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions.

In additional embodiments, the culture or collection of strains comprises a strain or a group of strains in which in aggregate at least one, at least 10, at least 20, at least 30, at least 50, at least 100, at least 300, or more than 300 gene products comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a
25 polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed, wherein each strain overexpresses or underexpresses one gene
30 product.

If desired, one or more of the strains in the culture or collection of strains may overexpress or underexpress more than one polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of
5 SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778.

The methods of the present invention may be used to identify the targets of
10 compounds which inhibit the proliferation of any desired cell or organism. In some embodiments, the methods of the present invention are employed to identify the targets of compounds which inhibit the proliferation of bacteria, fungi, or protozoans. In further embodiments, the methods of the present invention are employed to identify the targets of compounds which inhibit the growth of an organism selected from the
15 group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*,
20 *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*,
25 *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*,
30 *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,

Shigella sonnei, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

Overexpression may be obtained using a variety of techniques familiar to those skilled in the art. For example, overexpression may be obtained by operably linking a gene encoding the gene product to a promoter which transcribes a higher level of mRNA encoding or comprising the gene product than does a wild type cell. A variety of promoters may be used to overexpress the gene product. The promoters used to overexpress the gene product may be relatively strong promoters, promoters which possess a moderate level of activity, or relatively weak promoters and may be either constitutive or regulatable promoters. In some embodiments, several strains, each of which overexpresses the gene product to a different extent, may be used in order to optimize the degree of overexpression of the gene product.

In some embodiments, each of the gene products required for proliferation may be placed under the control of several different promoters of varying strengths to create several different strains which express the gene product at varying levels. The level of expression of the gene product in each of the strains is compared to that in wild type cells in order to identify a promoter which provides a desired level of expression relative to wild type cells (i.e. a desired level of overexpression or underexpression). The strain having the desired level of expression is then included in a culture or collection of strains to be contacted with a test compound as discussed below.

The promoter is selected to be active in the type of cell in which the gene product is to be expressed. For example, for overexpression of the gene product in mammalian cells, the gene encoding the gene product may be operably linked to promoters such as the SV40 promoter, the metallothionine promoter, the MMTV promoter, the RSV promoter, the tetP promoter, the adenovirus major late promoter or other promoters known to those skilled in the art. In yeast, the gene encoding the gene product may be operably linked to promoters such as the CYC1, ADHI, ADHII, GAL1, GAL10, PHO5, PGK or other promoters used in the art. Similarly, in bacteria,

the gene encoding the gene product may be operably linked to the , SP6, T3, trc promoter, lac promoter, temperature regulated lambda promoters, the *Bacillus* aprE and nprE promoters (U.S. Patent No. 5,387,521), the bacteriophage lambda P_L and P_R promoters (Renaut, et al., (1981) Gene 15: 81) the trp promoter (Russell, et al., (1982) Gene 20: 23), the tac promoter (de Boer et al., (1983) Proc. Natl. Acad. Sci. USA 80: 21), *B. subtilis* alkaline protease promoter (Stahl et al, (1984) J. Bacteriol. 158, 411-418) alpha amylase promoter of *B. subtilis* (Yang et al., (1983) Nucleic Acids Res. 11, 237-249) or *B. amyloliquefaciens* (Tarkinen, et al, (1983) J. Biol. Chem. 258, 1007-1013), the neutral protease promoter from *B. subtilis* (Yang et al, (1984) J. Bacteriol. 160, 15-21), T7 RNA polymerase promoter (Studier and Moffatt (1986) J Mol Biol. 189(1):113-30), *B. subtilis* xyl promoter or mutant tetR promoter active in bacilli (Geissendorfer & Hillen (1990) Appl. Microbiol. Biotechnol. 33:657-663), Staphylococcal enterotoxin D promoter (Zhang and Stewart (2000) J. Bacteriol. 182(8):2321-5), cap8 operon promoter from *Staphylococcus aureus* (Ouyang et al., (1999) J. Bacteriol. 181(8):2492-500), the lactococcal nisA promoter (Eichenbaum (1998) Appl Environ Microbiol. 64(8):2763-9), promoters from in *Acholeplasma laidlawii* (Jarhede et al., (1995) Microbiology 141 (Pt 9):2071-9), porA promoter of *Neisseria meningitidis* (Sawaya et al., (1999) Gene 233:49-57), the fbpA promoter of *Neisseria gonorrhoeae* (Forng et al., (1997) J. Bacteriol. 179:3047-3052), *Corynebacterium diphtheriae* toxin gene promoter (Schmitt and Holmes (1994) J. Bacteriol. 176(4):1141-9), the hasA operon promoter from Group A Streptococci (Alberti et al., (1998) Mol Microbiol 28(2):343-53), the rpoS promoter of *Pseudomonas putida* (Kojic and Venturi (2001) J. Bacteriol. 183:3712-3720), and the IPTG inducible promoter in pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997), In another embodiment, which may be useful in *Staphylococcus aureus*, the promoter is a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the xylO operator from the xylA promoter of *Staphylococcus aureus*. This promoter is described in U.S. Patent Application Serial Number 10/032,393, the disclosure of which is incorporated herein by reference in its entirety. In another embodiment the promoter may be a two-component inducible promoter system in

which the T7 RNA polymerase gene is integrated on the chromosome and is regulated by *lacUV5/ lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41, the disclosure of which is incorporated herein by reference in its entirety) and a T7 gene
10 promoter, which is transcribed by T7 RNA polymerase, is fused with a *lacO*
5 operator. In another embodiment the promoter may be the promoters from the plasmids pEPEF3 or pEPEF14, which harbor xylose inducible promoters functional in *E. faecalis*, described in U.S. Patent Application Serial No. 10/032,393, the disclosure of which is incorporated herein by reference in its entirety. Other promoters which may be used are familiar to those skilled in the art. In fungi, the gene encoding the
10 gene product may be operably linked to the CaACT1 promoter (Morschhauser, Mol. Gen. Genet. 257: 412-420 (1998), the disclosure of which is incorporated herein by reference in its entirety), the tetracycline regulatable promoter described in U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001, the disclosure of which is incorporated herein by reference in its entirety, or the promoters described in U.S.
15 Patent Application Serial Number 10/032,585 filed December 20, 2001, the disclosure of which is incorporated herein by reference in its entirety, or other promoters familiar to those skilled in the art. It will be appreciated that other combinations of organisms and promoters may also be used in the present invention.

In some embodiments, overexpression may be achieved by using homologous
20 recombination to replace the natural promoter which drives expression of the gene required for proliferation with a regulatable promoter. For example, the methods described in U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 (the disclosure
25 of which is incorporated herein by reference in its entirety), U.S. Patent Application 09/948,993 (the disclosure of which is incorporated herein by reference in its entirety) and U.S. Patent Application 09/948,993 (the disclosure of which is incorporated herein by reference in its entirety) may be used to place the gene required for proliferation under the control of a regulatable promoter. U.S. Patent Application
30 Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated

herein by reference in its entirety), U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/815,242 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application
5 Serial Number 09/492,709 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/711,164 (the disclosure of which is incorporated herein by reference in its entirety), and U.S. Patent Application Serial Number 09/741,669 (the disclosure of which is incorporated herein by reference in its entirety) disclose genes and gene products required for proliferation which may
10 be used in any of the methods of the present invention.

Briefly, in some embodiments of these methods, the cells may be haploid, such as bacterial cells. A linear promoter replacement cassette comprising a regulatable promoter flanked by nucleotide sequences having homology to the natural promoter is introduced into the cell. In some embodiments, the cassette also comprises a
15 nucleotide sequence encoding a selectable marker or a marker whose expression is readily identified. The cassette may be a double stranded nucleic acid or a single stranded nucleic acid as described in U.S. Patent Application Serial Number 09/948,993, the disclosure of which is incorporated herein by reference in its entirety. Upon homologous recombination, the natural promoter is replaced with the
20 regulatable promoter, leaving the gene required for proliferation under the control of the regulatable promoter. Strains in which the gene required for proliferation is under control of the regulatable promoter are grown under conditions in which the regulatable promoter provides a level of the proliferation-required gene product which is above the level in a wild type cell. For example, the strains may be grown in the
25 presence of an inducer which induces expression from the regulatable promoter, or under conditions in which the action of a repressor on the regulatable promoter is reduced or eliminated.

Alternatively, rather than replacing the native promoters each of the genes encoding gene product required for proliferation with a single desired replacement
30 promoter, a plurality of replacement promoters which provide desired expression

levels for the gene products to be overexpressed or underexpressed are used. The method is performed as described above except that rather than using a single labeled primer complementary to a nucleotide sequence within the single replacement promoter, a plurality of labeled primers complementary to suitable nucleotide sequences in the plurality of replacement promoters are used.

Alternatively, in embodiments in which the level or activity of gene products required for proliferation is reduced by transcribing an antisense nucleic acid complementary to at least a portion of the genes encoding such gene products, the strains may be designed such that the length of the nucleotide sequence encoding the antisense nucleic acid is different for each gene. Amplification reactions are performed as described above using primers at each end of the gene encoding the antisense nucleic acid such that the amplification product corresponding to each gene has a unique length or a dye which allows it to be distinguished from other amplification products of the same length. Alternatively, the lengths of the nucleotide sequences encoding the antisense nucleic acids may not be unique for each gene, but the primers used in the amplification reaction may be selected such that the length of the amplification product corresponding to each gene is unique.

In another embodiment, the native promoters may be replaced with promoters which include therein or adjacent thereto a unique nucleotide sequence which is distinct from that present in the other replacement promoters in the strains in the culture or collection of strains. In this embodiment, each promoter includes or has adjacent thereto a unique "tag" which may be used to identify strains which proliferate more rapidly or more slowly in the culture or collection of strains. The tag may be detected using hybridization based methods or amplification based methods, including the amplification method which generates amplification products having a unique size for each proliferation required gene described above.

Alternatively, the native promoter which directs the transcription of the gene required for proliferation may rendered regulatable by inserting a regulatory element into the chromosome of the cell via homologous recombination such that the regulatory element regulates the level of transcription from the promoter. The

regulatory element may be an operator which is recognized by a repressor (e.g. lac, tet, araBAD repressors) or a nucleotide sequence which is recognized by a transcriptional activator. In some embodiments, the regulatory element may be a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA or an upstream activating sequence. A linear regulatory element insertion cassette comprising a regulatory element flanked by nucleotide sequences having homology to the natural promoter is introduced into the cell. In some embodiments, the cassette also comprises a nucleotide sequence encoding a selectable marker or a marker whose expression is readily identified. The cassette may be a double stranded nucleic acid or a single stranded nucleic acid as described in U.S. Patent Application Serial Number 09/948,993, the disclosure of which is incorporated herein by reference in its entirety. Upon homologous recombination, the regulatory element is inserted into the chromosome, leaving the gene required for proliferation under the control of the regulatory element. Strains in which the gene required for proliferation is under control of the regulatory element are grown under conditions in which the regulatable promoter provides a level of the proliferation-required gene product which is above the level in a wild type cell. For example, the strains may be grown in the presence of an inducer which induces expression from the promoter, or under conditions in which the action of a repressor on the promoter is reduced or eliminated. It will be appreciated that the amplification method which generates amplification products having a unique size for each proliferation required gene may be used to detect strains which are overrepresented or underrepresented in the culture or collection of strains. For example, if desired, primers complementary to a nucleotide sequence within the regulatory element may be used in the amplification reaction.

The promoter replacement cassette or regulatory element insertion cassette may be a double stranded nucleic acid, such as an amplicon generated through PCR or other amplification methods, or a single stranded nucleic acid, such as an oligonucleotide. For example, single stranded nucleic acids may be introduced into the chromosome using the methods described in Ellis et al., PNAS 98: 6742-6746, 2001, the disclosure of which is incorporated herein by reference in its entirety.

In some embodiments, the cell into which the promoter replacement cassette or regulatory element insertion cassette is introduced has an enhanced frequency of recombination. For example, the cells may lack or have a reduced level or activity of one or more exonucleases which would ordinarily degrade the DNA to be inserted into the chromosome. In further embodiments, the cells may both lack or have reduced levels of exonucleases and express or overexpress proteins involved in mediating homologous recombination. For example, if the methods are performed in *Escherichia coli* or other enteric prokaryotes, cells in which the activity of exonuclease V of the RecBCD recombination pathway, which degrades linear nucleic acids, has been reduced or eliminated, such as recB, recC, or recD mutants may be used. In some embodiments, the cells have mutations in more than one of the recB, recC, and recD genes which enhance the frequency of homologous recombination. For example the cells may have mutations in both the recB and recC genes.

The promoter replacement or regulatory element insertion methods may also be performed in *Escherichia coli* cells in which the activity of the RecET recombinase system of the Rac prophage has been activated, such as cells which carry an sbcA mutation. The RecE gene of the rac prophage encodes ExoVIII a 5'-3' exonuclease, while the RecT gene of the Rac prophage encodes a single stranded DNA binding protein which facilitates renaturation and D-loop formation. Thus, the gene products of the RecE and RecT genes or proteins with analogous functions facilitate homologous recombination. The RecE and RecT genes lie in the same operon but are normally not expressed. However, sbcA mutants activate the expression the RecE and RecT genes. In some embodiments, the methods may be performed in cells which carry mutations in the recB and recC genes as well as the sbcA mutation. The RecE and RecT gene may be constitutively or conditionally expressed. For example, the methods may be performed in *E. coli* strain JC8679, which carries the sbcA23, recB21 and recC22 mutations.

In some embodiments, the methods may be performed in *Escherichia coli* cells in which recombination via the RecF pathway has been enhanced, such as cells which carry an sbcB mutation.

It will be appreciated that the recE and recT gene products, or proteins with analogous functions may be conditionally or constitutively expressed in prokaryotic organisms other than *E. coli*. In some embodiments, these proteins may be conditionally or constitutively expressed in *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, or *Yersinia pestis*. For example, plasmids encoding these gene products may be introduced into the organism. If desired, the coding sequences encoding these gene products may be optimized to reflect the codon preferences of the organism in which they are to be expressed. Similarly, in some embodiments, the organism may contain mutations analogous to the recB, recC, recD, sbcA or sbcB mutations which enhance the frequency of homologous recombination.

In further embodiments, the promoter replacement or regulatory element insertion methods may be conducted in cells which utilize the Red system of bacteriophage lambda (λ) or analogous systems from other phages to enhance the

frequency of homologous recombination. The Red system contains three genes, γ , β and *exo* whose products are the Gam, Bet and Exo proteins (see Ellis et al. PNAS 98:6742-6746, 2001, the disclosure of which is incorporated herein by reference in its entirety). The Gam protein inhibits the RecBCD exonuclease V, thus permitting Beta and Exo to gain access to the ends of the DNA to be integrated and facilitating homologous recombination. The Beta protein is a single stranded DNA binding protein that promotes the annealing of a single stranded nucleic acid to a complementary single stranded nucleic acid and mediates strand exchange. The Exo protein is a double-stranded DNA dependent 5'-3' exonuclease that leaves 3' overhangs that can act as substrates for recombination. Thus, constitutive or conditional expression of the λ red proteins or proteins having analogous functions facilitates homologous recombination.

It will be appreciated that the λ Beta, Gam and Exo proteins, or proteins with analogous functions may be expressed constitutively or conditionally in prokaryotic organisms other than *E. coli*. In some embodiments, these proteins may be conditionally or constitutively expressed in *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*

typhimurium, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, or *Yersinia pestis*. For example, plasmids encoding these gene products may be introduced into the organism. If desired, the coding sequences encoding these gene products may be optimized to reflect the codon preferences of the organism in which they are to be expressed.

In some embodiments, the cells may have an increased frequency of homologous recombination as a result of more than one of the aforementioned characteristics. In some embodiments, the enhanced frequency of recombination may be a conditional characteristic of the cells which depends on the culture conditions in which the cells are grown. For example, in some embodiments, expression of the λ Red Gam, Exo, and Beta proteins or recE and recT proteins may be regulated. Thus, the cells may have an increased frequency of homologous recombination as a result of any combination of the aforementioned characteristics. For example, in some embodiments, the cell may carry the sbcA and recBC mutations.

In some embodiments, a linear double stranded DNA to be inserted into the chromosome of the organism is introduced into an organism constitutively or conditionally expressing the recE and recT or the λ Beta, Gam and Exo proteins or proteins with analogous functions as described above. In some embodiments, the organism may be *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*,

Mycobacterium leprae, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*,
Neisseria meningitidis, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella*
multocida, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*,
Salmonella bongori, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella*
5 *paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*,
Moxarella catarrhalis, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,
Shigella sonnei, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*,
Streptococcus mutans, *Treponema pallidum*, *Yersinia enterocolitica*, or *Yersinia*
pestis. In some embodiments, the double stranded DNA may be introduced into an
10 organism having the recBC and sbcA mutations or analogous mutations.

In other embodiments, a single stranded DNA to be inserted into the
 chromosome of the organism is introduced into an organism expressing the λ Beta
 protein or a protein with an analogous function. In some embodiments the single
 stranded DNA is introduced into an organism expressing both the λ Beta and Gam
 15 proteins or proteins with analogous functions. In further embodiments, the single
 stranded DNA is introduced into an organism expressing the λ Beta, Gam and Exo
 proteins or proteins with analogous functions. The λ proteins or analogous proteins
 may be expressed constitutively or conditionally. In some embodiments, the organism
 may be *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides*
 20 *fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida*
albicans, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*,
Candida parapsilosis, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also
 called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*,
Chlamydia trachomatis, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium*
 25 *perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus*
neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*,
Escherichia coli, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma*
capsulatum, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*,
Mycobacterium tuberculosis, *Neisseria gonorrhoeae*, *Neisseria meningitidis*,
 30 *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis*

carinii, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
5 *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, or *Yersinia pestis*.

In some embodiments, the linear nucleic acid may be introduced into the chromosome of a first organism which has an enhanced frequency of homologous recombination and then transferred to a second organism which is less amenable to
10 direct application of the present methods. For example, the linear nucleic acid may be introduced into the chromosome of *E. coli* and transferred into a second organism via conjugation or transduction. After introduction into the second organism, the nucleic acid is inserted into the chromosome of the second organism via homologous recombination, thereby effectively transferring the regulatory element from the
15 chromosome of the first organism into the corresponding location in the chromosome of the second organism.

In other embodiments, the cells may be diploid cells, such as fungal cells. In some embodiments, one copy of the gene encoding the proliferation-required gene product may be disrupted, rendering it inactive. In further embodiments, one copy of
20 the gene encoding the proliferation-required gene product may be disrupted and the other copy of the gene encoding the proliferation-required gene product may be placed under the control of a regulatable promoter. Such strains may be generated by disrupting the first copy of the gene encoding the proliferation-required gene product by homologous recombination using a disruption cassette comprising a nucleotide
25 sequence encoding an expressible dominant selectable marker flanked on each side by nucleic acids homologous to the target sequence to be disrupted. The second copy of the gene encoding the proliferation-required gene product may be placed under the control of a regulatable promoter by homologous recombination using a promoter replacement cassette comprising a regulatable promoter flanked on each side by
30 nucleic acids homologous to the natural promoter for the proliferation-required gene.

The promoter replacement cassette may also include a nucleotide sequence encoding a selectable marker located 5' of the regulatable promoter but between the nucleic acids homologous to the natural promoter.

In other embodiments, overexpression may be achieved by operably linking
5 the gene required for proliferation to a desired promoter in a vector. The vector may be a vector which replicates extrachromosomally or a vector which integrates into the chromosome. For example, if the vector is to be used in bacterial cells, the vector may be a pBR322 based vector or a bacteriophage based vector such as P1 or lambda. If the vector is to be used in *Saccharomyces cerevisiae*, it may be a vector based on the
10 2 micron circle or a vector incorporating a yeast chromosomal origin of replication. If the vector is to be used in mammalian cells, it may be a retroviral vector, SV40 based vector, a vector based on bovine papilloma virus, a vector based on adenovirus, or a vector based on adeno-associated virus. If the vector is to be used in *Candida albicans* it may be a vector comprising a promoter selected from the group consisting
15 of the CaPCK1, MET25, MAL2, PHO5, GAL1,10, STE2 or STE3 promoters. In some embodiments, the vectors described in the following publications (the disclosures of which are incorporated herein by reference in their entireties) may be used: Clp10, an efficient and convenient integrating vector for *Candida albicans*. Murad et al., *Yeast* 16(4):325-7 (2000); Transforming vector pCPW7, Kvaal et al., :
20 *Infect Immun* 67(12):6652-62 (1999); Transforming vector pCWOP16, Kvaal et al., : *Infect Immun* 65(11):4668-75 (1997); double-ARS vector, pRM1, to be used for direct cloning in *Ca* by complementation of the histidine auxotrophy of strain CA9, Pla et al., *Gene* 165(1):115-20 (1995); pMK16, that was developed for the transformation of *C. albicans* and carries an ADE2 gene marker and a *Candida*
25 autonomously replicating sequence (CARS) element promoting autonomous replication (cited in Sanglard and Fiechter *Yeast* 8(12):1065-75 (1992); A plasmid vector (denoted pRC2312) was constructed, which replicates autonomously in *Escherichia coli*, *Saccharomyces cerevisiae* and *Candida albicans*. It contains LEU2, URA3 and an autonomously replicating sequence (ARS) from *C. albicans*, Cannon et al., *Mol Gen Genet* 235(2-3):453-7 (1992); Expression vector (Clp10-MAL2p) for use
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in *Candida albicans* has been constructed in which a gene of interest can be placed under the control of the CaMAL2 maltase promoter and stably integrated at the CaRP10 locus (Backen et al., *Yeast* 16(12):1121-9 (2000)); (Volker, R. S., A. Sonneborn, C. E. Leuker, and J. F. Ernst. 1997. Efg1p, an essential regulator of morphogenesis of the human pathogen *Candida albicans*, is a member of a conserved class of bHLH proteins regulating morphogenetic processes in fungi. *EMBO* 16:1982-1991.); and A *C. albicans* transformation vector containing the *C. albicans* URA3 gene, a *Candida* ARS sequence, and a portion of the *Saccharomyces cerevisiae* 2 microns circle containing the replication origin was constructed. Goshorn et al., *Infect Immun* 60(3):876-84 (1992). A variety of other vectors suitable for use in foregoing organisms or in any other organism in which the present invention is to be practiced are familiar to those skilled in the art.

Underexpression of the gene product may be obtained in a variety of ways. For example, in one embodiment underexpression of the gene product may be achieved by providing an agent which reduces the level or activity of the gene product within the cell. In one embodiment, the agent may comprise an antisense nucleic acid which is complementary to a nucleic acid encoding the gene product or complementary to a portion of a nucleic acid encoding the gene product. For example, a nucleic acid which encodes the antisense nucleic acid may be operably linked to a regulatable promoter. When grown under appropriate conditions, such as media containing an inducer of transcription or an agent which alleviates repression of transcription, the antisense nucleic acid is expressed in the cell, thereby reducing the level or activity of the gene product within the cell. In some embodiments, the concentration of the inducer of transcription or the agent which alleviates repression of transcription may be varied to provide optimal results. Such methods have been described in U.S. Patent Application Serial Number 09/815,242 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/492,709 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/711,164 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application

Serial Number 09/741,669 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), or U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 the disclosure of which is incorporated herein by reference in its entirety). Each of the Patent Applications cited in the preceding sentence disclose genes and gene products required for proliferation which may be used in any of the methods of the present invention.

Alternatively, underexpression of a gene product required for proliferation may be achieved by constructing strains in which the expression of the gene product is under the control of a constitutive or regulatable promoter using methods such as those described above with respect to methods in which the gene product is overexpressed. To provide cells which underexpress the gene product, the cells are grown under conditions in which expression the gene product is expressed at a level lower than that of a wild type cell. For example, the cells may be grown under conditions in which a repressor reduces the level of transcription from the regulatable promoter.

In other embodiments, underexpression may be achieved by operably linking the gene required for proliferation to a desired promoter in a vector as described above with respect to embodiments in which gene products required for proliferation are overexpressed. In some embodiments, the vector may be present in cells in which the chromosomal copy or copies of the gene has been disrupted.

Gene products required for proliferation may be identified using a variety of methods, including the methods described in U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/815,242 (the disclosure of which is incorporated herein by reference in its entirety), U.S. Patent Application Serial Number 09/492,709 (the disclosure of which is incorporated herein by reference in its

entirety), U.S. Patent Application Serial Number 09/711,164 (the disclosure of which is incorporated herein by reference in its entirety), and U.S. Patent Application Serial Number 09/741,669 (the disclosure of which is incorporated herein by reference in its entirety). Each of the proliferation-required genes and gene products disclosed in the applications listed in the preceding sentence may be used in any of the methods of the present invention. Briefly, in one embodiment, gene products required for proliferation are identified by operably linking random genomic fragments to a regulatable promoter in a vector. The random genomic fragments may be generated by a partial digestion with a restriction enzyme, mechanical shearing, using techniques such as sonication and nebulization, or DNaseI digestion. Upon induction of transcription from the promoter with a suitable agent, the expression vectors produce an RNA molecule corresponding to the inserted genomic fragments. In those instances where the inserted genomic fragments are in an antisense orientation with respect to the promoter, the transcript produced is complementary to at least a portion of an mRNA encoding a gene product such that they interact with sense mRNA produced from various genes and thereby decrease the translation efficiency or the level of the sense messenger RNA (mRNA) thus decreasing production of the protein encoded by these sense mRNA molecules. In cases where the sense mRNA encodes a protein required for proliferation, cells grown under inducing conditions fail to grow or grow at a substantially reduced rate. Additionally, in cases where the transcript produced is complementary to at least a portion of a non-translated RNA and where that non-translated RNA is required for proliferation, cells grown under inducing conditions also fail to grow or grow at a substantially reduced rate. In contrast, cells grown under non-inducing conditions grow at a normal rate. The genes to which the antisense nucleic acids are complementary are then identified and utilized in the methods of the present invention.

Alternatively, genes required for proliferation may be identified by replacing the natural promoter for the proliferation required gene with a regulatable promoter as described above. The growth of such strains under conditions in which the promoter is active or non-repressed is compared to the growth under conditions in which the

promoter is inactive or repressed. If the strains fail to grow or grow at a substantially reduced rate under conditions in which the promoter is inactive or repressed but grow normally under conditions in which the promoter is active or non-repressed, then the gene which is operably linked to the regulatable promoter encodes a gene product
5 required for proliferation. For example, proliferation-required genes and gene products identified using promoter replacement are described in U.S. Patent Application Serial Number 09/948,993 (the disclosure of which is incorporated herein by reference in its entirety) U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its
10 entirety), and U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety). Each of the genes and gene products described in the applications listed in the preceding sentence may be used in any of the methods of the present invention.

The present invention includes a method for identifying the gene product on
15 which a compound which inhibits the proliferation of an organism acts. The method employs a culture which comprises a mixture of strains of the organism. At least some of the strains in the culture overexpress a different gene product which is required for the proliferation of the organism. Preferably, each of the strains in the culture overexpresses a different gene product which is required for proliferation of
20 the organism (i.e. all of the strains in the culture overexpress a gene product which is required for proliferation of the organism). Such strains may be obtained using the methods described above. The culture may comprise any number of strains. For example the culture may comprise at least two strains, at least 10 strains, at least 20 strains, at least 30, strains, at least 50 strains, at least 100 strains, at least 300 strains or
25 more than 300 strains. In some embodiments, the culture may comprise strains which in aggregate overexpress all or most of the gene products required for proliferation of the organism.

The culture is contacted with a compound which inhibits proliferation of the organism. The compound may be a candidate drug compound obtained from any
30 source. For example, the compound may be a compound generated using

combinatorial chemistry, a compound from a natural product library, or an impure or partially purified compound, such as a compound in a partially purified natural extract. The culture is contacted with a sufficient concentration of the compound to inhibit the proliferation of strains of the organism in the culture which do not overexpress the gene product on which the compound acts, such that strains which overexpress said gene product on which the compound acts proliferate more rapidly in the culture than strains which do not overexpress said gene product on which said compound acts. Thus, after a sufficient period of time, the strain which overexpresses the gene product on which the compound acts will be more prevalent in the culture than strains which do not overexpress the gene product on which the compound acts. In a preferred embodiment, the growth conditions and incubation period are selected so that only one strain, the strain overexpressing the target of the compound, is recovered from the culture. Thus, in one embodiment, a plurality of cultures containing a plurality of strains each of which overexpresses a different proliferation-required gene product may be grown in the presence of varying concentrations of the compound. In addition to varying the compound concentrations, in embodiments where expression of the proliferation-required gene product is under the control of a regulatable promoter, the plurality of cultures may be grown at varying concentrations of an agent which regulates the level of expression from the promoter, such as an inducer or an agent which reduces the effect of a repressor on transcription from the promoter. It will be appreciated, that the cultures may be grown in liquid medium in the presence of the compound whose target is to be identified (and where appropriate in the presence of an agent which regulates the level of expression from the promoter) or alternatively, a liquid culture comprising the strains which overexpress the proliferation-required gene products may be grown in the absence of the compound whose target is to be identified and then introduced onto a solid medium containing the compound (and, where appropriate, also containing an agent which regulates the level of expression from the promoter).

The identity of the overexpressed gene product which is the target of the compound may be determined using a variety of methods. For example, in some

embodiments of the present invention, the nucleic acids present in the culture or collection of strains which was contacted with the compound may be compared to the nucleic acids present in a control culture or collection of strains which was not contacted with the compound to identify nucleic acids which are overrepresented in the culture or collection of strains contacted with the test compound relative to the control culture or collection of strains. Alternatively, in some embodiments, the nucleic acids present in a culture or collection of strains contacted with the test compound may be analyzed to identify those nucleic acids which are present without comparison to a control culture or collection of strains.

In some embodiments of the present invention, the strains which proliferated more rapidly in the culture or collection of strains, i.e. strains having an enhanced ability to proliferate in the presence of a test compound relative to other strains in the culture or collection of strains, are identified as follows. Amplification products which are correlated with each of the overexpressed genes and which are distinguishable from one another are obtained from a culture or collection grown in the presence of a test compound. The amplification products are distinguished from one another to determine whether a particular amplification product is overrepresented in the culture or collection of strains. In some embodiments, the amplification products corresponding to each of the gene products have lengths which permit them to be distinguished from one another. In another embodiment, one or more of the amplification products have similar or identical lengths but are distinguishable from one another based on a detectable agent, such as a dye, attached thereto. In some embodiments, amplification products which are overrepresented are identified by comparing the amplification products from the culture or collection of strains which was contacted with the test compound to the amplification products from a culture or collection of strains which was not contacted with the test compound. Alternatively, amplification products which are overrepresented may be identified by simply identifying the amplification products obtained from the culture or collection of strains contacted with the test compound (for example, only one or a few strains may have proliferated in the presence of the test compound). The above methods for

generating distinguishable amplification products may be used in conjunction with any of the methods for generating strains which overexpress gene products required for proliferation described herein in order to facilitate the identification of strains which proliferate more rapidly or more slowly in the presence of a test compound.

5 For example, in some embodiments of the present invention, each of the native promoters of each of the genes encoding gene product required for proliferation are replaced by a single desired replacement promoter. After growth of the culture or collection of strains containing the strains in which the promoters have been replaced in the presence of a test compound for a desired period of time, an amplification
10 reaction is performed on nucleic acids obtained from the culture as follows.

 The nucleic acids from the culture or collection of strains may be divided into at least two aliquots if desired. In a preferred embodiment the nucleic acids from the culture or collection of strains are divided into four aliquots. A single primer complementary to a nucleotide sequence within the replacement promoter, within the
15 proliferation required genes, or within nucleic acid sequences adjacent to the promoter or proliferation required genes is divided into at least two portions, one portion for each aliquot of nucleic acids. Each portion of the primer is labeled with a distinct detectable dye, such as the 6FAM™, TET™, VIC™, HEX™, NED™, and PET™ dyes obtainable from Applied Biosystems (Foster City, CA). For example, the DS-31
20 or DS-33 dye sets available from Applied Biosystems (Foster City, CA) may be used to label the primers. Alternatively, the HEX™, NED, JOE, TMR and TET™ dyes available from Amersham Biosciences may be used. Thus, if the nucleic acids from the culture are not divided into aliquots, a single primer labeled with a single dye may be used. If the nucleic acids from the culture are divided into aliquots, at least 2, at
25 least 3, at least 4 or more than 4 primers labeled with distinguishable dyes may be used. Each of the portions of labeled primers are added to each of the aliquots of the nucleic acids from the culture or collection of strains such that each aliquot of nucleic acid receives a single labeled primer with a single detectable dye thereon. In some embodiments, the primers are divided into 3 portions, 4 portions or more than 4

portions, with each portion having a dye which is distinguishable from the dyes on the other portions thereon.

Each of the aliquots of nucleic acids also receives a set of unlabeled primers, with each of the unlabeled primers being complementary to a nucleotide sequence
5 within the promoter, within a nucleotide sequence which is unique to one of the genes encoding gene products required for proliferation which were placed under the control of the replacement promoter, or within nucleotide sequences adjacent to the promoter or proliferation required genes. Each of the aliquots receives primers unique to $1/N$ proliferation required genes which were placed under the control of the replacement
10 promoter, where N is the number of aliquots (i.e. if the culture or collection of strains consisted of 100 strains in which a gene required for proliferation was placed under the control of the replacement promoter and was divided into four aliquots, then each of the four aliquots of nucleic acids from the culture or collection of strains would receive primers complementary to 25 of the genes). The unlabeled primers are
15 selected so that each will yield an amplification product having a length distinguishable from the length of the amplification product produced with the other unlabeled primers. Preferably, the amplification products are between about 100- about 400 nucleotides in length, but any lengths which may be distinguished from each other may be used. In addition, in some of the embodiments some of the
20 amplification products may have identical or very similar lengths but be distinguishable from one another due to labeling with distinguishable dyes.

A nucleic acid amplification reaction is conducted on each of the nucleic acid aliquots. The amplification products are then separated by length to identify amplification products having increased representation in the culture or collection of
25 strains (i.e. amplification products derived from cells which proliferated more rapidly in the culture or collection of strains). The amplification products are then correlated with the corresponding genes to determine which strains proliferated more rapidly in the culture or collection of strains. If desired, amplification products having increased representation in the culture may be identified by comparing the amplification
30 products obtained from a culture or collection of strains which was contacted with the

compound to amplification products obtained from a control culture or collection of strains which was not contacted with the compound. Alternatively, if desired, the amplification products which are obtained from a culture which was contacted with the compound may be directly identified without comparison to a control culture which was not contacted with the compound.

For example, in some embodiments, the amplification products from each of the nucleic acid aliquots are pooled and subjected to capillary electrophoresis. The amplification products are detected by detecting the fluorescent dyes attached thereto and their lengths are determined to identify those amplification products having increased or decreased representation in the culture or collection of strains. Figures 1A and 1B illustrate one embodiment of this method in which the absence of an amplification product from an amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation indicates that a test compound acts on the gene corresponding to the missing amplification product. It will be appreciated that the method may also be used to identify an amplification product which is overrepresented in an amplification reaction conducted on a culture or collection of strains overexpressing genes required for proliferation because the test compound acted on the corresponding gene.

Alternatively, in another embodiment, a first amplification reaction is performed on nucleic acids obtained from a culture or collection of strains which was contacted with the compound using a first primer complementary to a nucleotide sequence present upstream or downstream of all of the overexpressed genes (such as a primer complementary to a nucleotide sequence in a replacement promoter upstream of all of the overexpressed genes) and a set of primers complementary to a nucleotide sequence unique to each of the strains (such as a primer complementary to a nucleotide sequence within each of the proliferation-required genes). One of the two amplification primers for each of the proliferation required genes is labeled with a dye as described above. Preferably, the common primer complementary to a nucleotide sequence upstream or downstream of all of the overexpressed genes is labeled with the dye. The primers used in the amplification reaction are designed so that the

amplification product corresponding to each proliferation-required gene has a unique length or a dye which allows it to be distinguished from other amplification products of the same length. A second amplification reaction is conducted on a control culture or collection of strains which was not contacted with the compound using the same
5 primers as in the first amplification reaction. The amplification products from the first amplification reaction are compared to those from the second amplification reaction to identify one or more amplification products which are overrepresented in the culture or collection of strains. For example, the amplification products from the first amplification reaction may be run in a separate lane of a polyacrylamide gel or a
10 separate capillary than the amplification products from the second amplification reaction and the two lanes or capillaries are compared to one another. If desired, in the embodiment where the amplification products from the first amplification reaction are run in a different lane or capillary than the amplification products from the second amplification reaction, the same dye may be used to label the primers in the first and
15 second amplification reactions. Alternatively, if desired, different dyes may be used to label the primers in the first and second amplification reactions. If desired, in the embodiment where the amplification products from the first amplification reaction are run in a different lane or capillary than the amplification products from the second amplification reaction, the same dye may be used to label the primers in the first and
20 second amplification reactions. Alternatively, if desired, different dyes may be used to label the primers in the first and second amplification reactions.

Alternatively, in some embodiments, the primers in the second amplification reaction are labeled with a different dye which is distinguishable from the dye used in the first amplification reaction. In this embodiment, the amplification reactions may
25 be pooled and run in the same lane on a polyacrylamide gel or in the same capillary and the products from each amplification reaction are compared by comparing the amount of each dye present for each amplification product. Figures 2A and 2B illustrate one embodiment of this method in which the absence of an amplification product from the amplification reaction performed on a culture comprising a plurality
30 of strains underexpressing genes required for proliferation which was contacted with

the compound indicates that a test compound acts on the gene corresponding to the missing amplification product. It will be appreciated that the method may also be used to identify an amplification product which is overrepresented in an amplification reaction conducted on a culture or collection of strains overexpressing genes required for proliferation because the test compound acted on the corresponding gene.

If desired, rather than dividing the culture into aliquots, individual amplification reactions may be conducted on nucleic acids obtained from the culture or collection of strains. Each amplification reaction contains primers which will yield an amplification product specific for only one of the proliferation required genes. The resulting amplification products from each of the individual amplification reactions are pooled and amplification products having increased representation in the culture are identified as described above.

In another embodiment, a culture or collection of strains in which gene products required for proliferation are overexpressed from regulatable promoters which replaced the native promoters of the genes encoding these gene products is allowed to grow in the presence of a test compound for a desired number of generations. Preferably, the culture or collection of strains is allowed to grow in the presence of the test compound for at least 20 generations. Nucleic acids are isolated from the culture or collection of strains and an amplification reaction is performed using a primer which is complementary to a nucleotide sequence within the replacement promoter(s) or a nucleotide sequence adjacent to the a 5' end thereof and primers which are complementary to a nucleotide sequence within the proliferation required genes or nucleotide sequences adjacent thereto. The resulting amplification product(s) is directly sequenced using a primer complementary to a nucleotide sequence within the replacement promoter.

In one embodiment of the present invention, the vector containing the nucleotide sequence encoding the proliferation-required gene product is obtained from a strain which proliferated more rapidly in the culture using methods such as plasmid preparation techniques. Nucleic acid sequencing techniques are then employed to determine the nucleotide sequence of the gene which was overexpressed.

Alternatively, the identity of the overexpressed gene product which is the target of the compound may be determined by performing a nucleic acid amplification reaction, such as a polymerase chain reaction (PCR), to identify the nucleotide sequence of the gene which was overexpressed. For example, aliquots of a nucleic acid preparation, such as a purified plasmid, from the strain which is recovered from the culture may each be contacted with pairs of PCR primers which would amplify a different proliferation-required gene to determine which pair of primers yields an amplification product.

Yet another method for determining the identity of the gene product which is the target of the compound involves obtaining a nucleic acid array, such as a DNA chip, which contains each of the proliferation-required genes which were overexpressed in the strains in the culture. Each proliferation-required genes occupies a known location in the array. A nucleic acid preparation, such as a plasmid preparation, from the recovered strain is labeled with a detectable agent, such as radioactive or fluorescent moiety, and placed in contact with the nucleic acid array under conditions which permit the labeled nucleic acid to hybridize to complementary nucleic acids on the array. The location on the array to which the labeled nucleic acids hybridize is determined to identify the gene which was overexpressed in the recovered strain. If desired the hybridized nucleic acids from a culture which was contacted with the compound may be compared to the hybridized nucleic acids from a control culture which was not contacted with the compound. Alternatively, the hybridized nucleic acids from a culture which was contacted with the compound may be directly identified without comparison to nucleic acids from a control culture.

In some embodiments of the invention, more than one strain may proliferate more rapidly in the presence of the compound. This may result from a variety of causes. For example, the concentration of the compound may not have been high enough to restrict proliferation only to cells which overexpress one gene product (i.e. the target gene product). While strains which overexpress the target gene product will be the most prevalent strain in the culture, other strains may also have proliferated. In such instances, the identity of the gene product in the strain which is most prevalent in

the culture may be identified by quantitating the levels of each of the genes encoding proliferation-required proteins in the culture. This may be accomplished by quantitative PCR, DNA sequencing, hybridization, or array technology as described above.

5 In other instances, multiple strains will exhibit more rapid proliferation in the culture as a result of a common functional attribute. For example, the strains which proliferate more rapidly may each overexpress a gene product with a common enzymatic activity, such as serine protease activity for example. Alternatively, the strains which proliferate more rapidly may each overexpress a gene product with a
10 common functional domain, such as a cAMP binding domain. In such instances, the common attribute of the strains which proliferate more rapidly may provide information as to the mode of action of the compound or the biochemical activity of the target of the compound. For example, if all of the overexpressed genes in the strains which proliferated more rapidly are serine proteases, the compound acts by
15 inhibiting serine protease activity and the target protein is a serine protease. If desired, the compound may be derivatized and the efficacy of the derivatized compound against each of the strains which proliferated more rapidly may be assessed as described herein in order to identify derivatives which are capable of interacting with a wide range of targets sharing a common activity or binding site (i.e. derivatives
20 which have a greater ability to inhibit the proliferation of all the strains than the original compound) or to identify derivatives having greater specificity for a desired target (i.e. derivatives which have a greater specificity for one of the strains than the original compound). For example, it is possible that a nonessential gene product expressed in the cell might also bind to the initial test compound in addition to the
25 gene product required for proliferation. In such an instance, it is desirable to obtain a derivative of the initial test compound which is specific for the gene product required for proliferation. In addition, it is possible that two gene products required for proliferation might bind to the initial test compound but specificity for one of the gene products is desired.

In some embodiments, rather than employing a single culture which contains multiple strains each of which overexpresses a proliferation-required gene product, the methods of the present invention may be performed using an array of individual strains (i.e. a collection of strains) each of which overexpresses a different proliferation-required gene product. For example, individual strains each overexpressing a different proliferation-required gene product may be grown in different wells of a multiwell plate. Each well is contacted with the compound (and, where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of the strains in each of the wells is determined to identify a strain which proliferated more rapidly. The identity of the overexpressed gene product in the strain that proliferated more rapidly is determined as described above.

In another embodiment, individual strains each overexpressing a different proliferation-required gene product (i.e. a collection of strains) are grown at different locations on a solid medium, such as an agar plate. The medium contains the compound and where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of each of the strains is determined to identify a strain which proliferated more rapidly. The identity of the overexpressed gene product in the strain that proliferated more rapidly is determined as described above.

The above methods may be used to prioritize compound development or to determine whether the compound has been previously identified or whether the target of the compound is the target of a previously identified drug. In particular, if the product is a natural product, it is advantageous to determine whether it has been previously identified prior to investing significant effort in developing it. Thus, in some embodiments of the present invention, the target of a partially purified or purified natural product or a compound produced by combinatorial chemistry is identified using the methods described above and compared to the targets of known drugs. If the target is identical to that of a known drug, further development of the compound is halted.

In some embodiments of the present invention, an array of strains each of which overexpresses a different gene product (i.e. a collection of strains) is grown on solid medium containing a compound to be evaluated. The location of each strain in the array and the gene product overexpressed by that strain is known. The pattern of colonies which grow in the presence of the compound is evaluated and compared to the pattern of colonies which grow in the presence of previously identified drugs. If the pattern of colonies which grow in the presence of the compound being evaluated is the same as the pattern of colonies which grow in the presence of a previously identified drug, further development of the compound is halted.

In another embodiment, the sequence of the gene product in a strain which proliferated more rapidly in the assays described above is compared to the sequence of gene products from heterologous organisms to determine the likely spectrum of species whose growth would be inhibited by the compound. If the gene product has a high degree of homology to gene products from heterologous species, it is likely that the compound would also inhibit the growth of these heterologous species. Homology may be determined using any of a variety of methods familiar to those skilled in the art. For example, homology may be determined using a computer program such as BLASTP or FASTA. The ability of the compound to inhibit the growth of the heterologous species may then be confirmed by comparing the growth of cells of the heterologous species in the presence and absence of the compound.

In some embodiments, the present invention uses collections or cultures of strains comprising both strains which overexpress gene products required for cellular proliferation and strains which underexpress the same gene products required for cellular proliferation. The culture or collection of strains is contacted with a compound and the nucleic acids present in the culture or collection of strains are analyzed. Preferably, nucleic acids derived from overexpressing strains can be distinguished from those derived from underexpressing strains. For example, the overexpressing strains may be obtained using promoter replacement as described above while the underexpressing strains may be obtained by expressing antisense nucleic acids. Accordingly, in one embodiment, amplification primers may be

designed which will uniquely amplify nucleic acids from the overexpressing strains or the underexpressing strains. If a compound acts on a gene product which was overexpressed and underexpressed in the culture, then the amplification product obtained from the strain in the culture or collection which overexpressed gene product will be overrepresented in the culture or collection while the amplification product obtained from the strain which underexpressed the gene product will be underrepresented in the culture or collection. If desired, nucleic acids from a culture or collection which was contacted with the compound may be compared to nucleic acids from a control culture or collection which was not contacted with the compound. Alternatively, nucleic acids from a culture or collection which was contacted with the compound may be directly analyzed without comparison to a control culture or collection.

Current methods for identifying the target of compounds which inhibit cellular proliferation are laborious and time consuming. The above methods may be employed to allow the targets of a large number of compounds to be rapidly identified. In such methods, the methods described above are simultaneously performed for each of a large number of compounds. For example, the compounds may be members of a library of compounds generated using combinatorial chemistry or members of a natural product library. In such methods, a plurality of cultures each comprising a plurality of strains each of which overexpresses a different gene product required for proliferation or a plurality of collections of individual strains each of which overexpresses a different gene product required for proliferation is obtained. Each culture or collection of strains is contacted with a different compound in the library and the target of the compound is identified as described above.

In another embodiment of the present invention, the gene product on which a compound which inhibits the proliferation of an organism acts is identified using a culture which comprises a mixture of strains of the organism including strains which underexpress a different gene product which is required for proliferation of the organism (i.e. at least some of the strains in the culture underexpress a gene product which is required for proliferation of the organism). Preferably, each of the strains in

the culture underexpress a different a gene product which is required for the proliferation of the organism (i.e. all of the strains in the culture underexpress a gene product which is required for the proliferation of the organism). Such strains may be obtained using the methods described above. The culture may comprise any number of strains. For example the culture may comprise at least two strains, at least 10 strains, at least 20 strains, at least 30, strains, at least 50 strains, at least 100 strains, at least 300 strains or more than 300 strains. In some embodiments, the strains in the culture in aggregate may underexpress all or most of the gene products required for proliferation of the organism.

The culture is contacted with a compound which inhibits proliferation of the organism. The compound may be a candidate drug compound obtained from any source. For example, the compound may be a compound generated using combinatorial chemistry, a compound from a natural product library, or an impure or partially purified compound, such as a compound in a partially purified natural extract. The culture is contacted with a sufficient concentration of the compound to inhibit the proliferation of strains of the organism in the culture which underexpress the gene product on which the compound acts, such that strains which do not underexpress the gene product on which the compound acts proliferate more rapidly in the culture than strains which do underexpress said gene product on which said compound acts. Thus, after a sufficient period of time, the strain which underexpresses the gene product on which the compound acts will be less prevalent in the culture than strains which do not underexpress the gene product on which the compound acts. In one embodiment, the growth conditions and incubation period are selected so that only one strain, the strain underexpressing the target of the compound, proliferates at a reduced rate in the culture. In another embodiment, the growth conditions may be selected so that the strain underexpressing the target of the compound is not recovered from the culture. Thus, in one embodiment, a plurality of cultures containing a plurality of strains each of which underexpresses a different proliferation-required gene product may be grown in the presence of varying concentrations of the compound. In addition to varying the compound concentrations,

in embodiments where expression of the proliferation-required gene product is under the control of a regulatable promoter, the plurality of cultures may be grown at varying concentrations of an agent which regulates the level of expression from the promoter, such as an inducer or an agent which reduces the effect of a repressor on transcription from the promoter. It will be appreciated, that the cultures may be grown in liquid medium in the presence of the compound whose target is to be identified (and where appropriate in the presence of an agent which regulates the level of expression from the promoter) or alternatively, a liquid culture comprising the strains which underexpress the proliferation-required gene products may be grown in the absence of the compound whose target is to be identified and then introduced onto a solid medium containing the compound (and, where appropriate, also containing an agent which regulates the level of expression from the promoter).

The identity of the underexpressed gene product which is the target of the compound may be determined using a variety of methods. For example, in some embodiments of the present invention, the nucleic acids present in the culture or collection of strains which was contacted with the compound may be compared to the nucleic acids present in a control culture or collection of strains which was not contacted with the compound to identify nucleic acids which are underrepresented in the culture or collection of strains contacted with the test compound relative to the control culture or strains. Alternatively, in some embodiments, the nucleic acids present in a culture or collection of strains contacted with the test compound may be analyzed to identify those nucleic acids which are missing or present at reduced levels without comparison to a control culture or collection of strains.

In some embodiments of the present invention, the strains which proliferated more slowly in the culture or collection of strains ,i.e. strains having an decreased ability to proliferate in the presence of a test compound or which do not proliferate in the presence of a test compound, are identified as follows. Amplification products which are correlated with each of the underexpressed genes and which are distinguishable from one another are obtained from a culture or collection grown in the presence of a test compound. The amplification products are distinguished from

one another to determine whether a particular amplification product is underrepresented in the culture or collection of strains. In some embodiments, the amplification products corresponding to each of the gene products have lengths which permit them to be distinguished from one another. In another embodiment, one or more of the amplification products have similar or identical lengths but are distinguishable from one another based on a detectable agent, such as a dye, attached thereto. In some embodiments, amplification products which are underrepresented are identified by comparing the amplification products from the culture or collection of strains which was contacted with the test compound to the amplification products from a culture or collection of strains which was not contacted with the test compound. Alternatively, amplification products which are underrepresented in the culture or collection of strains may be identified simply by determining which amplification products are missing or present at reduced levels in the culture or collection of strains. The above methods for generating distinguishable amplification products may be used in conjunction with any of the methods for generating strains which underexpress gene products required for proliferation described herein in order to facilitate the identification of strains which proliferate more slowly in the presence of a test compound.

For example, in some embodiments of the present invention, each of the native promoters of each of the genes encoding gene product required for proliferation are replaced by a single desired replacement promoter. After growth of the culture or collection of strains containing the strains in which the promoters have been replaced in the presence of a test compound for a desired period of time, an amplification reaction is performed on nucleic acids obtained from the culture as follows.

The nucleic acids from the culture or collection of strains are divided into at least two aliquots. In a preferred embodiment the nucleic acids from the culture or collection of strains are divided into four aliquots. A single primer complementary to a nucleotide sequence within the replacement promoter, within the proliferation required genes, or within nucleic acid sequences adjacent to the promoter or proliferation required genes is divided into four groups. Each group is labeled with a

distinct detectable dye, such as the 6FAM™, TET™, VIC™, HEX™, NED™, and PET™ dyes obtainable from Applied Biosystems (Foster City, CA). For example, the DS-31 or DS-33 dye sets available from Applied Biosystems (Foster City, CA) may be used to label the primers. Each of the groups of labeled primers are added to each
5 of the aliquots of the nucleic acids from the culture or collection of strains such that each aliquot of nucleic acid receives a single labeled primer with a single detectable dye thereon.

Each of the aliquots of nucleic acids also receives a set of unlabeled primers, with each of the unlabeled primers being complementary to a nucleotide sequence
10 within the promoter, within a nucleotide sequence which is unique to one of the genes encoding gene products required for proliferation which were placed under the control of the replacement promoter, or within nucleotide sequences adjacent to the promoter or proliferation required genes. Each of the aliquots receives primers unique to 1/N proliferation required genes which were placed under the control of the replacement
15 promoter, where N is the number of aliquots (i.e. if the culture or collection of strains consisted of 100 strains in which a gene required for proliferation was placed under the control of the replacement promoter and was divided into four aliquots, then each of the four aliquots of nucleic acids from the culture or collection of strains would receive primers complementary to 25 of the genes). The unlabeled primers are
20 selected so that each will yield an amplification product having a length distinguishable from the length of the amplification product produced with the other unlabeled primers. Preferably, the amplification products are between about 100- about 400 nucleotides in length, but any lengths which may be distinguished from each other may be used. In addition, in some of the embodiments some of the
25 amplification products may have identical or very similar lengths but be distinguishable from one another due to labeling with distinguishable dyes.

A nucleic acid amplification reaction is conducted on each of the nucleic acid aliquots. The amplification products are then separated by length to identify
30 amplification products decreased representation or which are absent in the culture or collection of strains. The amplification products are then correlated with the

corresponding genes to determine which strains proliferated more slowly in the culture or collection of strains. If desired, amplification products having decreased representation in the culture may be identified by comparing the amplification products obtained from a culture or collection of strains which was contacted with the compound to amplification products obtained from a control culture or collection of strains which was not contacted with the compound. Alternatively, if desired, the amplification products which are missing or present at reduced levels in a culture which was contacted with the compound may be directly identified without comparison to a control culture which was not contacted with the compound.

For example, in some embodiments, the amplification products from each of the nucleic acid aliquots are pooled and subjected to capillary electrophoresis. The amplification products are detected by detecting the fluorescent dyes attached thereto and their lengths are determined to identify those amplification products having decreased representation in the culture or collection of strains. Figures 1A and 1B illustrate one embodiment of this method in which the absence of an amplification product from an amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation indicates that a test compound acts on the gene corresponding to the missing amplification product.

Alternatively, in another embodiment, a first amplification reaction is performed on nucleic acids obtained from a culture or collection of strains which was contacted with the compound using a first primer complementary to a nucleotide sequence present upstream or downstream of all of the overexpressed genes (such as a primer complementary to a nucleotide sequence in a replacement promoter upstream of all of the overexpressed genes) and a set of primers complementary to a nucleotide sequence unique to each of the strains (such as a primer complementary to a nucleotide sequence within each of the proliferation-required genes). One of the two amplification primers for each of the proliferation required genes is labeled with a dye as described above. Preferably, the common primer complementary to a nucleotide sequence upstream or downstream of all of the overexpressed genes is labeled with the dye. The primers used in the amplification reaction are designed so that the

amplification product corresponding to each proliferation-required gene has a unique length. A second amplification reaction is conducted on a control culture or collection of strains which was not contacted with the compound using the same primers as in the first amplification reaction. The amplification products from the first
5 amplification reaction are compared to those from the second amplification reaction to identify one or more amplification products which are underrepresented in the culture or collection of strains. For example, the amplification products from the first amplification reaction may be run in a separate lane of a polyacrylamide gel or a separate capillary than the amplification products from the second amplification
10 reaction and the two lanes or capillaries are compared to one another.

Alternatively, in some embodiments, the primers in the second amplification reaction are labeled with a different dye which is distinguishable from the dye used in the first amplification reaction. In this embodiment, the amplification reactions may be pooled and run in the same lane on a polyacrylamide gel or in the same capillary
15 and the products from each amplification reaction are compared by comparing the amount of each dye present for each amplification product. Figures 2A and 2B illustrate one embodiment of this method in which the absence of an amplification product from the amplification reaction performed on a culture comprising a plurality of strains underexpressing genes required for proliferation which was contacted with
20 the compound indicates that a test compound acts on the gene corresponding to the missing amplification product.

If desired, rather than dividing the culture into aliquots, individual amplification reactions may be conducted on nucleic acids obtained from the culture or collection of strains. Each amplification reaction contains primers which will yield
25 an amplification product specific for only one of the proliferation required genes. The resulting amplification products from each of the individual amplification reactions are pooled and amplification products having decreased representation in the culture are identified as described above.

In one embodiment the representation of each strain in the culture may be
30 assessed by hybridizing detectably labeled nucleic acids encoding the proliferation-

required gene products, or portions thereof, obtained from the culture to an array comprising nucleic acids encoding the gene products required for proliferation or portions thereof. Each nucleic acid encoding a gene product required for proliferation or portion thereof occupies a known location on the array. The signal from each location on the array is quantitated to identify those nucleic acids encoding a proliferation-required gene product which are underrepresented in the culture. If desired the hybridized nucleic acids from a culture which was contacted with the compound may be compared to the hybridized nucleic acids from a control culture which was not contacted with the compound. Alternatively, the hybridized nucleic acids from a culture which was contacted with the compound may be directly analyzed without comparison to nucleic acids from a control culture.

Alternatively, each strain underexpressing a gene product required for proliferation may be constructed to contain a unique nucleic acid sequence (referred to herein as a "tag"). The tag may be included in the chromosome of each strain or in an extrachromosomal vector. For example, the tag could be included in a vector encoding an antisense nucleic acid complementary to a gene encoding a gene product required for proliferation or a portion of such a gene or the tag may be included in the antisense nucleic acid itself. The representation of each strain in the culture may be assessed by performing an amplification reaction using primers complementary to each of the tags and quantitating the levels of the resulting amplification products to identify a tag which is underrepresented or absent from the culture. Since each tag corresponds to one strain, the strain which is underrepresented or absent from the culture may be identified. If desired the tags present in a culture which was contacted with the compound may be compared to the tags present in a control culture which was not contacted with the compound. Alternatively, the tags present in a culture which was contacted with the compound may be analyzed without comparison to a control culture.

It will be appreciated that, if desired, unique tags may also be used in embodiments in which gene products required for proliferation are overexpressed. In some aspects of such embodiments, the tags may be within or adjacent to the promoter

which drives expression of the gene encoding the gene product. In such embodiments, the gene product which is overexpressed in strains which proliferate more rapidly in the culture may be identified by detecting the presence or amount of the unique tag corresponding to that gene product in the culture.

5 In some embodiments of the invention, more than one strain may proliferate less rapidly in the presence of the compound. This may result from a variety of causes. For example, the concentration of the compound may not have been high enough to reduce the proliferation only in cells which underexpress one gene product (i.e. the target gene product). While strains which underexpress the target gene
10 product will be the least prevalent strain in the culture, other strains may also be underrepresented. In such instances, the identity of the gene product in the strain which is least prevalent in the culture (or not recovered from the culture) may be identified by quantitating the levels of each of the genes encoding proliferation-required proteins in the culture. This may be accomplished by quantitative PCR,
15 DNA sequencing, hybridization, or array technology as described above.

 In other instances, multiple strains will exhibit less rapid proliferation in the culture as a result of a common functional attribute. For example, the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may each underexpress a gene product with a common enzymatic activity, such as serine
20 protease activity for example. Alternatively, the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may each underexpress a gene product with a common functional domain, such as a cAMP binding domain. In such instances, the common attribute of the strains which proliferate less rapidly (or the strains which are not recovered from the culture) may provide information as to
25 the mode of action of the compound or the biochemical activity of the target of the compound. For example, if all of the underexpressed genes in the strains which proliferated less rapidly are serine proteases, the compound acts by inhibiting serine protease activity and the target protein is a serine protease. If desired, the compound may be derivatized and the efficacy of the derivatized compound against each of the
30 strains which proliferated more rapidly may be assessed as described herein in order to

identify derivatives which are capable of interacting with a wide range of targets sharing a common activity or binding site (i.e. derivatives which have a greater ability to inhibit the proliferation of all the strains than the original compound) or to identify derivatives having greater specificity for a desired target (i.e. derivatives which have a greater specificity for one of the strains than the original compound).

In some embodiments, rather than employing a single culture which contains multiple strains each of which underexpresses a proliferation-required gene product, the methods of the present invention may be performed using an array of individual strains (i.e. a collection of strains) each of which underexpresses a different proliferation-required gene product. For example, individual strains each underexpressing a different proliferation-required gene product may be grown in different wells of a multiwell plate. Each well is contacted with the compound (and, where appropriate an agent which regulates the level of expression from the promoter). The level of proliferation of the strains in each of the wells is determined to identify a strain which proliferated less rapidly or which did not proliferate at all. The identity of the underexpressed gene product in the strain that proliferated less rapidly or which did not proliferate at all is determined as described above.

In another embodiment, individual strains each underexpressing a different proliferation-required gene product (i.e. a collection of strains) are grown at different locations on a solid medium, such as an agar plate. The medium contains the compound and, where appropriate, an agent which regulates the level of expression from the promoter. The level of proliferation of each of the strains is determined to identify a strain which proliferated less rapidly (or a strain which is not recovered from the culture). The identity of the underexpressed gene product in the strain that proliferated less rapidly (or the strain which is not recovered from the culture) is determined as described above.

The above methods may be used to prioritize compound development or to determine whether the compound has been previously identified or whether the target of the compound is the target of a previously identified drug. In particular, if the product is a natural product is advantageous to determine whether it has been

previously identified prior to investing significant effort in developing it. Thus, in some embodiments of the present invention, the target of a partially purified or purified natural product or a compound produced by combinatorial chemistry is identified using the methods described above and compared to the targets of known drugs. If the target is identical to that of a known drug, further development of the compound is halted.

In some embodiments of the present invention, an array of strains each of which underexpresses a different gene product (i.e. a collection of strains) is grown on solid medium containing a compound to be evaluated. The location of each strain in the array and the gene product underexpressed by that strain is known. The pattern of colonies which grow less rapidly or fail to grow in the presence of the compound is evaluated and compared to the pattern of colonies which grow less rapidly or fail to grow in the presence of previously identified drugs. If the pattern of colonies which grow less rapidly or fail to grow in the presence of the compound being evaluated is the same as the pattern of colonies which grow less rapidly or fail to grow in the presence of a previously identified drug, further development of the compound is halted.

In another embodiment, the nucleotide sequence of the gene product in a strain which proliferated less rapidly (or a strain which was not recovered from the culture) in the assays described above is compared to the nucleotide sequence of gene products from heterologous organisms to determine the likely spectrum of species whose growth would be inhibited by the compound. If the gene product has a high degree of homology to gene products from heterologous species, it is likely that the compound would also inhibit the growth of these heterologous species. Homology may be determined using any of a variety of methods familiar to those skilled in the art. For example, homology may be determined using a computer program such as BLASTP or FASTA. The ability of the compound to inhibit the growth of the heterologous species may then be confirmed by comparing the growth of cells of the heterologous species in the presence and absence of the compound.

Current methods for identifying the target of compounds which inhibit cellular proliferation are laborious and time consuming. The above methods may be employed to allow the targets of a large number of compounds to be rapidly identified. In such methods, the methods described above are simultaneously
5 performed for each of a large number of compounds. For example, the compounds may be members of a library of compounds generated using combinatorial chemistry or members of a natural product library. In such methods, a plurality of cultures each comprising a plurality of strains each of which underexpresses a different gene product required for proliferation or a plurality of collections of individual strains each
10 of which underexpresses a different gene product required for proliferation is obtained. Each culture or collection of strains is contacted with a different compound in the library and the target of the compound is identified as described above.

In some embodiments of the present invention, strains are constructed in which a nucleic acid complementary to a gene encoding a gene product required for
15 proliferation, or a portion thereof (i.e. a nucleic acid encoding an antisense nucleic acid to the gene encoding the proliferation required gene product or a portion thereof) is operably linked to a regulatable promoter. A culture comprising a plurality of such strains wherein each strain expresses an antisense nucleic acid against a different gene product required for proliferation is grown in the presence of varying levels of a
20 compound which inhibits proliferation and in the presence of varying levels of an agent which regulates the level of transcription from the regulatable promoter. Nucleic acids samples are obtained from the culture, detectably labeled and hybridized to a solid support comprising nucleic acids containing the genes encoding the proliferation-required gene products or a portion thereof. The level of hybridization is
25 quantitated for each nucleic acid encoding each of the proliferation-required gene products to determine the rate at which each of the strains proliferated in the culture. If the antisense nucleic acid expressed by a strain in the culture is not complementary to all or a portion of the gene encoding the target of the compound (i.e. a nonspecific strain), then the hybridization intensity for that strain will not be correlated with the
30 concentration of the compound (see Figure 3), while if the antisense nucleic acid

expressed by a strain in the culture is complementary to all or a portion of the gene encoding the target of the compound, the hybridization intensity for that strain will be intimately correlated with the concentration of the compound (see Figure 4). In this manner, the target of the compound may be identified. It will be appreciated that, as
5 described above, rather than growing the strains in a single culture, each strain may be grown in a different location on a solid medium or in a different well of a multiwell plate.

The methods described herein may be performed simultaneously for each of a plurality of compounds which inhibit proliferation to allow the targets of those
10 compounds to be rapidly identified.

Some embodiments of the present invention are summarized on the following pages. It will be appreciated that the present invention may be applied to cultures of any organism and that any gene product required for proliferation of the organism may be overexpressed or underexpressed. Accordingly, the organisms and gene products
15 described in the following examples are exemplary only and do not limit the scope of the present invention.

Genes required for cellular proliferation for use in the present invention may be identified from the literature, may be identified using the following methods, or may be identified using other methods familiar to those skilled in the art. In some
20 embodiments of the present invention, the culture comprises a strain in which a gene product selected from the group consisting of a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
25 3796-3800, 3806-4860, 5916-10012, and 14111-14944, and a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed. The identification of nucleic acids comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising
30 a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-

3800, 3806-4860, 5916-10012, and 14111-14944 and gene products comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 are described below.

5

EXAMPLE 1

Identification of Genes Required for Cellular Proliferation by Expressing Antisense RNA Complementary to at least a Portion of a Gene Required for Cellular Proliferation

Random genomic fragments are obtained from the organism in which it is
10 desired to identify genes required for cellular proliferation. The random genomic fragments may be generated by a partial digestion with a restriction enzyme, mechanical shearing, using techniques such as sonication and nebulization, or DNaseI digestion. The random genomic fragments are operably linked to a regulatable promoter in a vector. In those instances where the inserted genomic fragments are in
15 antisense orientation with respect to the promoter, the transcript produced is complementary to at least a portion of an mRNA encoding a gene product such that they interact with sense mRNA produced from various genes and thereby decrease the translation efficiency or the level of the sense messenger RNA (mRNA) thus decreasing production of the protein encoded by these sense mRNA molecules. In cases where the
20 sense mRNA encodes a protein required for proliferation, cells grown under inducing conditions fail to grow or grow at a substantially reduced rate. Additionally, in cases where the transcript produced is complementary to at least a portion of a non-translated RNA and where that non-translated RNA is required for proliferation, cells grown under inducing conditions also fail to grow or grew at a substantially reduced rate. In contrast,
25 cells grown under non-inducing conditions grow at a normal rate. The genes to which the antisense nucleic acids are complementary are then identified and utilized in the methods of the present invention. Thus, to identify genes required for cellular proliferation, the extent of proliferation of cells containing the vectors in the presence of an agent which induces transcription from the regulatable promoter is compared to
30 the extent of proliferation of cells in the absence of the agent. Those cells which grow

well in the absence of the agent but exhibit significantly reduced proliferation in the presence of the agent contain a vector encoding an antisense nucleic acid complementary to at least a portion of a gene required for cellular proliferation.

The above method was used to identify genes required for cellular proliferation in *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*. The identification of genes required for cellular proliferation in *E. coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis* has been described in the following U.S. Patent Applications, the disclosures of which are incorporated herein by reference in their entireties: U.S. Patent Application Serial Number 09/815,242, filed March 21, 2001; U.S. Patent Application Serial Number 09/492709, filed January 27, 2000; U.S. Patent Application Serial Number 09/711164, filed November 9, 2000; U.S. Patent Application Serial Number 09/741669, filed December 19, 2000 and U.S. Patent Application Serial Number 09/815,242 filed March 21, 2001. The methods used to identify these genes required for cellular proliferation are summarized below.

To identify genes required for proliferation of *E. coli*, random genomic fragments were cloned into the IPTG-inducible expression vector pLEX5BA (Krause et al., J. Mol. Biol. 274: 365 (1997), the disclosure of which is incorporated herein by reference in its entirety) or a modified version of pLEX5BA, pLEX5BA-3' in which a synthetic linker containing a T7 terminator was ligated between the PstI and HindIII sites of pLEX5BA. In particular, to construct pLEX5BA-3', the following oligonucleotides were annealed and inserted into the PstI and HindIII sites of pLEX5BA:

5'-GTCTAGCATAACCCCTTGGGGCCTCTAAACGGGTCCTTGAGGGGTTTTTGA-3' (SEQ ID NO: 15779) **CORRECT SEQ ID NOS TO BE INSERTED THROUGHOUT THE APPLICATION**

5'-AGCTTCAAAAAACCCCTCAAGGACCGTTTGTAGAGGCCCAAGGGTTATGCTAGACTGCA-3' (SEQ ID NO: 15780)

Random fragments of *E. coli* genomic DNA were generated by DNaseI digestion or sonication, filled in with T4 polymerase, and cloned into the SmaI site of pLEX5BA or pLEX5BA-3'. Upon activation or induction, the promoter transcribed
5 the random genomic fragments

To study the effects of transcriptional induction in liquid medium, growth curves were carried out by back diluting cultures 1:200 into fresh media with or without 1 mM IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10², 10³, 10⁴, 10⁵, 10⁶, 10⁷ and 10⁸ fold
10 dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Of the numerous clones tested, some clones were identified as containing a
15 sequence that inhibited *E. coli* growth after IPTG induction. Accordingly, the gene to which the inserted nucleic acid sequence corresponds, or a gene within the operon containing the inserted nucleic acid, is required for proliferation in *E. coli*.

Nucleic acids required for proliferation of *Staphylococcus aureus*, *Salmonella typhimurium*, and *Klebsiella pneumoniae* were identified as follows. Randomly
20 generated fragments of *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic DNA were transcribed from inducible promoters.

In the case of *Staphylococcus aureus*, a novel inducible promoter system, XylT5, comprising a modified T5 promoter fused to the *xylO* operator from the *xylA*
25 promoter of *Staphylococcus aureus* was used. The promoter is described in U.S. Patent Application Serial Number 10/032,393, the disclosure of which is incorporated herein by reference in its entirety. Transcription from this hybrid promoter is inducible by xylose.

Randomly generated fragments of *Salmonella typhimurium* genomic DNA
30 were transcribed from an IPTG inducible promoter in pLEX5BA (Krause et al., J.

Mol. Biol. 274: 365 (1997) or a derivative thereof. Randomly generated fragments of *Klebsiella pneumoniae* genomic DNA were expressed from an IPTG inducible promoter in pLEX5BA-Kan. To construct pLEX5BA-kan, pLEX5BA was digested to completion with *ClaI* in order to remove the *bla* gene. Then the plasmid was treated with a partial *NotI* digestion and blunted with T4 DNA polymerase. A 3.2 kbp fragment was then gel purified and ligated to a blunted 1.3 kbp kan gene from pKan π . Kan resistant transformants were selected on Kan plates. Orientation of the kan gene was checked by *SmaI* digestion. A clone, which had the kan gene in the same orientation as the *bla* gene, was used to identify genes required for proliferation of *Klebsiella pneumoniae*.

Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were transcribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lacUV5/ lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41, the disclosure of which is incorporated herein by reference in its entirety). On a separate plasmid, a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, was fused with a *lacO* operator followed by a multiple cloning site.

In the case of *Staphylococcus aureus*, a shotgun library of *Staphylococcus aureus* genomic fragments was cloned into the vector pXyIT5-P15a, which harbors the XyIT5 inducible promoter. The vector was linearized at a unique *BamHI* site immediately downstream of the XyIT5 promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Staphylococcus aureus* strain RN450 was fully digested with the restriction enzyme *Sau3A*, or, alternatively, partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 0.1 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with supplemented with carbenicillin at 100 µg/ml. Resulting colonies numbering 5×10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

5 The purified library was then transformed into electrocompetent *Staphylococcus aureus* RN4220. Resulting transformants were plated on agar containing LB + 0.2% glucose (LBG medium) + chloramphenicol at 15 µg/ml (LBG+CM15 medium) in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384
10 well culture dishes. Each well contained 100µl of LBG + CM15 liquid medium. Inoculated 384 well dishes were incubated 16 hours at 37°C, and each well was robotically gridded onto solid LBG + CM15 medium with or without 2% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

15 Arrayed colonies that were growth-sensitive on medium containing 2% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing LBG + CM15, and were incubated for 16 hours at 37°C. These cultures
20 were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media containing 2% xylose or media lacking xylose. After growth for 16 hours at 37°C, the arrays that resulted on the two media were compared to each other. Clones that grew similarly at all dilutions on both media were scored as a
25 negative and were no longer considered. Clones that grew on xylose medium but failed to grow at the same serial dilution on the non-xylose plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the xylose plate and grow at a serial dilution of 10^8 or less on the non-xylose plate, then the corresponding clone received a score of "4" representing the log difference in
30 growth observed.

For *Salmonella typhimurium* and *Klebsiella pneumoniae* growth curves were carried out by back diluting cultures 1:200 into fresh media containing 1 mM IPTG or media lacking IPTG and measuring the OD₄₅₀ every 30 minutes (min). To study the effects of transcriptional induction on solid medium, 10², 10³, 10⁴, 10⁵, 10⁶, 10⁷ and 10⁸ fold dilutions of overnight cultures were prepared. Aliquots of from 0.5 to 3 µl of these dilutions were spotted on selective agar plates with or without 1 mM IPTG. After overnight incubation, the plates were compared to assess the sensitivity of the clones to IPTG.

Nucleic acids involved in proliferation of *Pseudomonas aeruginosa* were identified as follows. Randomly generated fragments of *Pseudomonas aeruginosa* genomic DNA were transcribed from a two-component inducible promoter system. Integrated on the chromosome was the T7 RNA polymerase gene regulated by *lacUV5/ lacO* (Brunschwig, E. and Darzins, A. 1992. Gene 111:35-41). On an expression plasmid there was a T7 gene 10 promoter, which is transcribed by T7 RNA polymerase, fused with a *lacO* operator followed by a multiple cloning site. Transcription from this hybrid promoter is inducible by IPTG. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of an mRNA encoding a gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *Pseudomonas aeruginosa* genomic fragments was cloned into the vectors pEP5, pEP5S, or other similarly constructed vectors which harbor the T7/*lacO* inducible promoter. The vector was linearized at a unique *Sma*I site immediately downstream of the T7/*lacO* promoter/operator. The linearized vector was treated with shrimp alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *Pseudomonas aeruginosa* strain PAO1 was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain XL1-Blue MRF' (Stratagene) and plated on LB medium with carbenicillin at 100 µg/ml or Streptomycin 100 µg/ml. Resulting colonies numbering 5×10^5 or greater were scraped and combined, and were then subjected to plasmid purification.

5 The purified library was then transformed into electrocompetent *Pseudomonas aeruginosa* strain PAO1. Resulting transformants were plated on LB agar with carbenicillin at 100 µg/ml or Streptomycin 40 µg/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384 well culture dishes. Each well contained 100 µl of LB +
10 CB 100 or Streptomycin 40 liquid medium. Inoculated 384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid LB + CB100 or Streptomycin 40 medium with or without 1 mM IPTG. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of IPTG.

15 Arrayed colonies that were growth-sensitive on medium containing 1 mM IPTG, yet were able to grow on similar medium lacking IPTG, were subjected to further growth sensitivity analysis as follows: Colonies from the plate lacking IPTG were manually picked and inoculated into individual wells of a 96 well culture dish containing LB + CB100 or Streptomycin 40, and were incubated for 16 hours at 30°C.
20 These cultures were robotically diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilutions in a 384 well array and then gridded onto media with and without 1 mM IPTG. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Clones that grew similarly at all dilutions on both
25 media were scored as a negative and were no longer considered. Clones that grew on IPTG medium but failed to grow at the same serial dilution on the non-IPTG plate were given a score based on the differential, i.e. should the clone grow at a serial dilution of 10^4 or less on the IPTG plate and grow at a serial dilution of 10^8 or less on the IPTG plate, then the corresponding clone received a score of "4" representing the
30 log difference in growth observed.

Following the identification of those vectors that, upon induction, negatively impacted *Pseudomonas aeruginosa* growth or proliferation, the inserts or nucleic acid fragments contained in those vectors were isolated for subsequent characterization. Vectors of interest were subjected to nucleic acid sequence determination.

5 Nucleic acids involved in proliferation of *E. faecalis* were identified as follows. Randomly generated fragments of genomic DNA were expressed from the vectors pEPEF3 or pEPEF14, which contain the CP25 or P59 promoter, respectively, regulated by the xyl operator/repressor. Should the genomic DNA downstream of the promoter contain, in an antisense orientation, at least a portion of a mRNA encoding a
10 gene product involved in proliferation, then induction of expression from the promoter will result in detectable inhibition of proliferation.

A shotgun library of *E. faecalis* genomic fragments was cloned into the vector pEPEF3 or pEPEF14, which harbor xylose inducible promoters. The vector was linearized at a unique *Sma*I site immediately downstream of the promoter/operator.
15 The linearized vector was treated with alkaline phosphatase to prevent reclosure of the linearized ends. Genomic DNA isolated from *E. faecalis* strain OG1RF was partially digested with DNase I and "blunt-ended" by incubating with T4 DNA polymerase. Random genomic fragments between 200 and 800 base pairs in length were selected by gel purification. The size-selected genomic fragments were added to the linearized
20 and dephosphorylated vector at a molar ratio of 2 to 1, and ligated to form a shotgun library.

The ligated products were transformed into electrocompetent *E. coli* strain TOP10 cells (Invitrogen) and plated on LB medium with erythromycin (Erm) at 150 μ g/ml. Resulting colonies numbering 5×10^5 or greater were scraped and combined,
25 and were then subjected to plasmid purification.

The purified library was then transformed into electrocompetent *E. faecalis* strain OG1RF. Resulting transformants were plated on Todd-Hewitt (TH) agar with erythromycin at 10 μ g/ml in order to generate 100 to 150 platings at 500 colonies per plating. The colonies were subjected to robotic picking and arrayed into wells of 384
30 well culture dishes. Each well contained 100 μ l of THB + Erm 10 μ g/ml. Inoculated

384 well dishes were incubated 16 hours at room temperature, and each well was robotically gridded onto solid TH agar + Erm with or without 5% xylose. Gridded plates were incubated 16 hours at 37°C, and then manually scored for arrayed colonies that were growth-compromised in the presence of xylose.

5 Arrayed colonies that were growth-sensitive on medium containing 5% xylose, yet were able to grow on similar medium lacking xylose, were subjected to further growth sensitivity analysis. Colonies from the plate lacking xylose were manually picked and inoculated into individual wells of a 96 well culture dish containing THB + Erm 10, and were incubated for 16 hours at 30°C. These cultures were robotically
10 diluted 1/100 into fresh medium and allowed to incubate for 4 hours at 37°C, after which they were subjected to serial dilution on plates containing 5% xylose or plates lacking xylose. After growth for 16 hours at 37°C, the arrays of serially diluted spots that resulted were compared between the two media. Colonies that grew similarly on both media were scored as a negative and corresponding colonies were no longer
15 considered. Colonies on xylose medium that failed to grow to the same serial dilution compared to those on the non-xylose plate were given a score based on the differential. For example, colonies on xylose medium that only grow to a serial dilution of -4 while they were able to grow to -8 on the non-xylose plate, then the corresponding transformant colony received a score of "4" representing the log
20 difference in growth observed.

 Following the identification of those vectors that, upon induction, negatively impacted *E. faecalis* growth or proliferation, the inserts or nucleic acid fragments contained in those expression vectors were isolated for subsequent characterization. The inserts in the vectors of interest were subjected to nucleotide sequence
25 determination.

 It will be appreciated that other restriction enzymes and other endonucleases or methodologies may be used to generate random genomic fragments. In addition, random genomic fragments may be generated by mechanical shearing. Sonication and nebulization are two such techniques commonly used for mechanical shearing of
30 DNA.

EXAMPLE 2

Nucleotide Sequence Determination of Identified Clones Transcribing Nucleic Acid
Fragments with Detrimental Effects on Proliferation of *Escherichia coli*,
Staphylococcus aureus, *Salmonella typhimurium*, *Klebsiella pneumoniae*,
5 *Pseudomonas aeruginosa* or *Enterococcus faecalis*

The nucleotide sequences of the nucleic acid sequences which inhibited the growth of *Escherichia coli* were determined using plasmid DNA isolated using QIAPREP (Qiagen, Valencia, CA) and methods supplied by the manufacturer. The primers used for sequencing the inserts were 5' - TGTTTATCAGACCGCTT - 3' (SEQ ID NO: 15781) and 5' - ACAATTTACACAGCCTC - 3' (SEQ ID NO: 15782).
10 These sequences flank the polylinker in pLEX5BA.

The nucleotide sequences of the nucleic acid sequences which inhibited the growth of *Staphylococcus aureus* were determined as follows. *Staphylococcus aureus* were grown in standard laboratory media (LB or TB with 15 ug/ml Chloramphenicol to select for the plasmid). Growth was carried out at 37°C overnight in culture tubes
15 or 2 ml deep well microtiter plates.

Lysis of *Staphylococcus aureus* was performed as follows. Cultures (2-5 ml) were centrifuged and the cell pellets resuspended in 1.5 mg/ml solution of lysostaphin (20 µl/ml of original culture) followed by addition of 250 µl of resuspension buffer (Qiagen). Alternatively, cell pellets were resuspended directly in 250 µl of
20 resuspension buffer (Qiagen) to which 5-20 µl of a 1 mg/ml lysostaphin solution were added.

DNA was isolated using Qiagen miniprep kits or Wizard (Qiagen) miniprep kits according to the instructions provided by the manufacturer.

25 The genomic DNA inserts were amplified from the purified plasmids by PCR as follows.

1 µl of Qiagen purified plasmid was put into a total reaction volume of 25 µl Qiagen Hot Start PCR mix. For *Staphylococcus aureus*, the following primers were used in the PCR reaction:

30 pXylT5F: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 15783)

LexL TGTTTTATCAGACCGCTT (SEQ ID NO: 15784)

Similar methods were conducted for *Salmonella typhimurium* and *Klebsiella pneumoniae*. For *Salmonella typhimurium* and *Klebsiella pneumoniae* the following primers were used:

- 5 5' - TGTTTTATCAGACCGCTT - 3' (SEQ ID NO: 15784) and
5'-ACAATTCACACAGCCTC-3' (SEQ ID NO: 15782)

PCR was carried out in a PE GenAmp with the following cycle times:

- Step 1. 95° C 15 min
Step 2. 94° C 45 sec
10 Step 3. 54° C 45 sec
Step 4. 72° C 1 minute
Step 5. Return to step 2, 29 times
Step 6. 72° C 10 minutes
Step 7. 4° C hold

- 15 The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

- For *Pseudomonas aeruginosa*, plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *Pseudomonas aeruginosa*
20 were grown in standard laboratory media (LB with carbenicillin at 100 µg/ml or Streptomycin 40 µg/ml to select for the plasmid). Growth was carried out at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 ul Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. For plasmid pEP5S the following primers were used in the PCR
25 reaction:

T7L1+: GTCGGCGATATAGGCGCCAGCAACCG (SEQ ID NO: 15785)

pStrA3: ATAATCGAGCATGAGTATCATACG (SEQ ID NO: 15786)

PCR was carried out in a PE GenAmp with the following cycle times:

- Step 1. 95° C 15 min
30 Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

Step 6. 72° C 10 minutes

5 Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the sequencing reaction:

10 T7/L2: ATGCGTCCGGCGTAGAGGAT (SEQ ID NO: 15787)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

Step 3. 50° C 5 sec

15 Step 4. 60 C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

20 For *E. faecalis*, plasmids from transformant colonies that received a dilution plating score of "2" or greater were isolated to obtain the genomic DNA insert responsible for growth inhibition as follows. *E. faecalis* were grown in THB 10 µg/ml Erm at 30°C overnight in 100 ul culture wells in microtiter plates. To amplify insert DNA 2 ul of culture were placed into 25 µl Qiagen Hot Start PCR mix. PCR reactions were in 96 well microtiter plates. The following primers were used in the PCR reaction:

25 pXyIT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 15783) and the pEP/pAK1 primer.

PCR was carried out in a PE GenAmp with the following cycle times:

30 Step 1. 95° C 15 min

Step 2. 94° C 45 sec

Step 3. 54° C 45 sec

Step 4. 72° C 1 minute

Step 5. Return to step 2, 29 times

5 Step 6. 72° C 10 minutes

Step 7. 4° C hold

The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

10 The purified PCR products were then directly cycle sequenced with Qiagen Hot Start PCR mix. The following primers were used in the PCR reaction:

pXyIT5: CAGCAGTCTGAGTTATAAAATAG (SEQ ID NO: 15783)

PCR was carried out in a PE GenAmp with the following cycle times:

Step 1. 94° C 15 min

Step 2. 96° C 10 sec

15 Step 3. 50° C 5 sec

Step 4. 60° C 4 min

Step 5. Return to step 2, 24 times

Step 6. 4° C hold

20 The PCR products were cleaned using Qiagen Qiaquick PCR plates according to the manufacturer's instructions.

The amplified genomic DNA inserts from each of the above procedures were subjected to automated sequencing. The nucleotide sequences of the antisense nucleic acids which inhibited the proliferation of *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and
25 *Enterococcus faecalis* are listed in the accompanying Sequence Listing as SEQ ID NOs.: 8-3795.

EXAMPLE 3

Comparison Of Isolated Nucleic Acids to Known Sequences

30 The nucleic acid sequences of the subcloned *E. coli* genomic fragments obtained from the vectors discussed above were compared to known *E. coli* sequences in

GenBank using BLAST version 1.4 or version 2.0.6 using the following default parameters: Filtering off, cost to open a gap=5, cost to extend a gap=2, penalty for a mismatch in the blast portion of run=3, reward for a match in the blast portion of run=1, expectation value (e)=10.0, word size=11, number of one-line descriptions=100, number of alignments to show (B)=100. BLAST is described in Altschul, J Mol Biol. 215:403-10 (1990), the disclosure of which is incorporated herein by reference in its entirety. The vectors were found to contain nucleic acid sequences in both the sense and antisense orientations. The presence of known genes, open reading frames, and ribosome binding sites was determined by comparison to public databases holding genetic information and various computer programs such as the Genetics Computer Group programs FRAMES and CODONPREFERENCE. Clones were designated as "antisense" if the cloned fragment was oriented to the promoter such that the RNA transcript produced was complementary to the expressed mRNA (or non-translated RNA) from a chromosomal locus. Clones were designated as "sense" if they coded for an RNA fragment that was identical to a portion of a wild type mRNA from a chromosomal locus.

The nucleotide sequences of the subcloned fragments from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* obtained from the expression vectors discussed above were compared to known sequences from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* and other microorganisms as follows. First, to confirm that each clone originated from one location on the chromosome and was not chimeric, the nucleotide sequences of the selected clones were compared against the *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* genomic sequences to align the clone to the correct position on the chromosome. The NCBI BLASTN v 2.0.9 program was used for this comparison, and the incomplete *Staphylococcus aureus* genomic sequences licensed from TIGR, as well as the NCBI nonredundant GenBank database were used as the source of genomic data. *Salmonella typhimurium* sequences were compared to sequences available from the Genome Sequencing Center

(<http://genome.wustl.edu/gsc/salmonella.shtml>), and the Sanger Centre (http://www.sanger.ac.uk/projects/S__typhi). *Pseudomonas aeruginosa* sequences were compared to a proprietary database and the NCBI GenBank database. The *E. faecalis* sequences were compared to a proprietary database.

5 The BLASTN analysis was performed using the default parameters except that the filtering was turned off. No further analysis was performed on inserts which resulted from the ligation of multiple fragments.

 In general, antisense molecules and their complementary genes are identified as follows. First, all possible full length open reading frames (ORFs) are extracted
10 from available genomic databases. Such databases include the GenBank nonredundant (nr) database, the unfinished genome database available from TIGR and the PathoSeq database developed by Incyte Genomics. The latter database comprises over 40 annotated bacterial genomes including complete ORF analysis. If databases are incomplete with regard to the bacterial genome of interest, it is not necessary to
15 extract all ORFs in the genome but only to extract the ORFs within the portions of the available genomic sequences which are complementary to the clones of interest. Computer algorithms for identifying ORFs, such as GeneMark, are available and well known to those in the art. Comparison of the clone DNA to the complementary ORF(s) allows determination of whether the clone is a sense or antisense clone.
20 Furthermore, each ORF extracted from the database can be compared to sequences in well annotated databases including the GenBank (nr) protein database, SWISSPROT and the like. A description of the gene or of a closely related gene in a closely related microorganism is often available in these databases. Similar methods are used to identify antisense clones corresponding to genes encoding non-translated RNAs.

25 Each of the cloned nucleic acid sequences discussed above which inhibited proliferation of *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* was used to identify the corresponding *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* ORFs in the
30 PathoSeq v.4.1 (March 2000 release) database of microbial genomic sequences. For

this purpose, the NCBI BLASTN 2.0.9 computer algorithm was used. The default parameters were used except that filtering was turned off. The default parameters for the BLASTN and BLASTX analyses were:

```

Expectation value (e)=10
5   Alignment view options: pairwise
   Filter query sequence (DUST with BLASTN, SEG with others)=T
   Cost to open a gap (zero invokes behavior)=0
   Cost to extend a gap (zero invokes behavior)=0
   X dropoff value for gapped alignment (in bits) (zero invokes behavior)=0
10  Show GI's in defines=F
   Penalty for a nucleotide mismatch (BLASTN only)=-3
   Reward for a nucleotide match (BLASTN only)=1
   Number of one-line descriptions (V)=500
   Number of alignments to show (B)=250
15  Threshold for extending hits=default
   Perform gapped alignment (not available with BLASTX)=T
   Query Genetic code to use=1
   DB Genetic code (for TBLAST[nx] only)=1
   Number of processors to use=1
20  SeqAlign file
   Believe the query define=F
   Matrix=BLOSUM62
   Word Size= default
   Effective length of the database (use zero for the real size)=0
25  Number of best hits from a region to keep=100
   Length of region used to judge hits=20
   Effective length of the search space (use zero for the real size)=0
   Query strands to search against database (for BLAST[nx] and TBLASTX), 3 is
both, 1 is top, 2 is bottom=3
30  Produce HTML output=F

```

Alternatively, ORFs were identified and refined by conducting a survey of the public and private data sources. Full-length gene protein and nucleotide sequences for these organisms were assembled from various sources. For *Pseudomonas aeruginosa*, gene sequences were adopted from the Pseudomonas genome sequencing project (downloaded from <http://www.pseudomonas.com>). For *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*, genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the

gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W., Suite B, Atlanta, GA, 30318, USA.

Antisense clones were identified as those clones for which transcription from the inducible promoter would result in the expression of an RNA antisense to a complementary ORF, intergenic or intragenic sequence.

It will be appreciated that ORFs may also be identified using databases other than PathoSeq. For example, the ORFs may be identified using the methods described in U.S. Provisional Patent Application Serial Number 60/191,078, filed March 21, 2000, the disclosure of which is incorporated herein by reference in its entirety.

The ORFs which correspond to the antisense nucleic acids which inhibited proliferation of *Escherichia coli*, *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* or *Enterococcus faecalis* are listed in the accompanying Sequence Listing as SEQ ID NOs.: 3796-3800, 3806-4860, and 5916-10012. The polypeptides encoded by the identified ORFs are provided in the accompanying Sequence Listing as SEQ ID NOs.: 3801-3805, 4861-5915, and 10013-14110.

In other embodiments, the culture comprises a strain in which a gene product encoded by a homologous coding nucleic acid as defined above is overexpressed or underexpressed. In further embodiments, the culture comprises a strain in which a homologous polypeptide as defined above is overexpressed or underexpressed.

Homologous coding nucleic acids may be obtained as described in Example 4 below.

EXAMPLE 4

Identification of Homologous Coding Nucleic Acids, Homologous Antisense Nucleic Acids or Homologous Polypeptides

Homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from other pathogenic microorganisms (including nucleic acids homologous to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids homologous to the antisense nucleic acids of SEQ ID NOs.: 8-3795, and polypeptides homologous to the polypeptides of SEQ ID

NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778) may be identified using methods such as those described below.

For example, in some embodiments, the proliferation-required nucleic acids, antisense nucleic acids, and polypeptides from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi*, or *Candida albicans* described herein (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, the antisense nucleic acids of SEQ ID NOs.: 8-3795, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778) may be used to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides required for proliferation in prokaryotes and eukaryotes. For example, nucleic acids or polypeptides required for the proliferation of protists, such as *Plasmodium* spp.; plants; animals, such as *Entamoeba* spp. and *Contracaecum* spp; and fungi including *Candida* spp., (e.g., *Candida albicans*), *Cryptococcus neoformans*, and *Aspergillus fumigatus* may be identified. In one embodiment of the present invention, monera, specifically bacteria, including both Gram positive and Gram negative bacteria, are probed to identify genes required for cellular proliferation. Likewise, homologous antisense nucleic acids may also be identified.

The genes and polypeptides required for the proliferation of *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi*, or *Candida albicans* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, the sequences complementary to the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, and the polypeptides of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778) can be used to identify

homologous coding nucleic acids or homologous polypeptides required for proliferation from these and other organisms using methods such as nucleic acid hybridization and computer database analysis. Likewise, the antisense nucleic acids which inhibit proliferation of *Staphylococcus aureus*, *Salmonella typhimurium*,
 5 *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, or *Salmonella typhi* (including the antisense nucleic acids of SEQ ID NOs.: 8-3795 or the sequences complementary thereto) may also be used to identify homologous antisense
 10 nucleic acids using nucleic acid hybridization or computer database analysis.

For example, the nucleic acid sequences from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*,
 15 *Staphylococcus aureus*, *Salmonella typhi*, or *Candida albicans* (including the nucleic acids of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and the antisense nucleic acids of SEQ ID NOs. 8-3795) are used to screen genomic libraries generated from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*,
 20 *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi*, or *Candida albicans* and other bacterial or fungal species of interest. For example, the genomic library may be from Gram positive bacteria, Gram negative bacteria or other organisms including *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*,
 25 *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,
 30

Cryptococcus neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*,
Enterococcus faecium, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*,
Histoplasma capsulatum, *Klebsiella pneumoniae*, *Listeria monocytogenes*,
Mycobacterium leprae, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*,
5 *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella*
multocida, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*,
Salmonella bongori, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella*
paratyphi, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*,
Moxarella catarrhalis, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*,
10 *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*,
Streptococcus mutans, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis*
or any species falling within the genera of any of the above species, including
coagulase negative species of *Staphylococcus*. In some embodiments, the genomic
library may be from an organism other than *E. coli*.

15 Standard molecular biology techniques are used to generate genomic libraries
from various cells or microorganisms. In one aspect, the libraries are generated and
bound to nitrocellulose paper. The nucleic acids of SEQ ID NOs. 3796-3800, 3806-
4860, 5916-10012, and 14111-14944 or SEQ ID NOs.: 8-3795, or portions thereof, can
then be used as probes to screen the libraries for homologous sequences.

20 For example, the libraries may be screened to identify homologous coding
nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences
which hybridize under stringent conditions to a nucleic acid selected from the group
consisting of SEQ ID NOs.: 8-3795, nucleic acids comprising nucleotide sequences
which hybridize under stringent conditions to a fragment comprising at least 10, 15,
25 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of
one of SEQ ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which
hybridize under stringent conditions to a nucleic acid complementary to one of SEQ
ID NOs. 8-3795, nucleic acids comprising nucleotide sequences which hybridize
under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40,
30 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence

complementary to one of SEQ ID NOS. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, and nucleic acids comprising nucleotide sequences which hybridize under stringent conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944.

The libraries may also be screened to identify homologous nucleic coding nucleic acids or homologous antisense nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid complementary to one of SEQ ID NOS. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40,

50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS. 8-3795, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and
5 14111-14944, nucleic acids comprising nucleic acid sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a nucleic acid
10 complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 and nucleic acids comprising nucleotide sequences which hybridize under moderate conditions to a fragment comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of the sequence complementary to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and
15 14111-14944.

The homologous nucleic coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides identified as above can then be used in the methods described herein. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides may be used to
20 identify genes which are required for the proliferation of more than one microorganism. Such genes are valuable targets for broad spectrum antibiotics effective against more than one microorganism.

For example, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide
25 sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 8-3795, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. The
30 preceding methods may also be used to isolate homologous coding nucleic acids or

homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleotide sequence selected from the group consisting of one of the nucleotide sequences of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. In some embodiments, the preceding methods may be used to isolate homologous coding nucleic acids or homologous antisense nucleic acids comprising a nucleotide sequence with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid sequence selected from the group consisting of one of the sequences of SEQ ID NOS. 3796-3800, 3806-4860, 5916-10012, and 14111-14944, fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, and the sequences complementary thereto. Identity may be measured using BLASTN version 2.0 with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety). For example, the homologous polynucleotides may comprise a coding sequence which is a naturally occurring allelic variant of one of the coding sequences described herein. Such allelic variants may have a substitution, deletion or addition of one or more nucleotides when compared to the nucleic acids of SEQ ID NOS: 8-3795, SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 or the nucleotide sequences complementary thereto.

Additionally, the above procedures may be used to isolate homologous coding nucleic acids which encode polypeptides having at least 99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid identity or similarity to a polypeptide comprising the sequence of one of SEQ ID NOS: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 or to a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOS: 8-3795 or fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or

150 consecutive amino acids thereof as determined using the FASTA version 3.0t78 algorithm with the default parameters. Alternatively, protein identity or similarity may be identified using BLASTP with the default parameters, BLASTX with the default parameters, or TBLASTN with the default parameters. (Altschul, S.F. et al. Gapped BLAST and PSI-BLAST: A New Generation of Protein Database Search Programs, Nucleic Acid Res. 25: 3389-3402 (1997), the disclosure of which is incorporated herein by reference in its entirety).

Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides may be identified by searching a database to identify sequences having a desired level of nucleotide or amino acid sequence homology to a nucleic acid or polypeptide involved in proliferation or an antisense nucleic acid to a nucleic acid involved in microbial proliferation. A variety of such databases are available to those skilled in the art, including GenBank and GenSeq. In some embodiments, the databases are screened to identify nucleic acids with at least 97%, at least 95%, at least 90%, at least 85%, at least 80%, or at least 70% nucleotide sequence identity to a nucleic acid required for proliferation, an antisense nucleic acid which inhibits proliferation, or a portion of a nucleic acid required for proliferation or a portion of an antisense nucleic acid which inhibits proliferation. For example, homologous coding sequences may be identified by using a database to identify nucleic acids homologous to one of SEQ ID Nos. 8-3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof, nucleic acids homologous to one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides of one of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, nucleic acids homologous to one of SEQ ID Nos. 8-3795, homologous to fragments comprising at least 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, 150, 200, 300, 400, or 500 consecutive nucleotides thereof or nucleic acids homologous to the sequences complementary to any of the preceding nucleic acids. In other embodiments, the databases are screened to identify polypeptides having at least

99%, 95%, at least 90%, at least 85%, at least 80%, at least 70%, at least 60%, at least 50%, at least 40% or at least 25% amino acid sequence identity or similarity to a polypeptide involved in proliferation or a portion thereof. For example, the database may be screened to identify polypeptides homologous to a polypeptide comprising one of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778, a polypeptide whose expression is inhibited by a nucleic acid of one of SEQ ID NOs: 8-3795 or homologous to fragments comprising at least 5, 10, 15, 20, 25, 30, 35, 40, 50, 75, 100, or 150 consecutive amino acids of any of the preceding polypeptides. In some embodiments, the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from cells or microorganisms other than the *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, or *Salmonella typhi* species from which they were obtained. For example the database may be screened to identify homologous coding nucleic acids, homologous antisense nucleic acids or homologous polypeptides from microorganisms such as *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*,

Pseudomonas aeruginosa, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species, including coagulase negative *Staphylococcus*. In some embodiments, the homologous coding nucleic acids, homologous antisense nucleic acids, or homologous polypeptides are from an organism other than *E. coli*.

In another embodiment, nucleic acid arrays and microarrays can be employed to identify homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides. Nucleic acid arrays are high density arrays of DNA samples deposited at specific locations on a glass chip, nylon membrane, or the like. An example of this technology is found in U.S. Patent No. 5807522, which is hereby incorporated by reference. In such embodiments, an array comprising nucleic acids from an organism in which it is desired to identify a homologous coding nucleic acid, homologous antisense nucleic acid or nucleic acid encoding a homologous polypeptide is contacted with a detectable probe comprising the nucleic acid, or a portion thereof, for which it is desired to identify a homologue under conditions which permit the probe to specifically hybridize to the homologue. For example, the arrays may consist of 12 x 24 cm nylon filters containing PCR products corresponding to ORFs from the organism in which it is desired to identify the homologous nucleic acid. For example, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified in *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium*

botulinum, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
Corynebacterium diphtheriae, *Cryptococcus neoformans*, *Enterobacter cloacae*,
Enterococcus faecalis, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus*
influenzae, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*,
5 *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*,
Neisseria gonorrhoeae, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella*
haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*,
Pseudomonas aeruginosa, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella*
enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*,
10 *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*,
Shigella flexneri, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus*
pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*,
Yersinia pestis or any species falling within the genera of any of the above species,
including coagulase negative *Staphylococcus*.

15 Alternatively, homologous coding nucleic acids, homologous antisense nucleic
acids or nucleic acids encoding homologous polypeptides can be identified by
transcribing an antisense nucleic acid comprising a nucleotide sequence complementary
to the proliferation-required sequences from *Staphylococcus aureus*, *Salmonella*
typhimurium, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus*
20 *faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*,
Helicobacter pylori, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*,
Staphylococcus aureus, or *Salmonella typhi* or a portion thereof in a heterologous cell
or microorganism and determining whether the antisense nucleic acid inhibits the
proliferation of the cell or microorganism.

25 Alternatively, homologous coding nucleic acids, homologous antisense nucleic
acids or nucleic acids encoding homologous polypeptides can be identified by
transcribing a homologous antisense nucleic acid such as an antisense nucleic acid
homologous to the nucleotide sequence complementary to one of SEQ ID NOs.: 3796-
3800, 3806-4860, 5916-10012, and 14111-14944, an antisense nucleic acid comprising
30 a nucleotide sequence homologous to one of SEQ ID Nos.: 8-3795, or an antisense

nucleic acid comprising a nucleotide sequence complementary to a portion of any of the preceding nucleic acids in a microorganism, such as the microorganism in which the homologous antisense nucleic acid was identified, and determining whether the proliferation of the microorganism is inhibited as described above.

5 In another embodiment, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides can be identified by using the conserved portions of nucleotide sequences required for proliferation to generate degenerate primers for use in the polymerase chain reaction (PCR). The PCR technique is well known in the art. The successful production of a
10 PCR product using degenerate probes generated from the nucleotide sequences identified herein indicates the presence of a homologous gene sequence in the species being screened. This homologous gene is then utilized in the present invention.

 The nucleic acids homologous to the genes required for the proliferation of *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*,
15 *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi* or *Candida albicans* or the sequences complementary thereto may be used to identify homologous coding nucleic acids, nucleic acids encoding homologous polypeptides, or
20 homologous antisense nucleic acids from cells or microorganisms other than *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi* or *Candida albicans* as described below. For example, the nucleic acids homologous to
25 proliferation-required genes from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi* or *Candida albicans* or the sequences complementary thereto may be used to
30

identify homologous coding nucleic acids, homologous antisense nucleic acids or
 nucleic acids encoding homologous polypeptides in *Anaplasma marginale*,
Aspergillus fumigatus, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*,
Burkholderia cepacia, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata*
 5 (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida*
guilliermondii, *Candida krusei*, *Candida kefyr* (also called *Candida*
pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia*
trachomatis, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
Coccidioides immitis, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
 10 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*,
Haemophilus influenzae, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella*
pneumoniae, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium*
tuberculosis, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*,
Pasteurella haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus*
 15 *vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*,
Salmonella enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
typhimurium, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella*
dysenteriae, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
Streptococcus pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia*
 20 *enterocolitica*, *Yersinia pestis* and any species falling within the genera of any of the
 above species. In some embodiments of the present invention, the nucleic acids
 homologous to proliferation-required sequences from *Staphylococcus aureus*,
Salmonella typhimurium, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and
Enterococcus faecalis, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus*
 25 *influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*,
Staphylococcus aureus, or *Salmonella typhi* (including nucleic acids homologous to
 one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944) or the
 sequences complementary thereto (including nucleic acids homologous to one of SEQ
 ID NOs.: 8-3795) are used to identify proliferation-required sequences in an organism
 30 other than *E. coli*.

In another embodiment of the present invention, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides are identified by transferring antisense nucleic acids complementary to the sequences identified as required for proliferation or portions thereof (including antisense nucleic acids comprising a nucleotide sequence complementary to one of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 or portions thereof, such as the nucleic acids of SEQ ID NOs.: 8-3795) to vectors capable of functioning within a species other than the species from which the sequences were obtained. For example, the vector may be functional in *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the vector may be functional in an organism other than *E. coli*. As would be appreciated by one of ordinary skill in the art, vectors may contain certain elements that are species specific.

These elements can include promoter sequences, operator sequences, repressor genes, origins of replication, ribosomal binding sequences, termination sequences, and others. To use the antisense nucleic acids, one of ordinary skill in the art would know to use standard molecular biology techniques to isolate vectors containing the sequences of interest from cultured bacterial cells, isolate and purify those sequences, and subclone those sequences into a vector adapted for use in the species of bacteria to be screened.

Vectors for a variety of other species are known in the art. For example, numerous vectors which function in *E. coli* are known in the art. Also, Pla et al. have reported an expression vector that is functional in a number of relevant hosts including: *Salmonella typhimurium*, *Pseudomonas putida*, and *Pseudomonas aeruginosa*. J. Bacteriol. 172(8):4448-55 (1990). Brunschwig and Darzins (Gene (1992) 111:35-4, the disclosure of which is incorporated herein by reference in its entirety) described a shuttle expression vector for *Pseudomonas aeruginosa*. Similarly many examples exist of expression vectors that are freely transferable among various Gram-positive microorganisms. Expression vectors for *Enterococcus faecalis* may be engineered by incorporating suitable promoters into a pAK80 backbone (Israelsen, H., S. M. Madsen, A. Vrang, E. B. Hansen and E. Johansen. 1995. Appl. Environ. Microbiol. 61:2540-2547, the disclosure of which is incorporated herein by reference in its entirety).

Following the subcloning of the antisense nucleic acids complementary to proliferation-required sequences from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi*, or *Candida albicans* or portions thereof into a vector functional in a second cell or microorganism of interest (i.e. a cell or microorganism other than the one from which the identified nucleic acids were obtained), the antisense nucleic acids are conditionally transcribed to test for bacterial growth inhibition. The nucleotide sequences of the nucleic acids from *Staphylococcus*

aureus, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*,
Enterococcus faecalis, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus*
influenzae, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* that, when
transcribed, inhibit growth of the second cell or microorganism are compared to the
5 known genomic sequence of the second cell or microorganism to identify the
homologous gene from the second organism. If the homologous sequence from the
second cell or microorganism is not known, it may be identified and isolated by
hybridization to the proliferation-required *Staphylococcus aureus*, *Salmonella*
typhimurium, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus*
10 *faecalis* *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*,
Helicobacter pylori, *Salmonella typhi* or *Candida albicans* sequence of interest or by
amplification using PCR primers based on the proliferation-required nucleotide
sequence of interest as described above. In this way, sequences which may be required
for the proliferation of the second cell or microorganism may be identified. For
15 example, the second microorganism may be *Anaplasma marginale*, *Aspergillus*
fumigatus, *Bacillus anthracis*, *Bacterioides fragilis* *Bordetella pertussis*, *Burkholderia*
cepacia, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called
Torulopsis glabrata), *Candida tropicalis*, *Candida parapsilosis*, *Candida*
guilliermondii, *Candida krusei*, *Candida kefyr* (also called *Candida*
20 *pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia*
trachomatis, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
Coccidioides immitis, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
Enterobacter cloacae, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*,
Haemophilus influenzae, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella*
25 *pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium*
tuberculosis, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*,
Pasteurella haemolytica, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus*
vulgaris, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*,
Salmonella enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
30 *typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella*

dysenteriae, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments of the present invention, the second

5 microorganism is an organism other than *E. coli*.

The homologous nucleic acid sequences from the second cell or microorganism which are identified as described above may then be operably linked to a promoter, such as an inducible promoter, in an antisense orientation and introduced into the second cell or microorganism. The techniques described herein for

10 identifying *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa* and *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Salmonella typhi* or *Candida albicans* genes required for proliferation may thus be employed to determine whether

15 the identified nucleotide sequences from a second cell or microorganism inhibit the proliferation of the second cell or microorganism. For example, the second microorganism may be *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*,

20 *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*,

25 *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*,

30 *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella*

enterica, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*,
Staphylococcus aureus, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*,
Shigella flexneri, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus*
pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*,
5 *Yersinia pestis* or any species falling within the genera of any of the above species. In
some embodiments of the present invention, the second microorganism may be an
organism other than *E. coli*.

Antisense nucleic acids required for the proliferation of microorganisms other
than *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*,
10 *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus*
faecalis, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida*
albicans or the genes corresponding thereto, may also be hybridized to a microarray
containing the *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella*
pneumoniae, *Pseudomonas aeruginosa*, *Enterococcus faecalis* *Escherichia coli*,
15 *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella*
typhi, or *Candida albicans* ORFs (including the nucleic acids of SEQ ID NOs.: 3796-
3800, 3806-4860, 5916-10012, and 14111-14944) to gauge the homology between the
Staphylococcus aureus, *Salmonella typhimurium*, *Klebsiella pneumoniae*,
Pseudomonas aeruginosa, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus*
20 *faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida*
albicans sequences and the proliferation-required nucleic acids from other cells or
microorganisms. For example, the proliferation-required nucleic acid may be from
Anaplasma marginale, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*
Bordetella pertussis, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*,
25 *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida*
parapsilosis, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called
Candida pseudotropicalis), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia*
trachomatis, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*,
Coccidioides immitis, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*,
30 *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*,

Haemophilus influenzae, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. In some embodiments, the proliferation-required nucleotide sequences from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* or homologous nucleic acids are used to identify proliferation-required sequences in an organism other than *E. coli*. In some embodiments of the present invention, the proliferation-required sequences may be from an organism other than *E. coli*. The proliferation-required nucleic acids from a cell or microorganism other than *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* may be hybridized to the array under a variety of conditions which permit hybridization to occur when the probe has different levels of homology to the nucleotide sequence on the microarray. This would provide an indication of homology across the cells or microorganisms as well as clues to other possible essential genes in these cells or microorganisms.

EXAMPLE 5**Identification of Nucleic Acids Homologous to Nucleic Acids Required for the
Proliferation of *E. coli* in other Bacterial Species**

Homologous coding nucleic acids, homologous antisense nucleic acids or
 5 nucleic acids encoding homologous polypeptides may be identified as follows. The
 ability of an antisense molecule identified in a first organism to inhibit the
 proliferation of a second organism (thereby confirming that a gene in the second
 organism which is homologous to the gene from the first organism is required for
 proliferation of the second organism) was demonstrated using some of the antisense
 10 nucleic acids which inhibit the growth of *E. coli*. Expression vectors which inhibited
 growth of *E. coli* upon induction of antisense RNA expression with IPTG were
 transformed directly into *Enterobacter cloacae*, *Klebsiella pneumonia* or *Salmonella*
typhimurium. The transformed cells were then assayed for growth inhibition
 according to the methods described above. After growth in liquid culture, cells were
 15 plated at various serial dilutions and a score determined by calculating the log
 difference in growth for INDUCED vs. UNINDUCED antisense RNA expression as
 determined by the maximum 10 fold dilution at which a colony was observed. The
 results of these experiments are listed below in Table I. If there was no effect of
 antisense RNA expression in a microorganism, the clone is minus in Table I. In
 20 contrast, a positive in Table I means that at least 10 fold more cells were required to
 observe a colony on the induced plate than on the non-induced plate under the
 conditions used and in that microorganism.

25 **TABLE I**
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit
Proliferation in *E. coli*

Mol. No.	<i>S. typhimurium</i>	<i>E. cloacae</i>	<i>K. pneumoniae</i>
EcXA001	+	+	-
EcXA004	+	-	-
EcXA005	+	+	+
EcXA006	-	-	-
EcXA007	-	+	-

EcXA008	+	-	+
EcXA009	-	-	-
EcXA010	+	+	+
EcXA011	-	+	-
EcXA012	-	+	-
EcXA013	+	+	+
EcXA014	+	+	-
EcXA015	+	+	+
EcXA016	+	+	+
EcXA017	+	+	+
EcXA018	+	+	+
EcXA019	+	+	+
EcXA020	+	+	+
EcXA021	+	+	+
EcXA023	+	+	+
EcXA024	+	-	+
EcXA025	-	-	-
EcXA026	+	+	-
EcXA027	+	+	-
EcXA028	+	-	-
EcXA029	-	-	-
EcXA030	+	+	+
EcXA031	+	-	-
EcXA032	+	+	-
EcXA033	+	+	+
EcXA034	+	+	+
EcXA035	-	-	-
EcXA036	+	-	+
EcXA037	+	+	-
EcXA038	+	+	+
EcXA039	+	-	-
EcXA041	+	+	+
EcXA042	-	+	+
EcXA043	-	-	-
EcXA044	-	-	-
EcXA045	+	+	+
EcXA046	-	-	-
EcXA047	+	+	-
EcXA048	-	-	-
EcXA049	+	-	-
EcXA050	-	-	-
EcXA051	+	-	-
EcXA052	+	-	-
EcXA053	+	+	+
EcXA054	-	-	+
EcXA055	+	-	-

EcXA056	+	-	+
EcXA057	+	+	-
EcXA058	-	-	-
EcXA059	+	+	+
EcXA060	-	-	-
EcXA061	-	-	-
EcXA062	-	-	-
EcXA063	+	+	-
EcXA064	-	-	-
EcXA065	+	+	-
EcXA066	-	-	-
EcXA067	-	+	-
EcXA068	-	-	-
EcXA069	-	+	-
EcXA070	-	-	-
EcXA071	+	-	-
EcXA072	+	-	+
EcXA073	+	+	+
EcXA074	+	+	+
EcXA075	+	-	-
EcXA076	-	+	-
EcXA077	+	+	-
EcXA079	+	+	+
EcXA080	+	-	-
EcXA082	-	+	-
EcXA083	-	-	-
EcXA084	-	+	-
EcXA086	-	-	-
EcXA087	-	-	-
EcXA088	-	-	-
EcXA089	-	-	-
EcXA090	-	-	-
EcXA091	-	-	-
EcXA092	-	-	-
EcXA093	-	-	-
EcXA094	+	+	+
EcXA095	+	+	-
EcXA096	-	-	-
EcXA097	+	-	-
EcXA098	+	-	-
EcXA099	-	-	-
EcXA100	-	-	-
EcXA101	-	-	-
EcXA102	-	-	-
EcXA103	-	+	-
EcXA104	+	+	+

EcXA106	+	+	-
EcXA107	-	-	-
EcXA108	-	-	-
EcXA109	-	-	-
EcXA110	+	+	-
EcXA111	-	-	-
EcXA112	-	+	-
EcXA113	+	+	+
EcXA114	-	+	-
EcXA115	-	+	-
EcXA116	+	+	-
EcXA117	+	-	-
EcXA118	-	-	-
EcXA119	+	+	-
EcXA120	-	-	-
EcXA121	-	-	-
EcXA122	+	-	+
EcXA123	+	-	-
EcXA124	-	-	-
EcXA125	-	-	-
EcXA126	-	-	-
EcXA127	+	+	-
EcXA128	-	-	-
EcXA129	-	+	-
EcXA130	+	+	-
EcXA132	-	-	-
EcXA133	-	-	-
EcXA136	-	-	-
EcXA137	-	-	-
EcXA138	+	-	-
EcXA139	-	-	-
EcXA140	+	-	-
EcXA141	+	-	-
EcXA142	-	-	-
EcXA143	-	+	-
EcXA144	+	+	-
EcXA145	-	-	-
EcXA146	-	-	-
EcXA147	-	-	-
EcXA148	-	-	-
EcXA149	+	+	+
EcXA150	-	-	-
EcXA151	+	-	-
EcXA152	-	-	-
EcXA153	+	+	-
EcXA154	-	-	-

EcXA155	-	-	ND
EcXA156	-	+	-
EcXA157	-	-	-
EcXA158	-	-	-
EcXA159	+	-	-
EcXA160	+	-	-
EcXA162	-	-	-
EcXA163	-	-	-
EcXA164	-	-	-
EcXA165	-	-	-
EcXA166	-	-	-
EcXA167	-	-	-
EcXA168	-	-	-
EcXA169	-	+	-
EcXA171	-	-	-
EcXA172	-	-	-
EcXA173	-	-	-
EcXA174	-	-	-
EcXA175	-	-	-
EcXA176	-	-	-
EcXA178	-	-	-
EcXA179	-	-	-
EcXA180	+	-	-
EcXA181	-	-	-
EcXA182	-	-	-
EcXA183	-	-	-
EcXA184	-	-	-
EcXA185	-	-	-
EcXA186	-	-	-
EcXA187	+	+	+
EcXA189	+	-	-
EcXA190	+	+	+
EcXA191	+	+	-
EcXA192	-	+	-

Thus, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides can be identified by measuring the ability of an antisense nucleic acid which inhibits the proliferation of

5 *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* to inhibit the growth of other organisms. This may be evaluated by

transforming the antisense nucleic acid directly into species other than the organism from which they were obtained. In particular, the ability of the antisense nucleic acid to inhibit the growth of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*,
5 *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*,
10 *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*,
15 *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*,
20 *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, *Yersinia pestis* or any species falling within the genera of any of the above species. may be evaluated. In some embodiments of the present invention, the ability of the antisense nucleic acid to inhibit the growth of an organism other than *E. coli* may be evaluated. In such embodiments, the antisense nucleic acids are inserted into
25 expression vectors functional in the organisms in which the antisense nucleic acids are evaluated.

It will be appreciated that the above methods for evaluating the ability of an antisense nucleic acid to inhibit the proliferation of a heterologous organism may be performed using antisense nucleic acids complementary to any of the proliferation-
30 required nucleic acids from *Staphylococcus aureus*, *Salmonella typhimurium*,

Klebsiella pneumoniae, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, such as the
5 antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

Those skilled in the art will appreciate that a negative result in a heterologous cell or microorganism does not mean that that cell or microorganism is missing that
10 gene nor does it mean that the gene is unessential. However, a positive result means that the heterologous cell or microorganism contains a homologous gene which is required for proliferation of that cell or microorganism. The homologous gene may be obtained using the methods described herein. For example, the homologous gene may be isolated by performing a PCR procedure using primers based on the antisense sequence which
15 reduced the level or activity of the gene product encoded by the homologous gene or by performing a Southern blot.

Those skilled in the art will appreciate that an antisense molecule which works in the microorganism from which it was obtained will not always work in a heterologous cell or microorganism.

20 **EXAMPLE 6**

Identification of Nucleic Acids Homologous to Nucleic Acids Required for the Proliferation of *Staphylococcus aureus* in other Bacterial Species

Nucleic acids homologous to proliferation-required nucleic acids from *Staphylococcus aureus* were identified as follows. Thirty-nine antisense nucleic acids
25 which inhibited the growth of *Staphylococcus aureus* were inserted into an expression vector such that their expression was under the control of a xylose-inducible Xyl-T5 promoter. A vector with Green Fluorescent Protein (GFP) under control of the Xyl-T5 promoter was used to show that expression from the Xyl-T5 promoter in *Staphylococcus epidermidis* was comparable to that in *Staphylococcus aureus*.

The vectors were introduced into *Staphylococcus epidermidis* by electroporation as follows: *Staphylococcus epidermidis* was grown in liquid culture to mid-log phase and then harvested by centrifugation. The cell pellet was resuspended in 1/3 culture volume of ice-cold EP buffer (0.625 M sucrose, 1 mM MgCl₂, pH=4.0), and then harvested again by centrifugation. The cell pellet was then resuspended with 1/40 volume EP buffer and allowed to incubate on ice for 1 hour. The cells were then frozen for storage at -80°C. For electroporation, 50 µl of thawed electrocompetent cells were combined with 0.5 µg plasmid DNA and then subjected to an electrical pulse of 10 kV/cm, 25 uFarads, 200 ohm using a biorad gene pulser electroporation device. The cells were immediately resuspended with 200 µl outgrowth medium and incubated for 2 hours prior to plating on solid growth medium with drug selection to maintain the plasmid vector. Colonies resulting from overnight growth of these platings were selected, cultured in liquid medium with drug selection, and then subjected to dilution plating analysis as described for *Staphylococcus aureus* above to test growth sensitivity in the presence of the inducer xylose.

The results are shown in Table II below. The first column indicates the Molecule Number of the *Staphylococcus aureus* antisense nucleic acid which was introduced into *Staphylococcus epidermidis*. The second column indicates whether the antisense nucleic acid inhibited the growth of *Staphylococcus epidermidis*, with a "+" indicating that growth was inhibited. Of the 39 *Staphylococcus aureus* antisense nucleic acids evaluated, 20 inhibited the growth of *Staphylococcus epidermidis*.

TABLE II
Sensitivity of Other Microorganisms to Antisense Nucleic Acids That Inhibit Proliferation of *Staphylococcus aureus*

Mol. No.	<i>S. epidermidis</i>
SaXA005	+
SaXA007	+
SaXA008	+
SaXA009	+

SaXA010	+
SaXA011	-
SaXA012	-
SaXA013	-
SaXA015	+
SaXA017	-
SaXA022	+
SaXA023	-
SaXA024	-
SaXA025	+
SaXA026	+
SaXA027	-
SaXA027b	-
SaXA02c	-
SaXA028	-
SaXA029	+
SaXA030	+
SaXA032	+
SaXA033	+
SaXA034	-
SaXA035	+
SaXA037	+
SaXA039	-
SaXA042	-
SaXA043	-
SaXA044	-
SaXA045	+
SaXA051	+
SaXA053	-

SaXA056b	-
SaXA059a	+
SaXA060	-
SaXA061	+
SaXA062	+
SaXA063	-
SaXA065	-

The above methods for identifying homologous genes using antisense nucleic acids complementary to any of the proliferation-required nucleic acids from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans*, (including antisense nucleic acids complementary to SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, such as the antisense nucleic acids of SEQ ID NOs.: 8-3795) or portions thereof, antisense nucleic acids complementary to homologous coding nucleic acids or portions thereof, or homologous antisense nucleic acids.

Homologous nucleic acids may also be identified using complementation analyses.

EXAMPLE 7

Identification of Homologous Nucleic Acids by Functional Complementation

Homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified as follows. Gene products whose activities may be complemented by a proliferation-required gene product from *Staphylococcus aureus*, *Salmonella typhimurium*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Enterococcus faecalis*, *Escherichia coli*, *Enterococcus faecalis*, *Haemophilus influenzae*, *Helicobacter pylori*, *Salmonella typhi* or *Candida albicans* or homologous polypeptides are identified using merodiploids,

created by introducing a plasmid or Bacterial Artificial Chromosome into an organism having a mutation in the essential gene which reduces or eliminates the activity of the gene product. In some embodiments, the mutation may be a conditional mutation, such as a temperature sensitive mutation, such that the organism proliferates under permissive conditions but is unable to proliferate under non-permissive conditions in the absence of complementation by the gene on the plasmid or Bacterial Artificial Chromosome. Alternatively, duplications may be constructed as described in Roth et al. (1987) Biosynthesis of Aromatic Amino Acids in *Escherichia coli* and *Salmonella typhimurium*, F. C. Neidhardt, ed., American Society for Microbiology, publisher, pp. 2269-2270, the disclosure of which is incorporated herein by reference in its entirety. Such methods are familiar to those skilled in the art. Alternatively, homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified by placing a gene required for proliferation or a nucleic acid complementary to at least a portion of a gene required for proliferation under the control of a regulatable promoter as described above, introducing a plasmid or Bacterial Artificial Chromosome into the cell, and identifying cells which are able to proliferate under conditions which would prevent or reduce proliferation in the absence of the plasmid or Bacterial Artificial Chromosome.

Homologous coding nucleic acids, homologous antisense nucleic acids or nucleic acids encoding homologous polypeptides may be identified using databases as follows.

EXAMPLE 8

Identification of Homologous Nucleic Acids by Database Analysis

As a demonstration of the database methodology used to find homologues to an essential gene, nine prokaryotic organisms were analyzed and compared in detail. First, the most reliable source of gene sequences for each organism was assessed by conducting a survey of the public and private data sources. The nine organisms studied are *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Klebsiella pneumoniae*, *Pseudomonas aeruginosa*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*. Full-length gene protein and nucleotide sequences

for these organisms were assembled from various sources. For *Escherichia coli*, *Haemophilus influenzae* and *Helicobacter pylori*, gene sequences were adopted from the public sequencing projects, and derived from the GenPept 115 database (available from NCBI). For *Pseudomonas aeruginosa*, gene sequences were adopted from the
5 *Pseudomonas* genome sequencing project (downloaded from <http://www.pseudomonas.com>). For *Klebsiella pneumoniae*, *Staphylococcus aureus*, *Streptococcus pneumoniae* and *Salmonella typhi*, genomic sequences from PathoSeq v 4.1 (Mar 2000 release) was reanalyzed for ORFs using the gene finding software GeneMark v 2.4a, which was purchased from GenePro Inc. 451 Bishop St., N.W.,
10 Suite B, Atlanta, GA, 30318, USA.

Subsequently, the essential genes found by the antisense methodology were compared to the derived proteomes of interest, in order to find all the homologous genes to a given gene. This comparison was done using the FASTA program v3.3. Genes were considered homologues if they were greater than 25% identical and the
15 alignment between the two genes covered more than 70% of the length of one of the genes. The best homologue for each of the nine organisms, defined as the most significantly scoring match which also fulfilled the above criteria, was reported in Table III. Table III lists the best ORF identified as described above (column labelled LOCUSID), the SEQ ID, % identity, and the amount of the protein which aligns well
20 with the query sequence (coverage) for the gene identified in each of the nine organisms evaluated as described above.

Table IV lists the PathoSeq cluster ID for genes identified as being required for proliferation in *Enterococcus faecalis*, *Escherichia coli*, *Pseudomonas aeruginosa*, and *Staphylococcus aureus* using the methods described herein. As indicated in the
25 column labelled PathoSeq cluster ID, these sequences share homology to one another and were consequently grouped within the same PathoSeq cluster. Thus, the methods described herein identified genes required for proliferation in several species which share homology.

TABLE III

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10000 1	SeqID IDENTITY COVERAGE	10430 27% 99%	10618 100% 100%	10998 28% 101%	11603 28% 79%	11739 29% 77%		12309 52% 98%	13524 55% 98%	14040 28% 98%
EFA10002 3	SeqID IDENTITY COVERAGE		10505 100% 100%					12860 27% 95%	13392 39% 101%	
EFA10006 5	SeqID IDENTITY COVERAGE	10322 49% 96%	10813 100% 100%	11177 49% 95%	11351 44% 96%		12018 48% 97%	12820 59% 97%	13186 65% 98%	13733 48% 96%
EFA10015 1	SeqID IDENTITY COVERAGE	10128 50% 99%	10516 100% 100%	11247 37% 100%	11340 46% 100%		11891 49% 100%	12529 54% 99%	13362 51% 100%	
EFA10015 7	SeqID IDENTITY COVERAGE		10673 100% 100%		11448 39% 98%			12352 64% 98%	13176 74% 99%	
EFA10016 5	SeqID IDENTITY COVERAGE	10031 31% 97%	10637 100% 100%	11189 33% 98%	11564 28% 100%		12009 32% 96%	12614 29% 90%	13399 27% 96%	14078 29% 97%
EFA10019	SeqID	10364	10480	11061	11408	11659	11996	12444	13232	13966

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
0	IDENTITY COVERAGE SeqID	54% 100% 10336	100% 101% 10540	57% 100% 11120	55% 99% 11426	55% 90% 90%	54% 100% 11989	78% 101% 12230	80% 101% 13222	54% 101% 14096
EFA100194	IDENTITY COVERAGE SeqID	60% 100% 10323	100% 101% 10798	62% 100% 11193	62% 102% 102%	60% 100% 12020	60% 100% 12020	85% 101% 12527	86% 92% 13561	61% 101% 13731
EFA100200	IDENTITY COVERAGE SeqID	39% 85% 10352	100% 100% 10560	38% 87% 11104			40% 85% 5171	50% 85% 12260	59% 88% 13204	39% 85% 13968
EFA100210	IDENTITY COVERAGE SeqID	53% 95% 10351	100% 101% 10523	53% 95% 11105	53% 94% 11438		54% 95% 11992	74% 101% 12214	93% 94% 13205	53% 95% 13968
EFA100211	IDENTITY COVERAGE SeqID	46% 87% 10284	100% 101% 10810	46% 87% 11105	39% 81% 11438		43% 87% 11827	69% 97% 13245	63% 81% 13245	
EFA100289	IDENTITY COVERAGE SeqID	30% 85% 10045	100% 100% 10517				31% 90% 11937		25% 84% 13616	
EFA100295	IDENTITY COVERAGE SeqID	43% 92% 10045	100% 101% 10641	41% 95% 11174	41% 97% 11601		45% 97% 11937	44% 99% 12390	45% 94% 13616	43% 72% 13911
EFA10031	SeqID							12178		

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
2	IDENTITY COVERAGE		100% 100%					33% 88%		
EFA10032 9	SeqID IDENTITY COVERAGE		10782 100% 100%							
EFA10039 4	SeqID IDENTITY COVERAGE	10465 43% 108%	10675 100% 100%	11238 43% 109%	11563 42% 101%		11961 44% 108%	13003 66% 99%	13684 72% 100%	13853 44% 108%
EFA10039 7	SeqID IDENTITY COVERAGE	10027 31% 96%	10773 100% 100%	11185 29% 98%			12012 29% 93%	12396 43% 91%	13478 46% 97%	14074 31% 93%
EFA10039 9	SeqID IDENTITY COVERAGE	10295 63% 98%	10766 100% 100%	11196 59% 98%	11483 59% 99%		11791 58% 101%	12281 72% 99%	13413 76% 100%	13739 63% 98%
EFA10042 6	SeqID IDENTITY COVERAGE	10224 28% 99%	10702 100% 101%			11638 29% 99%		12139 42% 91%	13348 41% 109%	13957 28% 99%
EFA10047 8	SeqID IDENTITY COVERAGE		10486 100% 100%	11135 29% 72%	11338 31% 70%			12986 44% 99%	13184 43% 98%	
EFA10061	SeqID		10501	11139			12028	12641	13331	

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
5	IDENTITY COVERAGE		100% 100%	44% 82%			47% 81%	61% 100%	78% 100%	
EFA10061 7	SeqID	10314	10764	11216	11391		5198	12322	13381	13765
	IDENTITY COVERAGE	43% 95%	100% 100%	43% 96%	44% 78%		51% 73%	63% 84%	69% 82%	44% 93%
EFA10064 1	SeqID	10205	10793				11896	12862	13334	
	IDENTITY COVERAGE	28% 79%	100% 100%				31% 74%	50% 85%	32% 82%	
EFA10064 2	SeqID		10792		11520		12023	12493	13367	
	IDENTITY COVERAGE		100% 100%		46% 100%		46% 101%	73% 100%	69% 100%	
EFA10066 8	SeqID	10026	10679	11184	11613		12013	12891	13505	14073
	IDENTITY COVERAGE	28% 83%	100% 100%	28% 76%	29% 78%		28% 92%	29% 82%	50% 99%	27% 95%
EFA10068 9	SeqID		10717					12523	13698	
	IDENTITY COVERAGE		100% 100%					33% 100%	33% 100%	
EFA10070 4	SeqID	10362	10482	11059	11415		11995	12442	13171	13964
	IDENTITY COVERAGE	78% 100%	100% 100%	78% 100%	77% 101%		75% 101%	90% 100%	78% 101%	77% 100%
EFA10073	SeqID	10111	10537	11052	11429	11651	11876	12228	13220	14010

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
9	IDENTITY COVERAGE	71% 83%	100% 101%	69% 83%	63% 86%	70% 87%	71% 83%	84% 87%	84% 87%	70% 87%
EFA100740	SeqID	10075	10536	11008	11348	11633	11942	12227	13219	13717
	IDENTITY COVERAGE	45% 94%	100% 100%	47% 94%	30% 93%	45% 94%	48% 82%	64% 94%	60% 93%	44% 94%
EFA100741	SeqID	10339	10535	11118	11430		11991	12226	13218	14098
	IDENTITY COVERAGE	40% 103%	100% 100%	37% 102%	34% 101%		39% 102%	48% 101%	60% 100%	40% 103%
EFA100742	SeqID	10340	10534	11116	11431		5160	12225	13217	14099
	IDENTITY COVERAGE	52% 99%	100% 101%	52% 99%	39% 92%		46% 99%	79% 101%	88% 101%	52% 99%
EFA100748	SeqID	10287	10483	11004	11523	11690	11944	12595		13868
	IDENTITY COVERAGE	41% 99%	100% 100%	39% 99%	29% 94%	42% 98%	44% 100%	52% 100%		41% 100%
EFA100756	SeqID	10112	10575		11396		11875	12327	13343	14009
	IDENTITY COVERAGE	49% 75%	100% 102%		43% 75%		45% 81%	64% 94%	62% 94%	47% 75%
EFA100757	SeqID	10155	10897							
	IDENTITY COVERAGE	27% 85%	100% 100%							
EFA10078	SeqID	10035	10811	10986	11543		11953	12738	13261	13914

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
3	IDENTITY COVERAGE	32% 104%	100% 100%	34% 83%	86% 100%		37% 78%	77% 100%	75% 99%	31% 99%
EFA10079	SeqID		10863						13416	
5	IDENTITY COVERAGE		100% 101%						50% 101%	
EFA10079	SeqID									
8	IDENTITY COVERAGE	10382 62% 95%	10818 100% 100%	11153 61% 95%	11550 56% 89%		11775 63% 92%		13641 85% 96%	
EFA10081	SeqID		10546					12236	13439	
1	IDENTITY COVERAGE		100% 101%					48% 98%	58% 99%	
EFA10087	SeqID							12446	13646	14042
0	IDENTITY COVERAGE	10439 47% 114%	10627 100% 100%	11036 46% 117%	11410 52% 79%		5179 46% 116%	72% 99%	78% 98%	46% 114%
EFA10091	SeqID		10579	11018	11617	11758	12111	12368	13230	14065
4	IDENTITY COVERAGE	10399 40% 102%	10579 100% 100%	11018 40% 102%	11617 34% 101%	11758 40% 102%	12111 40% 102%	12368 59% 101%	13230 63% 95%	14065 40% 102%
EFA10091	SeqID									
9	IDENTITY COVERAGE	10269 44% 101%	10491 100% 100%	11127 45% 101%	11419 40% 99%		11809 46% 101%	12556 55% 101%	13594 63% 100%	13874 45% 101%
EFA10095	SeqID									
		10333	10542	11123	11582	11627	5158	12232	13224	14093

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
5	IDENTITY COVERAGE	48% 98%	100% 101%	48% 98%	42% 98%	49% 79%	43% 98%	65% 99%	76% 101%	48% 98%
EFA100970	SeqID IDENTITY COVERAGE		10906 100% 100%							
EFA100978	SeqID IDENTITY COVERAGE	10334 46% 100%	10541 100% 100%	11122 46% 99%	11583 35% 98%		11987 45% 102%	12231 71% 101%	13223 70% 100%	14094 46% 100%
EFA100991	SeqID IDENTITY COVERAGE	10221 42% 91%	10681 100% 100%	11210 40% 93%	11607 29% 98%	11668 42% 94%	11801 39% 91%	12289 49% 93%	13191 56% 92%	14027 30% 93%
EFA101022	SeqID IDENTITY COVERAGE	10260 59% 85%	10875 100% 101%	10982 58% 85%	11401 50% 88%		11945 61% 85%	12715 76% 85%	13251 86% 89%	14086 56% 89%
EFA101060	SeqID IDENTITY COVERAGE		10722 100% 101%		11575 35% 83%	11646 37% 77%	11957 34% 97%	12504 71% 100%	13554 67% 101%	
EFA101086	SeqID IDENTITY COVERAGE	10315 37% 91%	10763 100% 100%	11215 37% 89%	11454 27% 98%	11716 38% 91%	12052 35% 92%	12953 57% 98%	13662 55% 95%	13764 36% 93%
EFA10112	SeqID	10017	10687	11219	11331		12057	12505	13498	14012

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
0	IDENTITY COVERAGE	30% 102%	100% 100%	31% 102%	27% 74%		29% 103%	26% 99%	64% 98%	29% 103%
EFA10112	SeqID		10686					12606	13600	
1	IDENTITY COVERAGE		100% 100%					38% 98%	50% 99%	
EFA10112	SeqID	10420	10748	11131	11478	11629	11820	12674	13265	13783
3	IDENTITY COVERAGE	43% 98%	100% 100%	39% 97%	33% 97%	43% 94%	40% 96%	70% 99%	70% 100%	42% 98%
EFA10114	SeqID	10436	10614	11071	11573		5181	12450	13246	14045
1	IDENTITY COVERAGE	35% 94%	100% 101%	40% 96%	35% 95%		40% 95%	60% 98%	70% 101%	31% 96%
EFA10115	SeqID	10174	10719	11221	11556		11880	12985	13385	13943
0	IDENTITY COVERAGE	35% 100%	100% 100%	36% 100%	26% 102%		33% 100%	45% 100%	58% 100%	36% 73%
EFA10115	SeqID	10359	10543	11097	11442		5176	12235	13197	13974
9	IDENTITY COVERAGE	55% 100%	100% 101%	52% 100%	48% 81%		49% 101%	58% 99%	89% 99%	53% 100%
EFA10116	SeqID	10358	10549	11098	11595		5175	12240	13198	13973
0	IDENTITY COVERAGE	43% 92%	100% 100%	43% 92%	33% 96%		45% 92%	62% 100%	74% 100%	43% 93%
EFA10116	SeqID	10357	10551	11099			11994	12242	13199	13972

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
1	IDENTITY COVERAGE	39% 86%	100% 101%	35% 99%				69% 93%	66% 103%	36% 100%
EFA10116	SeqID	10356	10555	11100	11441	11679	11993	12249	13200	13971
2	IDENTITY COVERAGE	58% 100%	100% 100%	58% 100%	59% 100%	59% 100%	57% 99%	78% 100%	84% 100%	58% 100%
EFA10116	SeqID	10355	10557	11101	11594		5174	12255	13201	
3	IDENTITY COVERAGE	66% 100%	100% 101%	68% 99%	60% 97%		70% 100%	84% 101%	90% 100%	
EFA10116	SeqID	10354	10558	11102	11593		5173	12258	13202	13970
4	IDENTITY COVERAGE	55% 91%	100% 101%	58% 91%	47% 91%		57% 85%	66% 91%	81% 97%	55% 91%
EFA10116	SeqID	10353	10559	11103	11592		5172	12259	13203	13969
5	IDENTITY COVERAGE	59% 95%	100% 100%	60% 95%	52% 99%		61% 95%	78% 100%	88% 100%	59% 95%
EFA10116	SeqID	10133	10574	11091			12025	12516		13849
9	IDENTITY COVERAGE	27% 93%	100% 100%	28% 97%			26% 94%	41% 100%		27% 93%
EFA10125	SeqID	10389	10852	11065	11551		11838	13072	13457	
3	IDENTITY COVERAGE	43% 97%	100% 100%	42% 97%	31% 96%		39% 99%	54% 97%	67% 99%	
EFA10125	SeqID	10124	10917	10976	11484		11914	12528	13357	14037

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
7	IDENTITY COVERAGE	40% 99%	100% 100%	39% 99%	39% 101%		37% 97%	39% 97%	58% 100%	38% 101%
EFA10125	SeqID	10127	10918	10973	11513		11892	12802	13358	13871
8	IDENTITY COVERAGE	40% 97%	100% 101%	40% 96%	39% 95%		36% 96%	41% 92%	66% 95%	29% 92%
EFA10132	SeqID		10620					12534	13328	
2	IDENTITY COVERAGE		100% 100%					66% 86%	65% 86%	
EFA10133	SeqID		10743		11448			12326	13391	
9	IDENTITY COVERAGE		100% 100%		33% 97%			46% 98%	60% 98%	
EFA10134	SeqID		10745							
0	IDENTITY COVERAGE		100% 102%							
EFA10135	SeqID	10047	10648	11089	11608		11935	12617	13345	13913
4	IDENTITY COVERAGE	33% 101%	100% 100%	33% 104%	32% 101%		34% 104%	38% 97%	36% 100%	32% 101%
EFA10137	SeqID		10738					13126		
0	IDENTITY COVERAGE		100% 101%					31% 98%		
EFA10140	SeqID		10662					12941		

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
3	IDENTITY COVERAGE		100% 100%					34% 100%		
EFA10140	SeqID	10210	10663	11214	11554		11921	12135	13418	13925
4	IDENTITY COVERAGE	29% 99%	100% 100%	28% 102%	39% 98%		27% 100%	59% 99%	64% 99%	30% 99%
EFA10140	SeqID	10350	10524	11106	11437		5170	12215	13207	
9	IDENTITY COVERAGE	54% 83%	100% 101%	58% 80%	44% 86%		53% 91%	81% 91%	87% 91%	
EFA10141	SeqID	10349	10525	11107	11436		5169	12216	13208	14108
0	IDENTITY COVERAGE	62% 101%	100% 101%	64% 101%	63% 100%		66% 100%	90% 101%	90% 101%	62% 102%
EFA10141	SeqID	10348	10526	11108			5168	12217	13209	14107
1	IDENTITY COVERAGE	50% 97%	100% 101%	43% 97%			49% 93%	66% 96%	71% 99%	46% 97%
EFA10141	SeqID	10347	10527	11109	11589	11654	5167	12218	13210	14106
2	IDENTITY COVERAGE	60% 100%	100% 101%	59% 100%	52% 98%	61% 101%	58% 99%	85% 92%	83% 100%	60% 101%
EFA10141	SeqID	10345	10528	11111	11435		5165	12219	13212	14104
4	IDENTITY COVERAGE	49% 99%	100% 101%	47% 99%	42% 99%		46% 100%	79% 101%	81% 101%	49% 101%
EFA10141	SeqID	10344	10529	11112	11434		5164	12220	13213	14103

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
5	IDENTITY COVERAGE	47% 98%	100% 101%	50% 98%	39% 100%		49% 98%	63% 101%	74% 101%	47% 98%
EFA10141	SeqID	10343	10530	11113	11433		5163	12221	13214	14102
6	IDENTITY COVERAGE	50% 97%	100% 101%	48% 97%	42% 91%		52% 94%	68% 99%	82% 101%	51% 98%
EFA10141	SeqID	10342	10531	11114	11432		5162	12222	13215	14101
7	IDENTITY COVERAGE	55% 100%	100% 101%	56% 95%	61% 84%		52% 92%	72% 95%	85% 94%	55% 100%
EFA10142	SeqID	10220	10784	11276		11765	11950	12350	13280	13934
4	IDENTITY COVERAGE	44% 99%	100% 101%	38% 97%		34% 73%	36% 78%	65% 101%	79% 99%	41% 99%
EFA10142	SeqID	10240	10785	11275			11925	12351	13281	13863
5	IDENTITY COVERAGE	49% 99%	100% 100%	50% 99%			39% 99%	63% 100%	78% 100%	47% 84%
EFA10147	SeqID	10263	10861	10965	11562		11948	13066	13525	14089
7	IDENTITY COVERAGE	52% 91%	100% 100%	50% 95%	41% 91%		49% 95%	59% 94%	72% 91%	50% 91%
EFA10153	SeqID	10281	10823							
6	IDENTITY COVERAGE	30% 86%	100% 100%							
EFA10153	SeqID									

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA101540	SeqID	10041	10487	11149	11456		11941	12314	13438	13907
	IDENTITY COVERAGE	51% 92%	100% 100%	50% 90%	50% 86%		49% 92%	73% 92%	76% 99%	51% 92%
EFA101541	SeqID	10042	10488	11150	11620		11940	12742	13437	13908
	IDENTITY COVERAGE	41% 100%	100% 100%	45% 98%	35% 121%		44% 101%	63% 100%	44% 116%	41% 100%
EFA101583	SeqID		10593							
	IDENTITY COVERAGE		100% 100%							
EFA101670	SeqID		10511							
	IDENTITY COVERAGE		100% 100%							
EFA101682	SeqID	10238	10789	11178	11517		11829	12811	13673	13864
	IDENTITY COVERAGE	45% 97%	100% 100%	45% 98%	40% 95%		44% 91%	57% 96%	57% 95%	45% 97%
EFA101685	SeqID		10791		11369		12022	12492	13368	
	IDENTITY COVERAGE		100% 100%		47% 92%		51% 98%	62% 97%	69% 99%	
EFA101686	SeqID	10237	10940	10999	11325		11901	12456	13455	13956
	IDENTITY COVERAGE	39% 99%	100% 100%	37% 99%	37% 99%		36% 99%	64% 99%	63% 99%	38% 99%

<i>LOCUSID</i>	<i>Data</i>	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10169 ₅	SeqID IDENTITY COVERAGE	10204 34% 104%	10629 100% 100%	11017 32% 106%	11479 34% 76%	11715 31% 93%	12106 35% 101%	12560 51% 100%	13284 75% 99%	13928 34% 105%
EFA10173 ₆	SeqID IDENTITY COVERAGE	10219 33% 100%	10775 100% 100%	11024 29% 100%			11924 27% 99%	12300 35% 98%	13340 32% 99%	13976 28% 100%
EFA10173 ₇	SeqID IDENTITY COVERAGE	10218 39% 98%	10778 100% 100%	11023 37% 98%			11923 42% 98%	12301 43% 100%	13341 43% 103%	13774 58% 96%
EFA10175 ₃	SeqID IDENTITY COVERAGE	10134 36% 91%	10552 100% 100%	11211 37% 89%			11895 36% 90%	12151 50% 94%	13693 50% 99%	13826 37% 91%
EFA10176 ₅	SeqID IDENTITY COVERAGE		10587 100% 100%					13010 28% 98%	13353 35% 97%	
EFA10179 ₀	SeqID IDENTITY COVERAGE	10414 42% 101%	10803 100% 100%	11085 41% 101%			11915 39% 101%	12306 46% 101%		13747 41% 101%
EFA10179 ₁	SeqID IDENTITY COVERAGE		10804 100% 101%					12359 37% 77%		

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10179	SeqID	10030	10805	11188	11458		5187	12360	13333	14077
2	IDENTITY COVERAGE	31% 98%	100% 100%	32% 96%	27% 98%		33% 99%	34% 101%	47% 100%	31% 98%
EFA10179	SeqID	10329	10922	11159	11322		12062	12581	13363	13886
5	IDENTITY COVERAGE	34% 98%	100% 101%	36% 98%	36% 99%		37% 98%	36% 98%	47% 99%	32% 97%
EFA10179	SeqID	10330	10924	11160	11321		12063	13127	13364	13885
7	IDENTITY COVERAGE	53% 98%	100% 100%	52% 98%	49% 98%		55% 98%	59% 98%	74% 99%	53% 98%
EFA10179	SeqID	10048	10926	11014	11339		11934	12908	13366	13897
9	IDENTITY COVERAGE	53% 97%	100% 100%	55% 97%	49% 94%		55% 97%	54% 97%	66% 97%	54% 97%
EFA10183	SeqID	10429	10720		11335		12039	12340	13451	14072
3	IDENTITY COVERAGE	31% 79%	100% 100%		36% 92%		35% 89%	51% 92%	59% 91%	31% 79%
EFA10186	SeqID		10829							
8	IDENTITY COVERAGE		100% 100%							
EFA10187	SeqID	10305	10815	11044	11343	11639	11797	12568	13288	13779
2	IDENTITY COVERAGE	62% 86%	100% 102%	62% 86%	38% 86%	61% 79%	60% 95%	93% 97%	92% 102%	62% 86%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10187 3	SeqID		10816				11796			
	IDENTITY COVERAGE		100% 101%				36% 94%			
EFA10189 2	SeqID	10454	10506	11048	11281		12005	12142	13190	14021
	IDENTITY COVERAGE	47% 100%	100% 101%	47% 100%	41% 97%		53% 100%	49% 101%	46% 100%	47% 100%
EFA10192 4	SeqID		10891		11532			12331	13463	
	IDENTITY COVERAGE		100% 100%		36% 101%			65% 100%	65% 94%	
EFA10192 5	SeqID		10893					12332		
	IDENTITY COVERAGE		100% 100%					59% 99%		
EFA10196 3	SeqID	10034	10848	11148	11536		12006	12552	13648	13901
	IDENTITY COVERAGE	48% 105%	100% 100%	47% 105%	49% 99%		47% 108%	57% 101%	69% 100%	48% 105%
EFA10200 6	SeqID		10580				11830	12804	13315	
	IDENTITY COVERAGE		100% 100%				33% 84%	42% 99%	43% 95%	
EFA10202 2	SeqID	10313	10881	11224	11502	11754	12051	12324	13485	13767
	IDENTITY COVERAGE	53% 88%	100% 101%	53% 88%	51% 87%	54% 89%	55% 88%	78% 89%	78% 89%	52% 89%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA102023	SeqID IDENTITY COVERAGE	10312 51% 98%	10882 100% 100%	10989 50% 99%	11576 38% 99%	11755 50% 84%	12050 50% 97%	12325 63% 99%	13699 70% 99%	13768 50% 97%
EFA102091	SeqID IDENTITY COVERAGE	10363 60% 101%	10481 100% 100%	11060 61% 101%	11568 63% 100%		11858 62% 101%	12443 75% 100%	13233 86% 100%	13965 59% 101%
EFA102110	SeqID IDENTITY COVERAGE	10193 32% 103%	10841 100% 100%	11255 34% 94%			12082 34% 100%		13430 62% 100%	13752 32% 99%
EFA102183	SeqID IDENTITY COVERAGE	10393 55% 84%	10952 100% 100%	11057 54% 86%	11330 50% 85%		11774 54% 86%	12695 67% 98%	13420 78% 100%	13920 55% 84%
EFA102185	SeqID IDENTITY COVERAGE	10458 27% 93%	10950 100% 101%	11051 29% 90%	11421 29% 94%	11632 28% 93%	12075 29% 91%	12413 63% 91%	13501 73% 96%	13858 27% 93%
EFA102186	SeqID IDENTITY COVERAGE	10448 29% 92%	10949 100% 101%	10995 29% 90%	11579 27% 94%			12412 53% 101%	13543 60% 92%	13817 30% 90%
EFA102205	SeqID IDENTITY COVERAGE	10108 46% 71%	10769 100% 102%	10985 38% 82%	11375 56% 73%				13375 55% 96%	13997 37% 104%

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA10225	SeqID	10275	10727	11175	11320		11933	12372	13376	13865
3	IDENTITY COVERAGE	53% 100%	100% 100%	55% 101%	48% 101%		53% 101%	67% 100%	80% 99%	54% 96%
EFA10228	SeqID		10729					12607	13424	
2	IDENTITY COVERAGE		100% 101%					40% 81%	46% 76%	
EFA10233	SeqID	10250	10651	11012	11488		11954	12940	13272	13705
8	IDENTITY COVERAGE	39% 95%	100% 100%	38% 92%	35% 86%		39% 98%	42% 99%	50% 99%	38% 99%
EFA10235	SeqID		10632							
0	IDENTITY COVERAGE		100% 101%							
EFA10235	SeqID		10634					12795	13406	
1	IDENTITY COVERAGE		100% 100%					33% 97%	38% 101%	
EFA10235	SeqID	10028	10635	11186	11328	11691	12011	12347	13409	14075
2	IDENTITY COVERAGE	40% 101%	100% 100%	39% 101%	35% 101%	40% 101%	39% 101%	51% 99%	55% 100%	40% 101%
EFA10235	SeqID	10029	10636	11187	11329		12010	12348	13398	14076
3	IDENTITY COVERAGE	32% 99%	100% 100%	34% 99%	28% 83%		32% 98%	50% 98%	61% 99%	31% 99%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10238 9	SeqID	10378	10904	11094			11781	12126	13263	
	IDENTITY COVERAGE	41% 97%	100% 100%	42% 83%			40% 98%	54% 82%	52% 100%	
EFA10245 3	SeqID		10931	10995	11579	11762		12412	13502	13819
	IDENTITY COVERAGE		100% 101%	29% 101%	33% 88%	33% 105%		54% 101%	54% 101%	29% 96%
EFA10250 1	SeqID	10438	10626	11037	11410		11997	12447	13187	14043
	IDENTITY COVERAGE	45% 112%	100% 100%	44% 111%	40% 114%		44% 113%	75% 93%	76% 96%	45% 112%
EFA10250 2	SeqID	10439	10627	11036	11410		5179	12446	13646	14042
	IDENTITY COVERAGE	47% 114%	100% 100%	46% 117%	52% 79%		46% 116%	72% 99%	78% 98%	46% 114%
EFA10250 3	SeqID	10016	10643		11446		12027	12995	13481	13947
	IDENTITY COVERAGE	45% 99%	100% 100%		37% 101%		43% 101%	61% 98%	65% 100%	41% 85%
EFA10251 8	SeqID	10288	10647			11681		12248	13229	13881
	IDENTITY COVERAGE	33% 105%	100% 100%			50% 71%		34% 102%	54% 100%	32% 105%

<i>LOCUSID</i>	<i>Data</i>	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10254 1	SeqID	10327	10602	11241	11471		5188	12237	13356	13729
	IDENTITY COVERAGE	59% 77%	100% 101%	59% 77%	49% 73%		59% 77%	69% 77%	82% 81%	56% 77%
EFA10254 2	SeqID	10326	10603	11240	11288		12016	12238	13361	13732
	IDENTITY COVERAGE	75% 95%	100% 105%	70% 95%	67% 100%		75% 95%	77% 105%	100% 100%	76% 100%
EFA10254 9	SeqID	10338	10538	11117	11428		5159			
	IDENTITY COVERAGE	63% 100%	100% 103%	63% 100%	71% 100%		68% 100%			
EFA10255 1	SeqID	10337	10539	11119	11427	11688	11990	12229	13221	14097
	IDENTITY COVERAGE	59% 96%	100% 101%	61% 91%	58% 99%	30% 74%	62% 96%	75% 101%	81% 101%	58% 96%
EFA10255 4	SeqID	10341	10532	11115			5161	12223	13216	
	IDENTITY COVERAGE	45% 93%	100% 102%	40% 93%			42% 97%	62% 102%	63% 100%	
EFA10265 5	SeqID	10049	10733	11086	11305		11813	12952	13228	13898
	IDENTITY COVERAGE	47% 97%	100% 100%	47% 99%	42% 99%		48% 99%	57% 98%	60% 108%	47% 97%
EFA10265 6	SeqID		10734					12321	13668	
	IDENTITY COVERAGE		100% 100%					55% 100%	55% 100%	

LOCUSID	Data	Escherichia coli	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA102698	SeqID	10082	10956			11807			14011
	IDENTITY COVERAGE	56% 96%	100% 100%			31% 96%			55% 96%
EFA102728	SeqID	10459	10948	11420		12074	12411	13503	13859
	IDENTITY COVERAGE	51% 89%	100% 101%	52% 73%		54% 82%	76% 96%	81% 100%	52% 90%
EFA102736	SeqID	10285	10556	11300		11943		13401	
	IDENTITY COVERAGE	53% 98%	100% 100%	44% 98%		51% 100%		71% 99%	
EFA102764	SeqID	10201	10478				12590	13425	13822
	IDENTITY COVERAGE	72% 99%	100% 100%				68% 99%	80% 100%	71% 99%
EFA102774	SeqID	10142	10896	11362		12040	12150	13235	13978
	IDENTITY COVERAGE	50% 96%	100% 100%	52% 94%		51% 95%	68% 98%	74% 97%	50% 96%
EFA102780	SeqID	10395	10908	11616		11772	12701	13552	
	IDENTITY COVERAGE	49% 77%	100% 100%	37% 77%		51% 75%	51% 101%	46% 98%	
EFA102788	SeqID	10176	10661	11297		11882	12630	13303	13941
	IDENTITY COVERAGE	59% 94%	100% 101%	54% 97%		63% 94%	70% 93%	81% 96%	59% 94%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
EFA10280 2	SeqID	10274	10854	11154	11298		11932	13128	13313	13866
	IDENTITY COVERAGE	66% 99%	100% 100%	64% 100%	58% 96%		64% 100%	74% 100%	83% 100%	65% 99%
EFA10281 3	SeqID	10191	10878	11005	11347		11815	12816	13492	13754
	IDENTITY COVERAGE	54% 100%	100% 100%	53% 100%	51% 99%		52% 99%	64% 99%	65% 99%	53% 100%
EFA10291 5	SeqID	10297	10640	10964	11323		11783	13090	13664	13737
	IDENTITY COVERAGE	27% 100%	100% 100%	32% 100%	30% 90%		31% 100%	50% 98%	52% 99%	28% 100%
EFA10302 1	SeqID	10434	10612	11039	11413		11999	12451	13517	
	IDENTITY COVERAGE	65% 101%	100% 101%	66% 101%	60% 99%		62% 101%	86% 101%	86% 99%	
EFA10303 3	SeqID	10221	10681	11210	11607	11668	11801	12289	13191	14027
	IDENTITY COVERAGE	42% 91%	100% 100%	40% 93%	29% 98%	42% 94%	39% 91%	49% 93%	56% 92%	30% 93%
EFA10303 8	SeqID	10435	10613	11038	11412		11998	12784	13397	14046
	IDENTITY COVERAGE	54% 99%	100% 100%	52% 100%	56% 99%		51% 100%	73% 100%	73% 100%	53% 99%
EFA10303 9	SeqID	10293	10850	11041	11482	11728	11793	12541	13377	13741
	IDENTITY COVERAGE	45% 99%	100% 100%	46% 101%	44% 98%	40% 99%	46% 99%	73% 102%	69% 101%	45% 99%

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA10306	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
2	IDENTITY	59%	100%	64%	54%		65%	64%	68%	59%
	COVERAGE	101%	101%	102%	102%		101%	99%	101%	102%
EFA10308	SeqID	10262	10862	10984	11403		11947		13415	14090
1	IDENTITY	41%	100%	41%	40%		41%		74%	40%
	COVERAGE	85%	101%	83%	82%		80%		95%	85%
EFA10317	SeqID	10251	10689	10969	11370		11955	12600	13518	13703
4	IDENTITY	32%	100%	32%	37%		33%	63%	77%	33%
	COVERAGE	93%	100%	94%	95%		96%	100%	100%	92%
EFA10321	SeqID	10071	10688	11019	11371		11850	12601	13319	13945
0	IDENTITY	56%	100%	63%	39%		57%	79%	76%	57%
	COVERAGE	97%	101%	98%	99%		97%	99%	101%	99%
EFA10326	SeqID	10365	10479	11062	11409		5178	12445	13231	13967
8	IDENTITY	69%	100%	70%	68%		70%	83%	93%	70%
	COVERAGE	100%	101%	100%	100%		99%	101%	101%	101%
EFA10329	SeqID	10319	10633	11140	11493		12029	12640	13320	13771
5	IDENTITY	66%	100%	58%	58%		70%	79%	86%	60%
	COVERAGE	77%	101%	85%	85%		77%	100%	96%	92%
EFA10334	SeqID		10873	10983	11402		11946			
8	IDENTITY		100%	39%	59%		39%			
	COVERAGE		103%	82%	85%		82%			

LOCUSID	Data	Escherichia coli	Enterococcus faecalis	Haemophilus influenzae	Helicobacter pylori	Klebsiella pneumoniae	Pseudomonas aeruginosa	Staphylococcus aureus	Streptococcus pneumoniae	Salmonella typhi
EFA10336	SeqID	10360	10533	11096	11443	11643	5177	12224	13196	13975
5	IDENTITY COVERAGE	57% 100%	100% 101%	58% 100%	53% 97%	58% 100%	58% 100%	82% 88%	82% 101%	58% 100%
EFA10337	SeqID	10177	10660	11222	11296		5120	12628	13302	
5	IDENTITY COVERAGE	50% 82%	100% 102%	52% 82%	36% 97%		50% 94%	66% 102%	78% 102%	
EFA10350	SeqID	10320	10671	11141	11492		12030	12638	13322	13766
4	IDENTITY COVERAGE	42% 97%	100% 101%	45% 97%	41% 96%		48% 97%	63% 98%	81% 100%	41% 100%
EFA10350	SeqID		10672						13321	
8	IDENTITY COVERAGE		100% 100%						30% 80%	
EFA10357	SeqID	10335	10879	11121	11425		11988	12578	13240	14095
1	IDENTITY COVERAGE	45% 102%	100% 100%	47% 102%	48% 103%		47% 102%	67% 99%	68% 100%	45% 102%
EFA10378	SeqID		10806					12361		
6	IDENTITY COVERAGE		100% 100%					59% 94%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1000 40	SeqID IDENTITY COVERAGE							12533 100% 101%		
SAU1000 53	SeqID IDENTITY COVERAGE	10366 32% 97%	10504 46% 100%	11075 30% 99%	11376 32% 81%	11723 33% 84%	11855 33% 81%	12143 100% 100%	13318 48% 100%	13814 32% 97%
SAU1000 56	SeqID IDENTITY COVERAGE		10930 39% 98%					12577 100% 100%	13477 33% 100%	
SAU1000 59	SeqID IDENTITY COVERAGE	10213 28% 71%	10598 70% 97%	11161 26% 95%	11528 26% 95%	11750 27% 71%	12064 28% 96%	12652 100% 100%	13433 25% 95%	13929 28% 71%
SAU1000 62	SeqID IDENTITY COVERAGE	10430 27% 103%	10618 52% 96%	10998 29% 103%	11603 29% 77%	11739 31% 76%		12309 100% 100%	13294 53% 97%	14040 28% 102%
SAU1000 77	SeqID IDENTITY COVERAGE		10565 64% 102%					12520 100% 100%	13464 62% 102%	
SAU1001 12	SeqID IDENTITY COVERAGE	10059 49% 97%			11477 52% 100%	11702 53% 77%	12096 46% 100%	12634 100% 100%		13895 49% 97%
SAU1001 14	SeqID IDENTITY COVERAGE	10152 44% 98%	10515 51% 98%	11279 43% 98%	11302 45% 98%		11851 43% 98%	12535 100% 100%	13387 25% 102%	13824 43% 98%
SAU1001 18	SeqID IDENTITY COVERAGE		10903 41% 101%				11828 27% 100%	12125 100% 100%	13262 37% 101%	
SAU1001 23	SeqID IDENTITY	10258 52%	10628 43%	11134 53%	11489 47%		5192 52%	12526 100%	13421 45%	14088 52%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1001	COVERAGE	98%	100%	97%	96%		98%	100%	82%	98%
31	SeqID	10466		11274			11960	12517		13854
	IDENTITY	35%		33%			40%	100%		35%
	COVERAGE	71%		97%			70%	100%		71%
SAU1001	SeqID	10311	10493	10990	11308	11703	11885	12574	13412	13769
33	IDENTITY	34%	44%	34%	33%	30%	31%	100%	43%	34%
	COVERAGE	79%	99%	80%	78%	82%	79%	100%	99%	79%
SAU1001	SeqID	10355	10557	11101	11594		5174	12255	13201	
39	IDENTITY	65%	84%	66%	64%		63%	100%	86%	
	COVERAGE	85%	86%	81%	83%		84%	101%	85%	
SAU1001	SeqID	10354	10558	11102	11440		5173	12258	13202	13970
40	IDENTITY	54%	66%	54%	40%		48%	100%	63%	54%
	COVERAGE	93%	91%	93%	94%		93%	101%	91%	93%
SAU1001	SeqID	10353	10559	11103	11592		5172	12259	13203	13969
41	IDENTITY	55%	78%	58%	54%		57%	100%	74%	55%
	COVERAGE	96%	101%	96%	96%		96%	100%	100%	96%
SAU1001	SeqID	10364	10480	11061	11408	11659	11996	12444	13232	13966
57	IDENTITY	60%	78%	60%	55%	62%	57%	100%	77%	60%
	COVERAGE	100%	101%	100%	99%	88%	100%	101%	101%	101%
SAU1001	SeqID	10363	10481	11060	11568		11858	12443	13233	13965
58	IDENTITY	60%	75%	59%	63%		59%	100%	77%	58%
	COVERAGE	98%	97%	98%	97%		98%	100%	97%	99%
SAU1001	SeqID	10069	10630	11239	11382		11971	12583	13597	14084
62	IDENTITY	43%	49%	44%	37%		43%	100%	46%	43%
	COVERAGE	92%	89%	88%	80%		83%	100%	89%	93%
SAU1001	SeqID	10250	10651	11012			11954	12582	13272	13705
75	IDENTITY	34%	42%	38%			34%	100%	42%	35%
	COVERAGE	98%	100%	93%			93%	100%	102%	99%
SAU1001	SeqID							12362		
82	IDENTITY							100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100186	COVERAGE									
	SeqID	10043	10489	11124	11423		11939	12317	13355	13909
	IDENTITY	46%	61%	44%	46%		45%	100%	54%	45%
	COVERAGE	99%	99%	99%	98%		100%	101%	99%	101%
SAU100198	SeqID				11445			12120	13414	
	IDENTITY				29%			100%	29%	
	COVERAGE				78%			101%	79%	
SAU100227	SeqID		10765					12525		
	IDENTITY		36%					100%		
	COVERAGE		100%					100%		
SAU100242	SeqID	10097		11201			11836	12336		14056
	IDENTITY	65%		62%			65%	100%		65%
	COVERAGE	94%		96%			95%	100%		94%
SAU100246	SeqID		10821					12496	13490	
	IDENTITY		35%					100%	38%	
	COVERAGE		101%					101%	93%	
SAU100251	SeqID							12363		
	IDENTITY							100%		
	COVERAGE							100%		
SAU100265	SeqID	10469						12122		
	IDENTITY	37%						100%		
	COVERAGE	88%						100%		
SAU100266	SeqID							12256		
	IDENTITY							100%		
	COVERAGE							101%		
SAU100272	SeqID		10617					12141		
	IDENTITY		26%					100%		
	COVERAGE		104%					100%		
SAU100275	SeqID	10041	10487	11149	11621		11941	12314	13438	13907
	IDENTITY	52%	73%	47%	51%		51%	100%	65%	51%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERAGE	88%	94%	93%	98%			100%	98%	88%
SAU100300	SeqID	10434	10612	11039	11413		11999	12451	13517	
	IDENTITY	67%	86%	68%	63%		65%	100%	82%	
	COVERAGE	99%	99%	99%	97%		99%	101%	97%	
SAU100301	SeqID	10433	10624	11083	11414		12000	12452	13168	
	IDENTITY	41%	58%	41%	35%		42%	100%	51%	
	COVERAGE	99%	98%	102%	96%		98%	101%	97%	
SAU100302	SeqID	10432		11082			12001	12453		
	IDENTITY	25%		34%			31%	100%		
	COVERAGE	92%		93%			103%	102%		
SAU100305	SeqID	10311	10774	10990			11885	12397	13491	13769
	IDENTITY	40%	50%	38%			40%	100%	49%	40%
	COVERAGE	94%	99%	94%			92%	100%	101%	94%
SAU100307	SeqID	10392	10725	10954		11685		12313	13252	13919
	IDENTITY	28%	32%	29%		28%		100%	29%	28%
	COVERAGE	99%	100%	99%		99%		100%	99%	99%
SAU100308	SeqID	10013	10814	10963				12312	13244	13711
	IDENTITY	26%	44%	30%				100%	40%	27%
	COVERAGE	90%	86%	86%				100%	92%	90%
SAU100313	SeqID		10757					12661	13293	
	IDENTITY		46%					100%	43%	
	COVERAGE		99%					100%	100%	
SAU100315	SeqID	10419	10802	11136	11326	11727	12087	12358	13521	13791
	IDENTITY	54%	73%	53%	53%	55%	53%	100%	74%	54%
	COVERAGE	96%	96%	96%	96%	82%	97%	100%	91%	96%
SAU100323	SeqID	10216	10855					12575		13933
	IDENTITY	32%	71%					100%		34%
	COVERAGE	88%	99%					100%		88%
SAU100347	SeqID		10895	10961			12077	12334	13206	
	IDENTITY		44%	30%			30%	100%	42%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100355	COVERAGE		106%	84%			100%	100%	100%	
	SeqID		10683					12155	13300	
	IDENTITY		42%					100%	31%	
	COVERAGE		93%					100%	109%	
SAU100359	SeqID		10757					12239	13293	
	IDENTITY		52%					100%	43%	
	COVERAGE		97%					100%	99%	
SAU100381	SeqID	10411	10674				11903	12276		14031
	IDENTITY	28%	29%				33%	100%		28%
	COVERAGE	101%	99%				92%	100%		101%
SAU100389	SeqID	10473	10737		11374			12279	13344	
	IDENTITY	27%	50%		41%			100%	27%	
	COVERAGE	75%	95%		99%			100%	71%	
SAU100401	SeqID	10090	10706	10980		11641		12576		14053
	IDENTITY	31%	30%	27%		33%		100%		31%
	COVERAGE	95%	99%	95%		95%		101%		99%
SAU100412	SeqID	10102	10563	11194	11360		5150	12197	13468	
	IDENTITY	31%	42%	30%	33%		35%	100%	40%	
	COVERAGE	74%	100%	80%	74%		73%	100%	97%	
SAU100414	SeqID	10453	10556	11205	11300		11943	12148	13401	13872
	IDENTITY	60%	80%	61%	60%		67%	100%	76%	60%
	COVERAGE	96%	99%	98%	99%		91%	101%	96%	96%
SAU100432	SeqID	10436	10614	11071	11411		5181	12450	13246	14045
	IDENTITY	34%	60%	33%	31%		39%	100%	55%	31%
	COVERAGE	98%	98%	100%	95%		99%	101%	98%	98%
SAU100433	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	IDENTITY	58%	64%	63%	57%		58%	100%	69%	58%
	COVERAGE	97%	99%	98%	99%		98%	101%	99%	98%
SAU100436	SeqID		10569					12154	13393	
	IDENTITY		27%					100%	27%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1004 43	COVERAGE		100%					100%	100%	
	SeqID	10272	10894	11081			11930	12333	13515	13869
	IDENTITY	40%	52%	39%			38%	100%	45%	40%
	COVERAGE	92%	100%	96%			92%	100%	100%	92%
SAU1004 44	SeqID	10440	10583	11016	11540		11967	12392	13403	14041
	IDENTITY	29%	30%	41%	41%		28%	100%	52%	29%
	COVERAGE	75%	88%	94%	90%		81%	100%	91%	75%
SAU1004 75	SeqID		10927				11911	12337		
	IDENTITY		33%				30%	100%		
	COVERAGE		101%				101%	100%		
SAU1004 78	SeqID			11273				12605		
	IDENTITY			25%				100%		
	COVERAGE			96%				100%		
SAU1004 89	SeqID	10332	10685	11074	11580	11729	11778	12566	13298	14100
	IDENTITY	33%	33%	31%	34%	34%	29%	100%	34%	33%
	COVERAGE	101%	102%	99%	94%	101%	99%	100%	97%	94%
SAU1004 96	SeqID		10744					12484		
	IDENTITY		40%					100%		
	COVERAGE		80%					100%		
SAU1004 97	SeqID	10245	10709	11171	11395		11792	12140		13740
	IDENTITY	46%	59%	49%	44%		48%	100%		45%
	COVERAGE	99%	101%	99%	100%		99%	100%		100%
SAU1005 14	SeqID	10215			11388		12036	12626		13932
	IDENTITY	52%			34%		51%	100%		51%
	COVERAGE	93%			95%		98%	100%		95%
SAU1005 21	SeqID	10251		10969	11370		11955	12600		13703
	IDENTITY	43%		39%	34%		39%	100%		42%
	COVERAGE	104%		108%	103%		103%	100%		104%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1005 22	SeqID IDENTITY COVERAGE	10114 36% 91%		11206 34% 89%		11680 30% 80%	11904 36% 90%	12599 100% 100%		14007 35% 91%
SAU1005 27	SeqID IDENTITY COVERAGE	10298 44% 98%	10721 48% 97%	10996 42% 99%			11782 41% 98%	12341 100% 101%	13452 43% 98%	13736 45% 97%
SAU1005 28	SeqID IDENTITY COVERAGE		10521 30% 83%					12507 100% 101%	13470 33% 71%	
SAU1005 32	SeqID IDENTITY COVERAGE	10235 39% 101%	10645 47% 100%	11128 29% 72%	11389 34% 90%			12580 100% 100%	13193 40% 97%	13744 31% 72%
SAU1005 42	SeqID IDENTITY COVERAGE	10371 52% 100%		11070 51% 98%	11422 46% 98%		12017 31% 102%	12532 100% 100%	13444 35% 102%	13806 52% 100%
SAU1005 46	SeqID IDENTITY COVERAGE	10359 43% 97%		11097 46% 97%	11596 34% 90%		5176 47% 99%	12235 100% 100%	13197 66% 99%	13974 46% 91%
SAU1005 47	SeqID IDENTITY COVERAGE	10358 41% 92%	10549 62% 100%	11098 39% 97%	11595 40% 96%		5175 46% 97%	12240 100% 100%	13198 63% 100%	13973 41% 93%
SAU1005 57	SeqID IDENTITY COVERAGE		10928 50% 99%					12565 100% 100%	13651 49% 99%	
SAU1005 82	SeqID IDENTITY COVERAGE							12503 100% 100%		
SAU1005 90	SeqID IDENTITY COVERAGE							12121 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100595	SeqID IDENTITY COVERAGE	10051 47% 88%	10832 66% 89%		11464 42% 89%		12109 50% 93%	12547 100% 100%	13174 46% 90%	13722 42% 91%
SAU100596	SeqID IDENTITY COVERAGE	10050 36% 99%	10833 50% 99%	11067 31% 100%	11624 41% 92%	11656 38% 89%	12110 42% 95%	12548 100% 100%	13173 30% 106%	13720 32% 95%
SAU100601	SeqID IDENTITY COVERAGE							12616 100% 100%		
SAU100608	SeqID IDENTITY COVERAGE	10032 30% 102%	10870 61% 96%	11190 29% 100%	11349 29% 98%		12008 34% 87%	12293 100% 100%	13507 50% 96%	14079 28% 104%
SAU100610	SeqID IDENTITY COVERAGE							12294 100% 100%		
SAU100613	SeqID IDENTITY COVERAGE	10378 44% 91%	10904 54% 88%	11094 43% 93%			11781 46% 73%	12126 100% 100%	13589 49% 89%	
SAU100617	SeqID IDENTITY COVERAGE		10502 26% 91%					12295 100% 100%	13314 25% 91%	
SAU100633	SeqID IDENTITY COVERAGE	10079 27% 92%	10589 42% 103%			11698 25% 89%	5107 29% 101%	12515 100% 100%	13644 35% 105%	13724 26% 103%
SAU100646	SeqID IDENTITY COVERAGE	10051 50% 95%	10570 48% 94%		11464 46% 97%		12109 49% 95%	12168 100% 100%	13174 42% 95%	14109 50% 96%
SAU100658	SeqID IDENTITY COVERAGE	10322 49% 100%	10813 59% 100%	11177 49% 100%	11351 46% 100%		12018 48% 100%	12388 100% 100%	13186 58% 100%	13733 49% 100%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100659	SeqID IDENTITY COVERAGE	10045 47% 92%	10923 54% 92%	11174 45% 95%	11601 40% 103%		11937 46% 97%	12390 100% 101%	13616 56% 95%	13911 44% 81%
SAU100679	SeqID IDENTITY COVERAGE	10303 32% 96%		10997 31% 99%	11453 32% 106%	11713 33% 96%	11799 35% 97%	12137 100% 100%	13329 42% 104%	13757 35% 96%
SAU100684	SeqID IDENTITY COVERAGE	10412 46% 97%			11486 40% 99%		12097 46% 99%	12632 100% 100%		13749 46% 97%
SAU100685	SeqID IDENTITY COVERAGE							12633 100% 100%		
SAU100689	SeqID IDENTITY COVERAGE		10694 55% 98%					12323 100% 100%	13311 46% 96%	
SAU100702	SeqID IDENTITY COVERAGE		10655 46% 97%					12196 100% 100%	13671 41% 91%	
SAU100710	SeqID IDENTITY COVERAGE						11908 27% 73%	12546 100% 101%		
SAU100714	SeqID IDENTITY COVERAGE	10465 48% 108%	10675 66% 100%	11238 41% 110%	11563 41% 102%		11961 44% 108%	12635 100% 103%	13382 60% 101%	13853 48% 108%
SAU100731	SeqID IDENTITY COVERAGE	10071 62% 99%	10688 79% 100%	11019 67% 100%	11371 40% 101%		11850 63% 99%	12601 100% 101%	13319 76% 100%	13945 60% 101%
SAU100733	SeqID IDENTITY COVERAGE	10415 41% 95%			11611 33% 92%	11636 42% 74%	12084 42% 95%	12602 100% 100%		13746 39% 95%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100734	SeqID IDENTITY COVERAGE	10321 28% 98%	10573 36% 95%	11142 29% 97%	11306 27% 90%		12031 28% 93%	12603 100% 100%	13273 31% 72%	13734 29% 101%
SAU100736	SeqID IDENTITY COVERAGE		10585 27% 97%					12391 100% 100%	13404 26% 97%	
SAU100738	SeqID IDENTITY COVERAGE	10188 48% 97%	10847 45% 98%	10953 46% 98%	11600 42% 97%	11634 48% 94%	11907 51% 97%	12624 100% 100%	13169 45% 97%	13981 49% 97%
SAU100741	SeqID IDENTITY COVERAGE	10081 65% 100%	10591 50% 101%		11459 35% 82%		11776 54% 100%	12409 100% 101%		13714 66% 101%
SAU100745	SeqID IDENTITY COVERAGE	10442 34% 98%	10484 53% 97%	11202 35% 100%	11607 31% 99%	11733 35% 101%	11906 34% 98%	12596 100% 100%	13453 49% 98%	13847 35% 101%
SAU100747	SeqID IDENTITY COVERAGE		10749 32% 74%					12597 100% 100%	13266 31% 73%	
SAU100751	SeqID IDENTITY COVERAGE	10425 62% 99%	10866 64% 99%	11080 59% 98%		11747 62% 87%	11927 62% 99%	12335 100% 100%	13431 63% 99%	13788 61% 99%
SAU100752	SeqID IDENTITY COVERAGE	10140 31% 71%					11976 35% 82%	12524 100% 100%		14022 38% 72%
SAU100767	SeqID IDENTITY COVERAGE	10290 43% 100%					12094 42% 90%	12579 100% 100%		13875 42% 100%
SAU100771	SeqID IDENTITY COVERAGE	10084 30% 88%					11821 29% 80%	12545 100% 101%	13306 28% 90%	13710 26% 94%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100773	SeqID IDENTITY COVERAGE	10055 47% 94%	10758 70% 100%	11093 41% 98%	11336 41% 96%	11763 46% 94%	11928 51% 93%	12377 100% 101%	13250 70% 96%	
SAU100776	SeqID IDENTITY COVERAGE							12482 100% 100%		
SAU100778	SeqID IDENTITY COVERAGE	10083 52% 89%		10957 52% 89%			11970 45% 88%	12514 100% 100%		14062 47% 89%
SAU100793	SeqID IDENTITY COVERAGE							12188 100% 100%	13392 27% 103%	
SAU100794	SeqID IDENTITY COVERAGE	10203 25% 101%						12189 100% 100%		
SAU100799	SeqID IDENTITY COVERAGE							12682 100% 100%		
SAU100808	SeqID IDENTITY COVERAGE							12345 100% 100%		14081 35% 70%
SAU100810	SeqID IDENTITY COVERAGE	10070 51% 94%					11824 49% 96%	12343 100% 100%		14080 50% 96%
SAU100813	SeqID IDENTITY COVERAGE	10314 47% 98%	10764 63% 94%	11216 47% 100%	11501 45% 91%		5198 48% 92%	12322 100% 100%	13381 58% 95%	13765 50% 92%
SAU100831	SeqID IDENTITY COVERAGE	10376 42% 97%	10741 58% 98%	11058 42% 102%			12093 42% 98%	12403 100% 100%	13349 51% 98%	13811 42% 101%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100836	SeqID IDENTITY COVERAGE							12212 100% 100%		
SAU100838	SeqID IDENTITY COVERAGE							12211 100% 100%		
SAU100839	SeqID IDENTITY COVERAGE		10794 42% 100%					12210 100% 100%	13183 44% 100%	
SAU100843	SeqID IDENTITY COVERAGE	10126 26% 101%	10921 28% 73%	10974 28% 101%	11342 28% 102%			12328 100% 100%	13601 26% 100%	14092 26% 104%
SAU100845	SeqID IDENTITY COVERAGE							12329 100% 100%		
SAU100858	SeqID IDENTITY COVERAGE	10256 37% 106%	10776 48% 98%		11367 35% 103%	11719 37% 106%		12401 100% 101%	13472 39% 100%	13796 39% 106%
SAU100859	SeqID IDENTITY COVERAGE	10446 33% 94%	10777 38% 94%	11254 33% 95%	11548 35% 96%		12071 34% 94%	12402 100% 100%	13473 38% 92%	14026 32% 95%
SAU100865	SeqID IDENTITY COVERAGE	10252 39% 100%	10877 49% 99%	11010 41% 100%	11406 28% 101%		11956 44% 99%	12648 100% 100%	13506 48% 99%	13704 38% 100%
SAU100866	SeqID IDENTITY COVERAGE	10191 54% 100%	10878 64% 100%	11005 51% 100%	11347 51% 100%		11815 53% 100%	12553 100% 100%	13492 57% 99%	13754 55% 100%
SAU100879	SeqID IDENTITY COVERAGE							12483 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1008 80	SeqID IDENTITY COVERAGE	10429 31% 81%	10720 51% 95%		11335 35% 97%		12039 36% 81%	12340 100% 100%	13451 45% 99%	14072 32% 85%
SAU1008 82	SeqID IDENTITY COVERAGE	10322 43% 98%	10750 54% 98%	11177 42% 98%	11351 40% 99%		12018 45% 98%	12374 100% 100%	13330 52% 98%	13733 43% 98%
SAU1008 85	SeqID IDENTITY COVERAGE	10410 52% 93%	10754 67% 74%	11001 53% 94%	11509 52% 96%		12095 53% 92%	12376 100% 100%		14032 52% 93%
SAU1008 86	SeqID IDENTITY COVERAGE	10224 38% 97%	10701 60% 83%	11213 38% 93%	11357 36% 99%		11905 36% 104%	12139 100% 100%	13348 52% 102%	13957 38% 98%
SAU1008 87	SeqID IDENTITY COVERAGE	10393 50% 85%	10952 51% 96%	11057 50% 82%	11330 49% 83%		11774 48% 83%	12138 100% 100%	13342 70% 96%	13920 50% 85%
SAU1008 99	SeqID IDENTITY COVERAGE							12277 100% 100%		
SAU1009 01	SeqID IDENTITY COVERAGE							12278 100% 100%		
SAU1009 16	SeqID IDENTITY COVERAGE	10209 32% 75%	10887 34% 72%					12394 100% 101%		13876 32% 75%
SAU1009 20	SeqID IDENTITY COVERAGE	10060 43% 91%	10772 48% 86%	11191 31% 87%	11530 28% 91%	11756 40% 86%	11983 30% 90%	12395 100% 100%		13896 43% 91%
SAU1009 21	SeqID IDENTITY COVERAGE	10027 32% 101%	10773 43% 96%	11185 33% 96%			12012 33% 96%	12396 100% 100%	13478 34% 98%	14074 32% 101%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1009 32	SeqID IDENTITY COVERAGE	10095 39% 101%		11271 36% 101%			11834 39% 102%	12615 100% 100%		14055 39% 101%
SAU1009 44	SeqID IDENTITY COVERAGE	10017 37% 80%	10687 26% 108%	11219 36% 79%	11506 36% 79%		12057 39% 83%	12505 100% 100%	13498 27% 83%	14012 39% 80%
SAU1009 52	SeqID IDENTITY COVERAGE		10717 33% 104%					12523 100% 100%	13312 31% 102%	
SAU1009 59	SeqID IDENTITY COVERAGE		10704 58% 99%					12485 100% 100%	13504 49% 101%	
SAU1009 61	SeqID IDENTITY COVERAGE	10320 42% 98%	10671 63% 99%	11141 47% 98%	11312 40% 97%		12030 50% 98%	12638 100% 101%	13322 57% 101%	13766 42% 99%
SAU1009 62	SeqID IDENTITY COVERAGE				11299 28% 80%			12639 100% 101%	13577 26% 92%	
SAU1009 63	SeqID IDENTITY COVERAGE	10319 60% 84%	10633 79% 96%	11140 59% 81%	11493 61% 81%		12029 63% 84%	12640 100% 101%	13320 81% 92%	13771 60% 88%
SAU1009 64	SeqID IDENTITY COVERAGE		10501 61% 101%	11139 45% 76%			12028 47% 77%	12641 100% 100%	13331 60% 101%	
SAU1009 65	SeqID IDENTITY COVERAGE							12642 100% 101%		
SAU1009 70	SeqID IDENTITY COVERAGE	10128 52% 99%	10516 54% 99%	11247 39% 100%	11512 47% 100%		11891 52% 99%	12529 100% 100%	13362 46% 99%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU100996	SeqID IDENTITY COVERAGE		10686 38% 97%		11350 34% 73%			12606 100% 100%	13600 39% 96%	
SAU101006	SeqID IDENTITY COVERAGE	10185 29% 84%	10572 40% 98%	11022 31% 87%	11473 26% 94%		5122 26% 79%	12190 100% 100%		13820 30% 91%
SAU101020	SeqID IDENTITY COVERAGE							12710 100% 100%		
SAU101024	SeqID IDENTITY COVERAGE							12711 100% 101%		
SAU101028	SeqID IDENTITY COVERAGE	10034 46% 106%	10848 57% 101%	11148 43% 107%	11364 46% 100%		12006 46% 108%	12552 100% 100%	13471 55% 100%	13901 45% 106%
SAU101034	SeqID IDENTITY COVERAGE		10578 36% 80%					12608 100% 100%	13654 37% 71%	
SAU101038	SeqID IDENTITY COVERAGE		10716 42% 96%				11822 35% 78%	12521 100% 101%	13428 36% 103%	
SAU101039	SeqID IDENTITY COVERAGE							12522 100% 100%		
SAU101065	SeqID IDENTITY COVERAGE	10221 37% 98%	10681 49% 103%	11210 40% 100%	11607 28% 108%	11668 38% 97%	11801 36% 98%	12289 100% 100%	13191 46% 102%	14027 31% 98%
SAU101067	SeqID IDENTITY COVERAGE		10682 41% 100%					12290 100% 100%	13394 40% 99%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101070	SeqID IDENTITY COVERAGE		10770 40% 89%					12291 100% 100%	13380 32% 82%	
SAU101084	SeqID IDENTITY COVERAGE	10066 36% 90%		11156 34% 102%			11974 35% 92%	12283 100% 100%		
SAU101085	SeqID IDENTITY COVERAGE	10170 37% 89%		11263 34% 88%	11462 37% 94%		11973 38% 94%	12284 100% 100%	13225 47% 101%	13993 32% 88%
SAU101086	SeqID IDENTITY COVERAGE				11366 42% 74%		11972 34% 94%	12285 100% 100%	13666 49% 101%	
SAU101090	SeqID IDENTITY COVERAGE		10755 36% 97%					12191 100% 100%	13188 31% 97%	
SAU101092	SeqID IDENTITY COVERAGE	10450 35% 71%	10567 33% 96%				11847 30% 72%	12192 100% 100%		
SAU101104	SeqID IDENTITY COVERAGE	10135 38% 98%	10768 45% 100%	11248 39% 100%	11404 37% 92%	11732 37% 99%	11869 42% 99%	12195 100% 100%	13482 38% 96%	13827 37% 99%
SAU101143	SeqID IDENTITY COVERAGE	10040 47% 99%		11157 27% 82%	11315 43% 98%		11968 44% 100%	12502 100% 100%		13906 47% 99%
SAU101145	SeqID IDENTITY COVERAGE		10548 42% 98%				12070 43% 96%	12299 100% 101%		
SAU101155	SeqID IDENTITY COVERAGE	10287 43% 95%	10697 49% 95%	11077 40% 95%	11352 30% 86%	11690 42% 95%	11944 42% 94%	12310 100% 100%	13549 37% 76%	13868 43% 95%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101156	SeqID IDENTITY COVERAGE	10426 56% 96%	10698 63% 101%	11032 60% 96%	11333 52% 97%		12083 58% 96%	12311 100% 101%		13790 55% 96%
SAU101159	SeqID IDENTITY COVERAGE		10891 65% 100%		11532 36% 100%			12331 100% 100%	13463 54% 104%	
SAU101175	SeqID IDENTITY COVERAGE							12213 100% 101%		
SAU101180	SeqID IDENTITY COVERAGE	10061 38% 72%	10888 50% 89%				11910 37% 70%	12656 100% 100%		
SAU101183	SeqID IDENTITY COVERAGE		10843 42% 102%					12304 100% 100%		
SAU101184	SeqID IDENTITY COVERAGE	10477 37% 86%	10711 46% 100%	11218 36% 102%	11376 30% 85%	11735 38% 82%	12033 35% 85%	12305 100% 100%	13499 44% 98%	13709 38% 82%
SAU101189	SeqID IDENTITY COVERAGE							12264 100% 100%		
SAU101197	SeqID IDENTITY COVERAGE	10180 31% 98%	10787 44% 98%	11024 31% 101%			11924 27% 100%	12300 100% 100%	13340 46% 98%	13976 30% 98%
SAU101198	SeqID IDENTITY COVERAGE	10218 43% 74%	10786 50% 98%	11023 43% 73%			11923 41% 75%	12301 100% 100%	13341 46% 102%	
SAU101199	SeqID IDENTITY COVERAGE	10088 29% 97%	10742 40% 86%	10970 31% 94%			11949 36% 97%	12302 100% 100%	13178 37% 87%	14052 30% 98%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1012 20	SeqID IDENTITY COVERAGE	10286 32% 74%	10864 37% 81%					12645 100% 100%	13390 39% 99%	13870 31% 74%
SAU1012 24	SeqID IDENTITY COVERAGE				11533 28% 77%			12647 100% 100%		
SAU1012 26	SeqID IDENTITY COVERAGE		10837 52% 96%			11658 28% 75%	11825 37% 90%	12298 100% 100%	13296 27% 77%	13721 27% 77%
SAU1012 31	SeqID IDENTITY COVERAGE	10301 32% 101%	10513 61% 100%				12079 32% 73%	12303 100% 101%		13759 31% 106%
SAU1012 35	SeqID IDENTITY COVERAGE		10616 37% 84%	11087 27% 90%				12561 100% 100%	13486 35% 97%	
SAU1012 36	SeqID IDENTITY COVERAGE	10089 42% 101%	10500 55% 77%			11673 29% 108%	11951 39% 100%	12564 100% 100%	13474 35% 103%	
SAU1012 39	SeqID IDENTITY COVERAGE				11361 33% 98%			12570 100% 100%		
SAU1012 40	SeqID IDENTITY COVERAGE							12573 100% 101%		
SAU1012 42	SeqID IDENTITY COVERAGE	10335 48% 104%	10879 67% 101%	11121 47% 104%	11425 48% 105%		11988 47% 104%	12578 100% 101%	13240 55% 101%	14095 47% 105%
SAU1012 47	SeqID IDENTITY COVERAGE		10919 32% 91%				11984 36% 90%	12512 100% 100%	13359 33% 85%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101262	SeqID IDENTITY COVERAGE	10137 28% 73%	10735 70% 100%		11399 47% 101%		11922 33% 97%	12488 100% 100%	13238 67% 100%	13837 28% 73%
SAU101266	SeqID IDENTITY COVERAGE	10238 45% 100%	10789 57% 99%	11178 46% 100%	11517 41% 98%		11829 43% 89%	12490 100% 100%	13317 51% 98%	13864 44% 100%
SAU101267	SeqID IDENTITY COVERAGE							12364 100% 100%		
SAU101270	SeqID IDENTITY COVERAGE	10175 50% 96%	10718 62% 99%	11220 47% 97%	11324 45% 93%		11881 52% 97%	12365 100% 100%	13383 61% 98%	13942 50% 96%
SAU101271	SeqID IDENTITY COVERAGE	10174 37% 100%	10719 46% 102%	11221 36% 100%	11556 25% 100%		11880 35% 100%	12366 100% 100%	13385 46% 101%	13943 37% 75%
SAU101275	SeqID IDENTITY COVERAGE	10232 35% 95%	10684 57% 101%	10981 38% 93%	11521 33% 98%	11708 34% 96%	11845 34% 94%	12604 100% 100%	13299 57% 101%	13954 35% 95%
SAU101286	SeqID IDENTITY COVERAGE		10884 47% 100%					12292 100% 101%	13189 40% 99%	
SAU101293	SeqID IDENTITY COVERAGE							12631 100% 101%		
SAU101300	SeqID IDENTITY COVERAGE		10751 57% 93%					12557 100% 101%	13194 54% 90%	
SAU101301	SeqID IDENTITY COVERAGE		10752 57% 96%				11785 27% 94%	12558 100% 101%	13195 54% 99%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101302	SeqID IDENTITY COVERAGE		10753 49% 101%		11317 33% 86%			12559 100% 101%	13611 26% 72%	
SAU101310	SeqID IDENTITY COVERAGE	10330 47% 98%	10924 52% 98%	11160 48% 98%	11321 43% 98%		12063 47% 98%	12562 100% 100%	13364 51% 98%	13885 47% 98%
SAU101311	SeqID IDENTITY COVERAGE	10094 46% 98%		11278 46% 98%			11859 42% 96%	12563 100% 100%		13891 46% 95%
SAU101320	SeqID IDENTITY COVERAGE	10263 50% 100%	10861 59% 99%	10965 49% 99%	11562 39% 100%		11948 51% 99%	12128 100% 100%	13254 56% 97%	14089 49% 100%
SAU101327	SeqID IDENTITY COVERAGE	10018 35% 100%	10710 46% 97%	11147 43% 101%			11779 34% 92%	12612 100% 101%	13495 35% 99%	14014 35% 100%
SAU101339	SeqID IDENTITY COVERAGE	10093 55% 99%	10520 30% 74%		11365 26% 74%		11839 54% 97%	12399 100% 100%	13405 27% 76%	13888 45% 99%
SAU101340	SeqID IDENTITY COVERAGE	10092 37% 106%					11840 35% 101%	12400 100% 101%		13889 39% 104%
SAU101341	SeqID IDENTITY COVERAGE	10230 47% 93%	10925 55% 92%	11212 48% 92%	11385 48% 98%		11898 45% 92%	12618 100% 100%	13365 48% 100%	13952 47% 93%
SAU101343	SeqID IDENTITY COVERAGE	10422 50% 99%	10649 55% 100%	11162 49% 99%		11721 50% 99%		12619 100% 100%	13346 58% 92%	13785 51% 99%
SAU101344	SeqID IDENTITY COVERAGE	10171 48% 81%	10650 62% 88%	11252 40% 79%			11826 37% 82%	12620 100% 100%	13347 44% 79%	13755 38% 81%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1013 46	SeqID IDENTITY COVERAGE	10058 36% 99%			11282 35% 103%		11803 43% 99%	12621 100% 100%		13894 36% 99%
SAU1013 47	SeqID IDENTITY COVERAGE	10139 63% 100%		11163 29% 96%	11283 62% 101%		11877 62% 100%	12622 100% 100%	13259 30% 91%	13839 62% 100%
SAU1013 50	SeqID IDENTITY COVERAGE	10184 61% 95%	10508 56% 98%		11318 32% 81%		12069 46% 100%	12487 100% 100%	13286 55% 97%	13982 60% 97%
SAU1013 51	SeqID IDENTITY COVERAGE		10507 60% 96%					12486 100% 100%	13285 59% 96%	
SAU1013 60	SeqID IDENTITY COVERAGE	10138 56% 98%	10571 70% 101%	10977 54% 98%	11598 35% 97%	11684 55% 88%	11878 58% 98%	12555 100% 100%	13175 71% 101%	13838 56% 98%
SAU1013 65	SeqID IDENTITY COVERAGE	10269 45% 101%	10491 55% 101%	11127 44% 101%	11577 40% 99%		11809 45% 101%	12556 100% 100%	13295 50% 100%	13874 45% 101%
SAU1013 66	SeqID IDENTITY COVERAGE	10147 49% 99%	10654 73% 98%					12266 100% 100%	13179 56% 99%	13843 48% 99%
SAU1013 69	SeqID IDENTITY COVERAGE							12274 100% 100%		
SAU1013 71	SeqID IDENTITY COVERAGE				11372 40% 86%		11902 32% 79%	12275 100% 100%	13243 34% 77%	
SAU1013 81	SeqID IDENTITY COVERAGE	10373 26% 98%						12145 100% 100%	13432 41% 99%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101382	SeqID IDENTITY COVERAGE	10239 53% 98%	10707 60% 99%	11179 50% 97%	11292 42% 97%	11635 39% 79%	11879 53% 98%	12146 100% 100%	13657 63% 96%	13862 52% 98%
SAU101383	SeqID IDENTITY COVERAGE	10317 37% 102%	10625 39% 90%	11226 36% 97%	11418 26% 98%		12055 38% 94%	12147 100% 100%	13422 37% 112%	13761 39% 94%
SAU101385	SeqID IDENTITY COVERAGE	10403 33% 99%	10830 52% 90%	11030 31% 92%	11368 27% 89%	11640 32% 96%	12115 29% 98%	12385 100% 100%	13508 38% 92%	14067 32% 99%
SAU101387	SeqID IDENTITY COVERAGE	10402 27% 87%	10839 35% 88%		11549 27% 71%		12114 27% 87%	12386 100% 101%	13509 32% 90%	14068 27% 87%
SAU101389	SeqID IDENTITY COVERAGE	10401 55% 98%	10801 72% 99%	11029 57% 99%	11400 60% 100%		12113 57% 98%	12387 100% 100%	13510 74% 94%	14069 55% 98%
SAU101398	SeqID IDENTITY COVERAGE	10313 55% 100%	10881 78% 101%	11224 54% 100%	11502 51% 99%	11754 57% 101%	12051 56% 100%	12324 100% 101%	13485 68% 101%	13767 54% 101%
SAU101399	SeqID IDENTITY COVERAGE	10312 50% 99%	10882 63% 100%	10989 48% 98%	11416 38% 97%	11755 51% 85%	12050 51% 97%	12325 100% 100%	13699 58% 99%	13768 49% 99%
SAU101400	SeqID IDENTITY COVERAGE		10743 46% 96%		11448 32% 95%			12326 100% 100%	13391 41% 96%	
SAU101408	SeqID IDENTITY COVERAGE	10267 37% 100%	10509 43% 99%					12308 100% 100%	13278 42% 101%	14050 39% 100%
SAU101421	SeqID IDENTITY COVERAGE		10676 38% 93%					12498 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1014 27	SeqID IDENTITY COVERAGE							12500 100% 100%	13234 48% 100%	
SAU1014 32	SeqID IDENTITY COVERAGE			11046 57% 99%	11286 60% 100%	11744 63% 101%	12065 68% 99%	12184 100% 101%	13538 26% 73%	
SAU1014 36	SeqID IDENTITY COVERAGE	10271 27% 90%		11045 62% 99%	11285 61% 97%		12067 59% 98%	12183 100% 100%		13873 27% 90%
SAU1014 38	SeqID IDENTITY COVERAGE	10146 30% 88%	10825 29% 94%	11042 29% 89%				12379 100% 100%	13337 27% 94%	13842 30% 88%
SAU1014 44	SeqID IDENTITY COVERAGE	10254 60% 100%	10827 66% 101%	11144 57% 100%	11301 54% 100%		12034 60% 100%	12381 100% 100%	13335 61% 99%	13792 59% 100%
SAU1014 45	SeqID IDENTITY COVERAGE	10248 52% 99%	10828 70% 100%	11207 52% 96%			12037 54% 99%	12382 100% 100%	13408 72% 100%	13949 51% 100%
SAU1014 46	SeqID IDENTITY COVERAGE	10411 50% 98%	10674 59% 100%				11903 33% 97%	12383 100% 100%		14031 50% 99%
SAU1014 47	SeqID IDENTITY COVERAGE							12683 100% 101%		
SAU1014 52	SeqID IDENTITY COVERAGE							12684 100% 100%		
SAU1014 55	SeqID IDENTITY COVERAGE							12686 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1014 61	SeqID IDENTITY COVERAGE		10705 54% 93%				11790 26% 86%	12680 100% 101%		
SAU1014 63	SeqID IDENTITY COVERAGE	10268 29% 77%	10708 45% 98%				11919 26% 91%	12679 100% 101%	13584 26% 88%	14051 29% 77%
SAU1014 76	SeqID IDENTITY COVERAGE	10469 38% 84%	10905 29% 94%					12254 100% 100%	13454 25% 95%	13905 26% 73%
SAU1014 81	SeqID IDENTITY COVERAGE	10125 40% 93%	10920 39% 95%	10975 40% 96%	11290 32% 93%		11894 39% 96%	12130 100% 100%	13580 41% 96%	
SAU1014 82	SeqID IDENTITY COVERAGE	10126 55% 98%	10921 51% 100%	10974 52% 98%	11342 44% 98%	11738 36% 77%	11893 52% 98%	12123 100% 100%	13360 48% 99%	14092 37% 101%
SAU1014 83	SeqID IDENTITY COVERAGE	10127 65% 88%	10918 41% 90%	10973 59% 90%	11341 58% 90%		11892 61% 87%	12124 100% 101%	13674 51% 92%	13871 31% 94%
SAU1014 88	SeqID IDENTITY COVERAGE		10730 28% 95%				11868 25% 74%	12164 100% 100%	13450 33% 98%	13799 28% 73%
SAU1014 91	SeqID IDENTITY COVERAGE		10580 42% 104%					12165 100% 100%	13315 42% 95%	
SAU1014 92	SeqID IDENTITY COVERAGE	10073 38% 98%	10581 52% 101%	11020 37% 98%	11284 29% 78%		11831 37% 94%	12166 100% 101%	13323 43% 85%	13715 38% 98%
SAU1014 93	SeqID IDENTITY COVERAGE	10074 42% 96%		11021 41% 97%	11381 30% 94%		11832 43% 98%	12167 100% 101%	13564 64% 91%	13716 44% 96%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101495	SeqID IDENTITY COVERAGE	10030 32% 92%	10805 34% 92%	11188 36% 90%	11458 29% 86%		5187 33% 90%	12360 100% 100%	13333 32% 94%	14077 32% 92%
SAU101497	SeqID IDENTITY COVERAGE		10806 59% 100%					12361 100% 100%		
SAU101509	SeqID IDENTITY COVERAGE	10121 34% 104%				11712 36% 104%		12418 100% 100%	13249 49% 83%	
SAU101526	SeqID IDENTITY COVERAGE		10901 38% 88%					12179 100% 100%	13465 34% 89%	
SAU101529	SeqID IDENTITY COVERAGE							12544 100% 100%		
SAU101541	SeqID IDENTITY COVERAGE	10024 41% 101%	10631 63% 100%	11182 42% 101%	11526 38% 98%		12014 42% 101%	12344 100% 100%	13647 59% 101%	14019 40% 100%
SAU101543	SeqID IDENTITY COVERAGE	10025 26% 78%	10634 33% 97%	11183 27% 78%			11867 27% 73%	12346 100% 100%	13406 32% 96%	14091 28% 76%
SAU101545	SeqID IDENTITY COVERAGE	10029 31% 98%	10636 50% 99%	11187 32% 97%	11329 27% 83%		12010 28% 97%	12348 100% 100%	13633 47% 97%	14076 30% 98%
SAU101546	SeqID IDENTITY COVERAGE		10638 27% 80%					12349 100% 100%		
SAU101549	SeqID IDENTITY COVERAGE	10443 40% 70%	10762 38% 95%	11228 30% 88%		11767 38% 70%	12049 29% 92%	12549 100% 102%	13460 39% 92%	14030 38% 70%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1015 51	SeqID IDENTITY COVERAGE	10172 52% 97%	10490 77% 98%	11194 26% 98%	11360 27% 89%		12019 26% 96%	12550 100% 100%	13326 76% 98%	13939 52% 97%
SAU1015 54	SeqID IDENTITY COVERAGE		10485 48% 83%		11485 26% 81%			12551 100% 101%	13672 46% 91%	
SAU1015 61	SeqID IDENTITY COVERAGE	10400 44% 99%	10937 57% 99%	11073 44% 99%	11355 38% 100%	11759 42% 99%	12112 44% 100%	12149 100% 100%	13307 49% 99%	14064 43% 99%
SAU1015 65	SeqID IDENTITY COVERAGE	10134 37% 93%	10552 50% 96%	11211 35% 94%			11895 36% 92%	12151 100% 100%	13448 44% 99%	13826 36% 92%
SAU1015 67	SeqID IDENTITY COVERAGE							12144 100% 100%		
SAU1015 70	SeqID IDENTITY COVERAGE	10037 32% 100%	10690 48% 100%	11208 31% 99%		11700 34% 95%	11835 33% 102%	12584 100% 100%	13563 37% 100%	13900 30% 100%
SAU1015 71	SeqID IDENTITY COVERAGE		10691 45% 98%				11917 33% 94%	12585 100% 100%	13308 31% 97%	
SAU1015 72	SeqID IDENTITY COVERAGE	10068 26% 75%	10692 56% 101%			11689 46% 89%	11864 43% 96%	12586 100% 100%	13309 45% 98%	14083 25% 75%
SAU1015 73	SeqID IDENTITY COVERAGE	10096 31% 98%	10693 49% 103%	11270 35% 98%			11865 30% 101%	12587 100% 100%		14054 31% 98%
SAU1015 74	SeqID IDENTITY COVERAGE							12588 100% 101%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101575	SeqID IDENTITY COVERAGE		10869 31% 98%					12589 100% 100%	13638 27% 96%	
SAU101576	SeqID IDENTITY COVERAGE		10762 32% 93%				12049 29% 98%	12554 100% 102%	13460 39% 98%	
SAU101586	SeqID IDENTITY COVERAGE							12598 100% 101%	13487 34% 78%	
SAU101592	SeqID IDENTITY COVERAGE	10249 51% 101%	10605 74% 100%	10987 53% 100%	11555 53% 100%	11741 51% 101%	11952 52% 101%	12406 100% 100%	13283 70% 100%	13950 51% 101%
SAU101599	SeqID IDENTITY COVERAGE							12478 100% 100%		
SAU101610	SeqID IDENTITY COVERAGE	10449 38% 105%			11390 38% 101%		12048 40% 99%	12629 100% 100%		13816 38% 105%
SAU101612	SeqID IDENTITY COVERAGE							12637 100% 100%		
SAU101614	SeqID IDENTITY COVERAGE	10167 49% 100%	10678 55% 98%	11262 29% 93%	11534 29% 94%		11978 39% 95%	12649 100% 100%	13462 53% 99%	13851 48% 100%
SAU101616	SeqID IDENTITY COVERAGE	10186 33% 102%	10667 28% 99%		11407 32% 88%	11695 29% 104%	11872 34% 96%	12432 100% 100%		13903 33% 100%
SAU101622	SeqID IDENTITY COVERAGE	10162 69% 100%			11619 29% 104%	11710 67% 78%	12104 43% 101%	12430 100% 100%		13832 70% 100%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1016 24	SeqID IDENTITY COVERAGE	10193 26% 101%		11255 27% 106%	11316 38% 97%			12429 100% 100%	13430 26% 103%	13752 26% 107%
SAU1016 30	SeqID IDENTITY COVERAGE							12410 100% 100%		
SAU1016 32	SeqID IDENTITY COVERAGE							12407 100% 100%		
SAU1016 37	SeqID IDENTITY COVERAGE		10886 44% 99%					12201 100% 101%	13384 38% 98%	
SAU1016 41	SeqID IDENTITY COVERAGE	10223 51% 92%					11918 53% 95%	12193 100% 100%		
SAU1016 51	SeqID IDENTITY COVERAGE		10790 38% 97%		11552 28% 89%		12021 34% 90%	12491 100% 101%	13369 42% 100%	
SAU1016 52	SeqID IDENTITY COVERAGE		10791 62% 97%		11369 49% 91%		12022 50% 95%	12492 100% 100%	13368 56% 98%	
SAU1016 53	SeqID IDENTITY COVERAGE		10792 73% 100%		11520 46% 100%		12023 49% 100%	12493 100% 100%	13367 63% 100%	
SAU1016 55	SeqID IDENTITY COVERAGE	10205 31% 84%	10793 50% 97%				11896 30% 83%	12494 100% 100%	13334 33% 93%	
SAU1016 63	SeqID IDENTITY COVERAGE							12261 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101664	SeqID IDENTITY COVERAGE	10202 37% 98%	10512 41% 97%	11138 36% 108%			11863 38% 106%	12262 100% 101%	13685 38% 105%	13823 36% 98%
SAU101674	SeqID IDENTITY COVERAGE	10067 27% 103%					11846 27% 101%	12594 100% 100%		14082 27% 103%
SAU101679	SeqID IDENTITY COVERAGE	10190 41% 90%	10644 53% 100%	11055 42% 99%	11398 36% 86%		12105 45% 90%	12593 100% 100%	13264 45% 98%	13756 40% 90%
SAU101681	SeqID IDENTITY COVERAGE	10464 39% 100%	10746 46% 102%				11861 31% 95%	12592 100% 100%	13419 44% 102%	13987 40% 97%
SAU101682	SeqID IDENTITY COVERAGE	10156 28% 94%	10670 30% 96%	11265 28% 102%				12591 100% 100%	13488 34% 80%	13884 26% 94%
SAU101685	SeqID IDENTITY COVERAGE		10590 26% 88%				11920 37% 97%	12152 100% 100%	13396 56% 100%	
SAU101717	SeqID IDENTITY COVERAGE	10129 33% 101%	10586 51% 100%	11027 35% 93%	11610 31% 70%		11890 38% 99%	12131 100% 100%	13352 49% 93%	14070 34% 101%
SAU101724	SeqID IDENTITY COVERAGE	10309 44% 97%	10588 44% 99%	11268 41% 97%	11337 36% 87%		12015 43% 80%	12136 100% 100%	13678 45% 98%	13772 43% 97%
SAU101726	SeqID IDENTITY COVERAGE	10130 37% 101%	10664 50% 100%	11026 42% 101%	11461 36% 101%		11889 40% 100%	12134 100% 100%	13550 48% 100%	14071 41% 77%
SAU101727	SeqID IDENTITY COVERAGE		10665 50% 101%					12133 100% 101%	13551 49% 101%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1017 28	SeqID IDENTITY COVERAGE	10019 34% 86%	10666 54% 95%	11053 35% 88%		11734 35% 85%	11800 34% 90%	12132 100% 100%	13182 53% 94%	14015 34% 86%
SAU1017 36	SeqID IDENTITY COVERAGE	10225 28% 72%					11817 38% 99%	12519 100% 100%		13958 29% 72%
SAU1017 37	SeqID IDENTITY COVERAGE				11405 32% 78%		11817 30% 96%	12518 100% 101%		
SAU1017 44	SeqID IDENTITY COVERAGE		10562 44% 101%					12367 100% 100%		
SAU1017 51	SeqID IDENTITY COVERAGE	10474 30% 85%	10606 46% 100%			11671 30% 82%		12448 100% 100%	13165 45% 99%	13706 31% 79%
SAU1017 52	SeqID IDENTITY COVERAGE	10438 46% 115%	10626 75% 99%	11037 47% 114%	11410 40% 120%		11997 45% 116%	12447 100% 100%	13187 69% 99%	14043 46% 115%
SAU1017 54	SeqID IDENTITY COVERAGE	10439 46% 116%	10627 72% 100%	11036 46% 117%	11571 53% 80%		5179 46% 118%	12446 100% 100%	13646 68% 101%	14042 46% 116%
SAU1017 56	SeqID IDENTITY COVERAGE	10365 65% 91%	10479 83% 93%	11062 66% 91%	11409 65% 91%		5178 68% 91%	12445 100% 101%	13231 82% 93%	13967 65% 93%
SAU1017 71	SeqID IDENTITY COVERAGE	10220 43% 91%	10784 65% 101%	11276 37% 77%		11765 35% 82%	11950 36% 80%	12350 100% 101%	13280 67% 98%	13934 41% 91%
SAU1017 72	SeqID IDENTITY COVERAGE	10240 50% 100%	10785 63% 101%	11275 51% 100%	11294 27% 77%		11925 38% 100%	12351 100% 100%	13281 61% 101%	13863 48% 84%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101777	SeqID IDENTITY COVERAGE		10673 64% 97%		11448 43% 88%			12352 100% 100%	13176 62% 98%	
SAU101781	SeqID IDENTITY COVERAGE		10495 67% 99%				111917 38% 93%	12353 100% 100%	13308 28% 85%	
SAU101782	SeqID IDENTITY COVERAGE		10496 75% 100%			111689 44% 89%	111916 41% 99%	12354 100% 100%	13309 40% 96%	
SAU101784	SeqID IDENTITY COVERAGE	10037 44% 97%	10498 65% 100%	11208 45% 97%		111700 35% 92%	111866 42% 99%	12355 100% 100%	13563 37% 99%	13900 44% 97%
SAU101790	SeqID IDENTITY COVERAGE	10350 51% 86%	10524 81% 99%	11106 55% 86%	11437 48% 86%		5170 55% 90%	12215 100% 101%	13207 79% 99%	
SAU101791	SeqID IDENTITY COVERAGE	10349 67% 101%	10525 90% 101%	11107 69% 101%	11436 62% 100%		5169 66% 100%	12216 100% 101%	13208 89% 101%	14108 67% 102%
SAU101792	SeqID IDENTITY COVERAGE	10348 53% 96%	10526 66% 94%	11108 52% 95%			5168 49% 97%	12217 100% 101%	13209 68% 94%	14107 50% 96%
SAU101793	SeqID IDENTITY COVERAGE	10347 64% 100%	10527 85% 101%	11109 65% 99%	11589 51% 99%	11654 64% 101%	5167 63% 99%	12218 100% 101%	13210 79% 100%	14106 64% 101%
SAU101795	SeqID IDENTITY COVERAGE	10345 51% 99%	10528 79% 101%	11111 47% 99%	11435 44% 98%		5165 44% 100%	12219 100% 101%	13212 76% 101%	14104 51% 101%
SAU101797	SeqID IDENTITY COVERAGE	10343 45% 100%	10530 68% 101%	11113 41% 99%	11433 41% 93%		5163 48% 96%	12221 100% 101%	13214 66% 101%	14102 46% 101%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101798	SeqID IDENTITY COVERAGE	10342 55% 99%	10531 72% 95%	11114 55% 99%	11432 62% 87%		5162 52% 99%	12222 100% 101%	13215 66% 96%	14101 55% 99%
SAU101799	SeqID IDENTITY COVERAGE	10341 51% 100%	10532 62% 102%	11115 42% 100%			5161 42% 97%	12223 100% 102%	13216 69% 98%	
SAU101800	SeqID IDENTITY COVERAGE	10340 47% 99%	10534 79% 101%	11116 46% 99%	11431 40% 90%		5160 42% 99%	12225 100% 101%	13217 84% 101%	14099 47% 99%
SAU101802	SeqID IDENTITY COVERAGE	10075 48% 97%	10536 64% 97%	11008 52% 97%	11348 31% 93%	11633 47% 97%	11942 53% 84%	12227 100% 100%	13219 56% 96%	13717 47% 97%
SAU101803	SeqID IDENTITY COVERAGE	10111 71% 97%	10537 84% 101%	11052 71% 97%	11429 60% 100%	11651 70% 101%	11876 71% 97%	12228 100% 101%	13220 82% 101%	14010 70% 101%
SAU101805	SeqID IDENTITY COVERAGE	10337 53% 96%	10539 75% 101%	11119 52% 99%	11427 58% 99%		11990 60% 96%	12229 100% 101%	13221 74% 101%	14097 52% 96%
SAU101806	SeqID IDENTITY COVERAGE	10336 62% 100%	10540 85% 101%	11120 64% 100%	11426 60% 102%		11989 61% 100%	12230 100% 101%	13222 85% 92%	14096 63% 101%
SAU101807	SeqID IDENTITY COVERAGE	10334 42% 99%	10541 71% 100%	11122 42% 99%	11583 37% 94%		11987 42% 99%	12231 100% 100%	13223 58% 99%	14094 42% 99%
SAU101808	SeqID IDENTITY COVERAGE	10333 48% 98%	10542 65% 103%	11123 49% 98%	11582 46% 99%	11627 48% 78%	5158 45% 98%	12232 100% 101%	13224 67% 106%	14093 48% 98%
SAU101810	SeqID IDENTITY COVERAGE	10053 35% 76%	10544 52% 88%	11229 34% 78%	11625 32% 77%	11666 36% 73%	11909 33% 72%	12233 100% 100%	13441 47% 88%	14110 36% 73%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101811	SeqID IDENTITY COVERAGE	10196 38% 78%	10545 49% 87%	11068 33% 82%	11463 32% 82%	11666 33% 83%	11888 32% 82%	12234 100% 100%	13440 45% 87%	13721 34% 76%
SAU101814	SeqID IDENTITY COVERAGE	10327 58% 94%	10602 69% 96%	11241 57% 94%	11471 47% 92%	11655 56% 71%	5188 55% 97%	12237 100% 101%	13356 65% 99%	13729 56% 94%
SAU101815	SeqID IDENTITY COVERAGE	10326 49% 98%		11240 48% 98%	11288 46% 93%		12016 53% 93%	12238 100% 101%	13361 69% 99%	13732 51% 99%
SAU101818	SeqID IDENTITY COVERAGE			11231 32% 95%	11307 33% 90%		11814 31% 96%	12369 100% 101%	13494 35% 93%	
SAU101824	SeqID IDENTITY COVERAGE	10158 33% 71%					12004 28% 75%	12371 100% 100%		
SAU101833	SeqID IDENTITY COVERAGE	10207 42% 100%	10747 49% 102%	11040 28% 95%	11481 44% 107%		11794 35% 117%	12373 100% 100%	13388 46% 103%	13775 44% 89%
SAU101839	SeqID IDENTITY COVERAGE	10398 30% 94%	10849 33% 78%	11236 32% 90%			12100 25% 98%	12495 100% 100%	13291 32% 83%	13924 28% 94%
SAU101842	SeqID IDENTITY COVERAGE	10105 45% 98%	10942 70% 95%	11075 33% 95%	11376 48% 99%	11723 33% 94%	11855 47% 97%	12510 100% 100%	13445 65% 82%	13999 45% 99%
SAU101845	SeqID IDENTITY COVERAGE	10231 30% 101%	10739 47% 102%		11567 40% 102%		11899 26% 101%	12506 100% 100%	13544 43% 102%	13953 28% 101%
SAU101849	SeqID IDENTITY COVERAGE	10015 56% 103%	10740 77% 99%	11209 54% 103%	11472 56% 101%		12058 56% 103%	12567 100% 100%	13379 75% 98%	13713 56% 104%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1018 57	SeqID IDENTITY COVERAGE							12569 100% 100%		
SAU1018 62	SeqID IDENTITY COVERAGE	10257 40% 98%	10817 63% 100%	10955 40% 98%	11334 33% 101%		11802 39% 98%	12571 100% 100%	13305 62% 99%	13797 39% 98%
SAU1018 64	SeqID IDENTITY COVERAGE							12572 100% 100%		
SAU1018 65	SeqID IDENTITY COVERAGE	10044 43% 85%	10834 58% 88%	11151 45% 88%	11417 40% 87%		11938 40% 87%	12318 100% 100%	13227 54% 88%	13910 41% 88%
SAU1018 66	SeqID IDENTITY COVERAGE		10835 42% 102%				11873 29% 99%	12319 100% 100%	13586 40% 100%	
SAU1018 68	SeqID IDENTITY COVERAGE	10049 45% 101%	10733 56% 99%	11086 45% 101%	11305 42% 96%		11813 48% 100%	12320 100% 100%	13228 49% 108%	13898 45% 99%
SAU1018 69	SeqID IDENTITY COVERAGE		10734 55% 100%					12321 100% 100%	13668 49% 101%	
SAU1018 76	SeqID IDENTITY COVERAGE							12169 100% 101%		
SAU1018 81	SeqID IDENTITY COVERAGE	10325 42% 98%					12081 41% 97%	12162 100% 100%		13728 42% 98%
SAU1018 82	SeqID IDENTITY COVERAGE	10246 33% 96%	10824 30% 89%			11743 31% 73%	12080 31% 94%	12163 100% 100%		13727 33% 95%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101890	SeqID IDENTITY COVERAGE	10374 53% 91%		11125 49% 92%			12091 47% 93%	12280 100% 100%		13809 53% 91%
SAU101891	SeqID IDENTITY COVERAGE	10295 63% 91%	10766 72% 91%	11196 62% 90%	11483 60% 90%		11791 58% 93%	12281 100% 100%	13413 67% 92%	13739 64% 91%
SAU101893	SeqID IDENTITY COVERAGE	10300 46% 87%	10724 47% 100%			11748 41% 78%	11981 35% 93%	12282 100% 100%	13290 40% 95%	13825 43% 96%
SAU101904	SeqID IDENTITY COVERAGE	10047 34% 98%	10648 38% 101%	11089 33% 102%	11451 31% 105%		11935 31% 104%	12617 100% 100%	13345 34% 93%	13913 33% 98%
SAU101907	SeqID IDENTITY COVERAGE	10362 75% 100%	10482 90% 101%	11059 76% 100%	11415 74% 101%		11995 73% 101%	12442 100% 100%	13171 75% 101%	13964 74% 100%
SAU101909	SeqID IDENTITY COVERAGE	10390 41% 99%		11249 32% 88%	11346 29% 90%		11789 36% 93%	12441 100% 100%		14063 32% 73%
SAU101910	SeqID IDENTITY COVERAGE	10199 56% 97%					11818 60% 97%	12440 100% 100%		
SAU101915	SeqID IDENTITY COVERAGE		10838 26% 90%					12439 100% 100%		
SAU101922	SeqID IDENTITY COVERAGE							12438 100% 100%		
SAU101948	SeqID IDENTITY COVERAGE							12709 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU101966	SeqID IDENTITY COVERAGE	10101 45% 88%	10561 31% 91%	11007 32% 92%	11538 37% 86%	11705 43% 88%	11897 45% 88%	12186 100% 101%		14003 45% 88%
SAU101968	SeqID IDENTITY COVERAGE	10106 30% 90%	10568 31% 92%	11242 33% 90%	11480 27% 88%		11965 30% 83%	12187 100% 100%		13998 31% 76%
SAU101991	SeqID IDENTITY COVERAGE		10938 40% 101%					12454 100% 101%	13500 25% 80%	
SAU101995	SeqID IDENTITY COVERAGE	10388 46% 72%	10939 47% 78%	11066 49% 73%	11575 58% 72%	11646 46% 72%	11957 57% 76%	12455 100% 100%	13386 51% 74%	
SAU101996	SeqID IDENTITY COVERAGE	10237 38% 98%	10940 64% 99%	10999 36% 98%	11325 38% 98%		11901 35% 99%	12456 100% 100%	13455 58% 100%	13956 37% 98%
SAU101999	SeqID IDENTITY COVERAGE	10476 48% 97%	10941 61% 98%	11259 46% 98%	11304 49% 91%		12035 51% 96%	12423 100% 100%	13241 64% 97%	13708 48% 97%
SAU102001	SeqID IDENTITY COVERAGE	10258 47% 105%	10628 58% 98%	11134 47% 106%	11489 43% 105%		11787 49% 98%	12424 100% 100%	13636 46% 98%	14088 47% 105%
SAU102002	SeqID IDENTITY COVERAGE							12425 100% 100%		
SAU102003	SeqID IDENTITY COVERAGE							12426 100% 101%		
SAU102006	SeqID IDENTITY COVERAGE			11267 44% 92%	11555 28% 74%			12427 100% 101%	13260 47% 105%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102007	SeqID IDENTITY COVERAGE			11266 60% 97%				12428 100% 100%	13258 61% 97%	
SAU102032	SeqID IDENTITY COVERAGE						12086 62% 99%	12198 100% 100%		13989 58% 75%
SAU102035	SeqID IDENTITY COVERAGE	10299 60% 98%	10933 50% 99%	10974 26% 85%	11514 29% 84%		11860 41% 97%	12199 100% 100%	13360 31% 86%	13763 56% 99%
SAU102044	SeqID IDENTITY COVERAGE	10141 56% 100%	10916 67% 102%	11011 59% 100%	11344 50% 101%		12041 58% 101%	12414 100% 100%	13447 69% 102%	13977 56% 100%
SAU102046	SeqID IDENTITY COVERAGE	10103 32% 74%	10723 28% 86%				12089 29% 90%	12415 100% 100%		14001 29% 89%
SAU102049	SeqID IDENTITY COVERAGE	10427 36% 101%	10518 39% 99%	10962 49% 97%	11291 40% 99%		11784 41% 100%	12416 100% 100%	13652 46% 98%	13781 36% 101%
SAU102054	SeqID IDENTITY COVERAGE	10280 53% 100%	10494 50% 79%	11095 55% 100%	11356 51% 100%	11676 53% 70%	11856 55% 100%	12417 100% 100%		13877 53% 100%
SAU102059	SeqID IDENTITY COVERAGE	10085 43% 107%	10771 72% 100%	11152 43% 107%	11622 40% 102%		11969 41% 109%	12286 100% 100%	13226 72% 71%	14059 40% 89%
SAU102067	SeqID IDENTITY COVERAGE	10380 32% 95%	10564 52% 98%	11155 31% 98%			11795 28% 97%	12287 100% 100%	13407 44% 98%	13798 31% 94%
SAU102068	SeqID IDENTITY COVERAGE		10680 29% 101%					12288 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102102	SeqID IDENTITY COVERAGE							12696 100% 100%		
SAU102113	SeqID IDENTITY COVERAGE		10641 34% 110%					12178 100% 101%		
SAU102116	SeqID IDENTITY COVERAGE		10642 29% 85%					12180 100% 100%	13480 31% 81%	
SAU102117	SeqID IDENTITY COVERAGE	10016 43% 101%	10643 61% 100%		11604 38% 102%		12027 42% 103%	12181 100% 100%	13481 55% 100%	13947 41% 85%
SAU102129	SeqID IDENTITY COVERAGE		10859 60% 98%					12176 100% 100%	13400 56% 99%	
SAU102132	SeqID IDENTITY COVERAGE		10760 39% 101%					12177 100% 100%	13304 41% 101%	
SAU102142	SeqID IDENTITY COVERAGE	10154 37% 99%						12457 100% 100%		
SAU102143	SeqID IDENTITY COVERAGE	10154 32% 100%						12458 100% 100%		
SAU102144	SeqID IDENTITY COVERAGE							12459 100% 100%		
SAU102162	SeqID IDENTITY COVERAGE							12462 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102165	SeqID IDENTITY COVERAGE							12460 100% 100%		
SAU102200	SeqID IDENTITY COVERAGE							12665 100% 101%		
SAU102201	SeqID IDENTITY COVERAGE							12666 100% 101%		
SAU102222	SeqID IDENTITY COVERAGE	10447 58% 99%	10797 68% 99%	10994 58% 99%	11358 52% 99%		11986 59% 99%	12511 100% 100%	13192 67% 99%	13818 58% 99%
SAU102231	SeqID IDENTITY COVERAGE	10323 41% 94%	10798 50% 93%	11193 42% 89%			12020 38% 94%	12527 100% 100%	13561 46% 99%	13731 41% 94%
SAU102232	SeqID IDENTITY COVERAGE	10100 36% 75%	10799 40% 79%			11687 35% 74%		12530 100% 100%	13562 42% 79%	14004 34% 75%
SAU102233	SeqID IDENTITY COVERAGE		10800 61% 98%					12531 100% 100%	13496 45% 91%	
SAU102241	SeqID IDENTITY COVERAGE	10163 28% 74%	10845 43% 99%					12539 100% 100%		
SAU102242	SeqID IDENTITY COVERAGE	10188 47% 100%	10847 72% 99%	10953 44% 101%	11600 38% 100%	11634 47% 98%	11907 47% 100%	12540 100% 100%	13593 70% 100%	13981 47% 100%
SAU102246	SeqID IDENTITY COVERAGE	10274 59% 99%	10854 74% 100%	11154 60% 97%	11476 54% 96%		11932 62% 100%	12542 100% 100%	13313 81% 101%	13866 58% 99%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1022 47	SeqID IDENTITY COVERAGE							12543 100% 101%	13180 28% 74%	
SAU1022 52	SeqID IDENTITY COVERAGE	10300 39% 79%	10677 48% 93%			11748 39% 73%	11981 37% 91%	12241 100% 100%	13290 43% 95%	13825 41% 98%
SAU1022 56	SeqID IDENTITY COVERAGE	10451 33% 97%			11515 32% 97%			12243 100% 101%	13531 75% 101%	
SAU1022 57	SeqID IDENTITY COVERAGE	10451 38% 81%			11515 29% 75%			12244 100% 101%	13274 85% 101%	
SAU1022 59	SeqID IDENTITY COVERAGE		10844 65% 97%					12245 100% 100%	13519 72% 97%	13782 25% 87%
SAU1022 60	SeqID IDENTITY COVERAGE	10182 34% 96%	10646 37% 87%			11682 32% 96%		12246 100% 101%	13275 83% 100%	13984 32% 87%
SAU1022 61	SeqID IDENTITY COVERAGE	10183 25% 79%	10731 30% 80%					12247 100% 100%	13276 74% 99%	13983 26% 79%
SAU1022 62	SeqID IDENTITY COVERAGE	10270 35% 104%	10759 39% 103%			11724 31% 84%		12248 100% 100%	13277 82% 100%	13881 34% 104%
SAU1022 64	SeqID IDENTITY COVERAGE	10160 45% 100%					5103 44% 100%	12250 100% 100%		13830 43% 101%
SAU1022 65	SeqID IDENTITY COVERAGE						11926 37% 100%	12251 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1022 68	SeqID IDENTITY COVERAGE							12252 100% 101%		
SAU1022 70	SeqID IDENTITY COVERAGE							12253 100% 100%		
SAU1022 80	SeqID IDENTITY COVERAGE							12378 100% 100%		
SAU1022 81	SeqID IDENTITY COVERAGE	10316 45% 99%		11227 48% 99%	11469 39% 100%		12054 45% 99%	12384 100% 100%	13497 61% 100%	13762 44% 99%
SAU1022 83	SeqID IDENTITY COVERAGE	10260 41% 88%	10875 59% 88%	10982 43% 88%	11560 41% 92%		11945 41% 95%	12119 100% 102%	13251 54% 88%	14086 41% 88%
SAU1022 84	SeqID IDENTITY COVERAGE							12389 100% 100%		
SAU1022 86	SeqID IDENTITY COVERAGE	10385 37% 104%	10595 42% 99%					12393 100% 100%	13688 39% 101%	
SAU1022 87	SeqID IDENTITY COVERAGE	10220 42% 81%	10594 45% 95%	11025 40% 88%		11663 39% 89%	11925 41% 84%	12398 100% 101%	13427 41% 94%	13934 39% 83%
SAU1022 92	SeqID IDENTITY COVERAGE	10399 41% 101%	10579 59% 100%	11018 40% 101%	11455 37% 100%	11758 41% 101%	12111 42% 101%	12368 100% 100%	13230 57% 94%	14065 41% 101%
SAU1022 94	SeqID IDENTITY COVERAGE							12610 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102297	SeqID IDENTITY COVERAGE	10405 52% 99%	10912 66% 100%	11063 51% 100%	11303 46% 99%		12117 50% 98%	12704 100% 100%	13686 64% 100%	14066 48% 77%
SAU102298	SeqID IDENTITY COVERAGE	10404 36% 72%	10914 62% 99%	11031 33% 87%		11686 35% 89%	12116 28% 87%	12705 100% 100%	13255 54% 100%	
SAU102308	SeqID IDENTITY COVERAGE	10077 38% 88%	10577 46% 100%	11248 37% 86%	11625 33% 87%	11732 39% 88%	12032 38% 90%	12706 100% 100%	13350 45% 100%	13995 39% 95%
SAU102318	SeqID IDENTITY COVERAGE	10122 32% 90%	10795 75% 97%				11806 37% 72%	12707 100% 100%	13242 63% 97%	14039 31% 89%
SAU102333	SeqID IDENTITY COVERAGE	10057 41% 96%	10550 43% 97%				12102 40% 96%	12657 100% 100%	13316 31% 90%	13829 38% 95%
SAU102334	SeqID IDENTITY COVERAGE	10056 50% 91%					12101 50% 92%	12658 100% 100%		
SAU102336	SeqID IDENTITY COVERAGE							12659 100% 101%		
SAU102340	SeqID IDENTITY COVERAGE							12660 100% 100%		
SAU102345	SeqID IDENTITY COVERAGE						11843 37% 86%	12655 100% 101%		
SAU102350	SeqID IDENTITY COVERAGE							12433 100% 101%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1023 52	SeqID IDENTITY COVERAGE		10657 55% 100%					12434 100% 100%	13426 39% 91%	
SAU1023 55	SeqID IDENTITY COVERAGE		10726 39% 87%					12435 100% 100%		
SAU1023 56	SeqID IDENTITY COVERAGE	10227 43% 95%	10669 60% 100%	11203 45% 95%	11546 48% 98%		11805 43% 95%	12436 100% 100%	13324 56% 99%	13960 43% 95%
SAU1023 78	SeqID IDENTITY COVERAGE							12437 100% 100%		
SAU1023 80	SeqID IDENTITY COVERAGE						11870 32% 71%	12265 100% 100%		
SAU1023 88	SeqID IDENTITY COVERAGE	10367 36% 96%		11157 33% 90%	11386 27% 101%		11808 39% 99%	12267 100% 100%		13802 36% 96%
SAU1023 89	SeqID IDENTITY COVERAGE	10063 33% 99%	10547 59% 97%	10988 31% 97%			11837 36% 95%	12268 100% 100%	13395 35% 98%	13917 33% 99%
SAU1023 90	SeqID IDENTITY COVERAGE	10192 41% 100%				11678 26% 97%		12269 100% 101%		13753 42% 100%
SAU1023 92	SeqID IDENTITY COVERAGE	10131 50% 73%	10500 42% 80%			11673 32% 80%	11951 42% 74%	12270 100% 100%	13474 42% 76%	
SAU1023 94	SeqID IDENTITY COVERAGE		10807 32% 102%					12271 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102396	SeqID IDENTITY COVERAGE	10243 37% 101%	10809 62% 99%					12272 100% 100%	13467 27% 98%	13794 37% 98%
SAU102401	SeqID IDENTITY COVERAGE							12209 100% 100%		
SAU102417	SeqID IDENTITY COVERAGE		10934 31% 79%				12068 25% 72%	12204 100% 100%		
SAU102418	SeqID IDENTITY COVERAGE					11760 25% 89%		12205 100% 100%		
SAU102420	SeqID IDENTITY COVERAGE							12206 100% 100%		
SAU102422	SeqID IDENTITY COVERAGE	10308 30% 92%				11665 30% 72%	11977 27% 93%	12207 100% 100%		13776 31% 92%
SAU102423	SeqID IDENTITY COVERAGE			11084 27% 94%	11491 25% 92%		12099 27% 93%	12208 100% 100%		
SAU102433	SeqID IDENTITY COVERAGE	10395 42% 101%	10908 51% 100%	11167 39% 100%	11616 37% 73%		11772 52% 72%	12701 100% 100%	13552 44% 98%	
SAU102434	SeqID IDENTITY COVERAGE	10394 26% 99%	10907 44% 100%	11166 28% 99%			11773 26% 100%	12700 100% 100%	13446 40% 101%	13921 27% 99%
SAU102437	SeqID IDENTITY COVERAGE	10393 55% 86%	10952 67% 99%	11057 57% 88%	11330 51% 86%		11774 55% 87%	12695 100% 100%	13420 64% 99%	13920 56% 86%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1024 40	SeqID IDENTITY COVERAGE						12085 41% 98%	12692 100% 100%		13990 39% 99%
SAU1024 47	SeqID IDENTITY COVERAGE		10947 38% 98%					12685 100% 100%	13436 32% 98%	
SAU1024 48	SeqID IDENTITY COVERAGE	10460 32% 101%	10946 55% 102%	11049 31% 101%	11332 35% 101%		12073 34% 101%	12681 100% 101%	13435 46% 102%	13860 32% 102%
SAU1024 49	SeqID IDENTITY COVERAGE	10445 45% 97%	10945 55% 98%	11253 43% 98%	11444 35% 99%	11731 43% 76%	12072 44% 97%	12677 100% 100%	13434 51% 100%	14028 45% 97%
SAU1024 50	SeqID IDENTITY COVERAGE	10456 47% 100%	10943 70% 100%	11264 46% 100%	11487 43% 99%		12076 47% 99%	12675 100% 100%	13237 68% 100%	13857 47% 100%
SAU1024 52	SeqID IDENTITY COVERAGE	10420 41% 97%	10748 70% 98%	11143 37% 97%	11478 32% 97%	11629 40% 94%	11820 40% 97%	12674 100% 100%	13265 62% 100%	13783 38% 99%
SAU1024 53	SeqID IDENTITY COVERAGE		10749 43% 101%				12107 29% 70%	12669 100% 100%	13266 41% 71%	
SAU1024 60	SeqID IDENTITY COVERAGE	10063 34% 98%	10547 35% 100%	10988 34% 100%			11837 34% 100%	12171 100% 100%	13395 34% 101%	13917 34% 98%
SAU1024 69	SeqID IDENTITY COVERAGE	10217 58% 98%						12172 100% 100%		
SAU1024 73	SeqID IDENTITY COVERAGE		10868 28% 88%					12173 100% 100%	13475 35% 83%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102474	SeqID IDENTITY COVERAGE	10713 26% 96%	10971 26% 105%					12174 100% 100%	13476 26% 89%	14025 27% 97%
SAU102476	SeqID IDENTITY COVERAGE							12175 100% 100%		
SAU102479	SeqID IDENTITY COVERAGE	10306 26% 84%						12405 100% 100%		
SAU102480	SeqID IDENTITY COVERAGE	10310 28% 100%	10935 33% 88%				11871 30% 100%	12404 100% 100%		13770 27% 100%
SAU102481	SeqID IDENTITY COVERAGE	10289 26% 102%	10831 29% 94%					12422 100% 101%		13879 26% 102%
SAU102485	SeqID IDENTITY COVERAGE	10457 28% 86%	10890 53% 100%					12421 100% 100%	13512 56% 99%	13961 60% 93%
SAU102486	SeqID IDENTITY COVERAGE	10294 36% 95%	10889 38% 97%	11025 27% 95%				12420 100% 101%	13513 42% 93%	13962 37% 95%
SAU102487	SeqID IDENTITY COVERAGE							12419 100% 100%		
SAU102498	SeqID IDENTITY COVERAGE	10241 36% 93%	10597 35% 94%	10974 35% 93%	11342 33% 92%	11706 37% 94%	11842 38% 94%	12688 100% 100%	13387 35% 93%	14092 36% 93%
SAU102502	SeqID IDENTITY COVERAGE						12060 26% 85%	12689 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU1025 03	SeqID IDENTITY COVERAGE						12059 32% 92%	12690 100% 100%		
SAU1025 26	SeqID IDENTITY COVERAGE							12691 100% 100%		
SAU1025 27	SeqID IDENTITY COVERAGE	10352 54% 93%	10560 74% 101%	11104 55% 93%	11439 56% 94%		5171 58% 93%	12260 100% 101%	13204 75% 94%	13968 54% 93%
SAU1025 31	SeqID IDENTITY COVERAGE		10765 34% 102%					12667 100% 100%		
SAU1025 41	SeqID IDENTITY COVERAGE	10076 41% 93%	10520 49% 102%	11000 38% 91%	11498 37% 93%		11966 44% 100%	12668 100% 100%	13405 45% 81%	13718 41% 93%
SAU1025 51	SeqID IDENTITY COVERAGE			11013 47% 87%	11353 38% 84%		11816 39% 84%	12672 100% 101%	13271 41% 95%	
SAU1025 54	SeqID IDENTITY COVERAGE		10494 47% 99%					12673 100% 100%	13466 44% 98%	
SAU1025 75	SeqID IDENTITY COVERAGE	10166 28% 98%		11232 29% 91%	11618 35% 99%		11777 30% 96%	12609 100% 100%		13836 27% 98%
SAU1025 78	SeqID IDENTITY COVERAGE	10459 59% 88%	10948 76% 95%	11050 60% 88%	11420 51% 89%		12074 65% 81%	12411 100% 101%	13503 73% 94%	13859 59% 89%
SAU1025 84	SeqID IDENTITY COVERAGE							12537 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102585	SeqID IDENTITY COVERAGE						12611 100% 100%		
SAU102593	SeqID IDENTITY COVERAGE	10889 27% 87%					12463 100% 100%	13513 27% 88%	
SAU102598	SeqID IDENTITY COVERAGE	10187 30% 102%	10958 32% 85%		11710 27% 75%	11979 31% 92%	12464 100% 100%		13833 31% 86%
SAU102599	SeqID IDENTITY COVERAGE	10206 36% 89%	10958 30% 93%	11619 30% 73%		11975 33% 79%	12466 100% 100%	13653 32% 77%	13773 32% 101%
SAU102601	SeqID IDENTITY COVERAGE	10273 27% 95%	11076 30% 93%		11722 28% 95%	11931 28% 93%	12467 100% 100%	13256 51% 97%	13867 27% 92%
SAU102602	SeqID IDENTITY COVERAGE	10356 58% 100%	10555 78% 100%	11441 57% 100%	11679 59% 100%	11993 60% 99%	12249 100% 100%	13200 77% 100%	13971 58% 99%
SAU102603	SeqID IDENTITY COVERAGE						12469 100% 100%		
SAU102605	SeqID IDENTITY COVERAGE		10836 47% 96%				12470 100% 100%		
SAU102606	SeqID IDENTITY COVERAGE	10273 27% 95%	11076 30% 92%		11722 27% 95%	11931 25% 93%	12471 100% 100%	13256 50% 97%	13867 26% 94%
SAU102607	SeqID IDENTITY COVERAGE						12472 100% 100%	13579 43% 98%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102609	SeqID IDENTITY COVERAGE							12473 100% 100%		
SAU102610	SeqID IDENTITY COVERAGE							12474 100% 100%		
SAU102613	SeqID IDENTITY COVERAGE	10461 26% 97%		11272 28% 95%				12475 100% 100%		13988 26% 97%
SAU102614	SeqID IDENTITY COVERAGE	10211 33% 89%	10600 55% 100%					12476 100% 100%		13927 32% 89%
SAU102615	SeqID IDENTITY COVERAGE	10234 32% 98%	10601 40% 100%			11720 32% 92%	12098 26% 87%	12477 100% 100%		13926 31% 100%
SAU102620	SeqID IDENTITY COVERAGE							12479 100% 100%		
SAU102621	SeqID IDENTITY COVERAGE	10288 61% 100%	10519 62% 101%			11724 58% 81%		12480 100% 100%	13370 59% 101%	13881 61% 100%
SAU102629	SeqID IDENTITY COVERAGE		10885 26% 108%					12481 100% 100%		
SAU102631	SeqID IDENTITY COVERAGE		10522 27% 83%			11657 44% 83%	11841 32% 81%	12712 100% 100%		
SAU102636	SeqID IDENTITY COVERAGE							12650 100% 100%	13696 29% 102%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102637	SeqID IDENTITY COVERAGE							12651 100% 100%	13697 39% 98%	
SAU102652	SeqID IDENTITY COVERAGE							12653 100% 101%		
SAU102658	SeqID IDENTITY COVERAGE	10283 45% 97%	10910 54% 92%	11064 42% 97%			12090 39% 97%	12654 100% 100%	13514 49% 96%	13855 41% 100%
SAU102663	SeqID IDENTITY COVERAGE	10304 43% 99%	10840 58% 99%	11043 44% 96%	11626 34% 95%		11798 45% 91%	12158 100% 100%	13172 56% 97%	13780 41% 99%
SAU102669	SeqID IDENTITY COVERAGE	10022 42% 96%	10756 26% 91%	11257 43% 95%			12045 41% 94%	12160 100% 100%	13371 54% 95%	14035 41% 93%
SAU102671	SeqID IDENTITY COVERAGE	10409 34% 91%		11079 32% 91%	11319 44% 96%	11683 35% 74%	12043 56% 99%	12161 100% 100%	13373 69% 96%	14033 33% 91%
SAU102674	SeqID IDENTITY COVERAGE	10020 55% 102%		11164 54% 103%		11648 46% 101%	5127 55% 105%	12156 100% 101%		14016 53% 102%
SAU102693	SeqID IDENTITY COVERAGE	10178 53% 82%	10659 74% 87%		11474 38% 86%		11883 49% 86%	12627 100% 101%	13301 61% 90%	13940 49% 72%
SAU102694	SeqID IDENTITY COVERAGE	10177 48% 97%	10660 66% 102%	11222 50% 97%	11296 44% 94%		5120 55% 94%	12628 100% 102%	13302 60% 102%	
SAU102725	SeqID IDENTITY COVERAGE	10418 40% 96%	10514 72% 100%	11137 39% 96%	11507 38% 103%		12088 37% 104%	12338 100% 100%	13378 66% 100%	13789 40% 96%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102764	SeqID IDENTITY COVERAGE	10179 44% 99%	10929 67% 99%	11234 42% 99%	11295 41% 90%		11884 42% 97%	12625 100% 100%	13484 63% 99%	13938 43% 99%
SAU102812	SeqID IDENTITY COVERAGE		10860 48% 100%					12127 100% 101%	13253 49% 96%	
SAU102870	SeqID IDENTITY COVERAGE	10113 29% 92%	10880 35% 83%					12170 100% 100%	13270 29% 93%	14008 28% 87%
SAU102880	SeqID IDENTITY COVERAGE	10360 60% 100%	10533 82% 101%	11096 61% 100%	11443 57% 97%	11643 61% 100%	5177 58% 100%	12224 100% 101%	13196 85% 101%	13975 61% 100%
SAU102881	SeqID IDENTITY COVERAGE	10357 38% 89%	10551 69% 98%	11099 37% 89%			11994 38% 89%	12242 100% 101%	13199 54% 102%	13972 38% 89%
SAU102883	SeqID IDENTITY COVERAGE	10396 63% 86%		11168 70% 88%	11449 60% 86%		12118 65% 86%	12702 100% 102%	13181 76% 90%	
SAU102905	SeqID IDENTITY COVERAGE		10732 31% 92%	11217 26% 80%	11373 38% 87%			12273 100% 100%		
SAU102909	SeqID IDENTITY COVERAGE	10042 59% 95%	10488 68% 95%	11150 60% 95%	11457 69% 130%	11637 59% 95%	11940 60% 98%	12315 100% 101%	13437 73% 124%	13908 59% 95%
SAU102933	SeqID IDENTITY COVERAGE	10448 33% 104%	10949 53% 113%	10995 35% 101%	11579 32% 108%	11762 31% 107%	11985 29% 101%	12412 100% 101%	13502 50% 101%	13817 31% 103%
SAU102936	SeqID IDENTITY COVERAGE	10236 33% 97%	10872 66% 100%				11804 60% 96%	12356 100% 101%		13955 33% 98%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU102942	SeqID IDENTITY COVERAGE	10136 52% 100%	10492 55% 100%	11230 43% 99%		11696 50% 99%		12296 100% 100%	13339 51% 99%	13834 51% 99%
SAU102944	SeqID IDENTITY COVERAGE							12468 100% 100%	13257 42% 99%	
SAU102979	SeqID IDENTITY COVERAGE	10014 33% 88%		10979 37% 87%	11384 32% 87%		11936 41% 87%	12536 100% 100%	13429 33% 87%	13712 33% 90%
SAU102983	SeqID IDENTITY COVERAGE		10883 28% 70%					12676 100% 100%	13269 27% 76%	
SAU102992	SeqID IDENTITY COVERAGE	10176 62% 99%	10661 70% 92%	11223 62% 99%	11297 48% 97%		11882 59% 99%	12630 100% 101%	13303 63% 99%	13941 61% 101%
SAU103010	SeqID IDENTITY COVERAGE							12194 100% 100%		
SAU103024	SeqID IDENTITY COVERAGE					11670 44% 89%	12042 26% 72%	12200 100% 101%		
SAU103025	SeqID IDENTITY COVERAGE							12202 100% 100%		
SAU103037	SeqID IDENTITY COVERAGE		10867 27% 99%					12613 100% 101%	13267 26% 86%	
SAU103077	SeqID IDENTITY COVERAGE							12408 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU103115	SeqID IDENTITY COVERAGE							12508 100% 101%	13469 32% 101%	
SAU103144	SeqID IDENTITY COVERAGE		10936 42% 84%					12663 100% 100%		
SAU103159	SeqID IDENTITY COVERAGE	10110 43% 115%	10783 48% 100%	11134 38% 112%	11489 48% 117%		11787 48% 98%	12670 100% 100%	13411 63% 101%	13994 43% 116%
SAU103169	SeqID IDENTITY COVERAGE							12678 100% 100%	13239 34% 84%	
SAU103175	SeqID IDENTITY COVERAGE	10157 36% 96%						12687 100% 100%		
SAU103191	SeqID IDENTITY COVERAGE							12465 100% 102%	13332 42% 75%	
SAU103204	SeqID IDENTITY COVERAGE							12499 100% 101%		
SAU103226	SeqID IDENTITY COVERAGE							12713 100% 100%		
SAU103232	SeqID IDENTITY COVERAGE	10368 36% 102%				11704 35% 98%	11848 48% 101%	12697 100% 101%		13803 35% 102%
SAU200006	SeqID IDENTITY COVERAGE	10033 53% 78%	10639 70% 80%	11192 47% 84%	11553 43% 82%		12007 50% 89%	12723 100% 100%	13479 65% 77%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU200028	SeqID IDENTITY COVERAGE							12694 100% 100%		
SAU200030	SeqID IDENTITY COVERAGE	10372 42% 84%	10553 74% 98%	11056 39% 84%	11447 43% 93%	11672 41% 86%	12092 35% 93%	12745 100% 102%	13449 73% 95%	13807 42% 84%
SAU200058	SeqID IDENTITY COVERAGE		10621 39% 79%					12719 100% 101%	13327 37% 78%	
SAU200059	SeqID IDENTITY COVERAGE	10259 31% 73%	10622 33% 97%	10978 32% 73%			12026 36% 74%	12720 100% 100%	13325 40% 96%	14087 31% 73%
SAU200088	SeqID IDENTITY COVERAGE	10262 51% 82%		10984 56% 91%	11403 57% 93%		11947 45% 93%	12724 100% 102%	13415 68% 100%	14090 49% 82%
SAU200042	SeqID IDENTITY COVERAGE		10712 28% 99%					12734 100% 100%		
SAU200097	SeqID IDENTITY COVERAGE	10109 33% 95%	10756 64% 100%	11257 34% 98%			11982 33% 95%	12739 100% 100%	13371 33% 95%	13996 32% 95%
SAU200045	SeqID IDENTITY COVERAGE							12751 100% 100%		
SAU200092	SeqID IDENTITY COVERAGE	10164 26% 97%	10584 30% 80%	10968 25% 96%	11566 27% 98%		11912 33% 93%	12755 100% 100%		13892 26% 98%
SAU200068	SeqID IDENTITY COVERAGE	10201 78% 74%	10478 75% 75%	11054 62% 74%			12061 36% 81%	12937 100% 101%	13425 76% 75%	13822 78% 74%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU200558	SeqID IDENTITY COVERAGE	10039 28% 72%	10728 31% 102%	11277 26% 80%			12046 30% 75%	12777 100% 100%	13423 32% 99%	13904 29% 72%
SAU200561	SeqID IDENTITY COVERAGE							12693 100% 100%		
SAU200564	SeqID IDENTITY COVERAGE	10099 33% 87%		11170 31% 87%	11602 31% 82%	11645 34% 86%	11788 32% 93%	12780 100% 100%		13992 34% 87%
SAU200565	SeqID IDENTITY COVERAGE	10098 32% 97%		11250 34% 96%	11386 35% 98%		11786 39% 97%	12781 100% 100%		13991 33% 97%
SAU200593	SeqID IDENTITY COVERAGE	10435 53% 99%	10613 73% 100%	11038 50% 99%	11412 53% 98%		11998 52% 100%	12784 100% 100%	13397 64% 99%	14046 52% 99%
SAU200628	SeqID IDENTITY COVERAGE	10173 32% 92%	10856 31% 97%					12790 100% 100%	13297 29% 97%	13937 34% 94%
SAU200685	SeqID IDENTITY COVERAGE							12801 100% 100%	13185 31% 94%	
SAU200721	SeqID IDENTITY COVERAGE	10208 40% 92%	10582 33% 79%	11015 41% 99%	11541 36% 94%			12797 100% 100%	13681 42% 100%	13922 41% 94%
SAU200725	SeqID IDENTITY COVERAGE	10118 30% 98%	10761 46% 100%	10966 30% 97%			11780 25% 98%	12933 100% 100%	13632 47% 100%	14020 29% 98%
SAU200731	SeqID IDENTITY COVERAGE	10283 55% 99%	10822 54% 100%	11064 44% 98%			12090 43% 98%	12342 100% 100%	13514 51% 100%	13855 46% 99%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU2007 40	SeqID IDENTITY COVERAGE	10318 48% 86%	10554 56% 102%	11225 48% 86%	11393 49% 73%		12056 50% 87%	12798 100% 100%	13695 55% 93%	13760 48% 86%
SAU2007 52	SeqID IDENTITY COVERAGE							12809 100% 100%		
SAU2009 14	SeqID IDENTITY COVERAGE	10383 26% 96%	10714 28% 98%			11747 27% 79%	11927 27% 90%	12837 100% 100%	13431 25% 91%	13788 25% 90%
SAU2009 16	SeqID IDENTITY COVERAGE							12838 100% 100%		
SAU2009 28	SeqID IDENTITY COVERAGE	10439 54% 86%	10627 73% 99%	11036 55% 87%	11571 53% 86%		5179 49% 102%	12815 100% 100%	13646 69% 100%	14042 54% 86%
SAU2009 34	SeqID IDENTITY COVERAGE	10212 44% 72%	10780 60% 93%				11964 42% 82%	12842 100% 100%		13835 42% 88%
SAU2009 49	SeqID IDENTITY COVERAGE							12846 100% 100%		
SAU2009 60	SeqID IDENTITY COVERAGE				11500 42% 70%		11886 33% 91%	12431 100% 102%		
SAU2009 94	SeqID IDENTITY COVERAGE	10036 36% 100%	10497 62% 101%	11270 32% 100%			11865 37% 102%	12935 100% 100%	13310 35% 73%	14054 33% 99%
SAU2011 67	SeqID IDENTITY COVERAGE		10779 37% 98%					12887 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU2011 68	SeqID IDENTITY COVERAGE		10819 53% 102%					12889 100% 100%	13626 56% 100%	
SAU2011 84	SeqID IDENTITY COVERAGE	10448 40% 70%	10715 52% 108%	10995 35% 97%	11579 37% 82%		11985 37% 70%	12807 100% 101%	13502 53% 111%	13819 32% 111%
SAU2011 97	SeqID IDENTITY COVERAGE	10330 58% 99%	10924 66% 99%	11160 60% 99%	11321 53% 98%		5215 58% 99%	12938 100% 101%	13364 63% 96%	13885 58% 99%
SAU2012 25	SeqID IDENTITY COVERAGE		10812 41% 93%	11090 33% 80%				12896 100% 100%	13170 38% 87%	
SAU2012 36	SeqID IDENTITY COVERAGE	10026 32% 92%	10679 29% 96%	11184 33% 93%	11613 33% 89%		12013 34% 95%	12891 100% 100%	13505 30% 95%	14073 32% 90%
SAU2013 01	SeqID IDENTITY COVERAGE							12899 100% 100%		
SAU2013 33	SeqID IDENTITY COVERAGE	10192 41% 100%				11678 28% 96%		12905 100% 101%		13753 41% 100%
SAU2013 75	SeqID IDENTITY COVERAGE						11929 36% 95%	12926 100% 100%		
SAU2013 80	SeqID IDENTITY COVERAGE	10379 34% 94%	10499 25% 93%		11313 26% 95%		12024 25% 89%	12922 100% 100%		13801 25% 101%
SAU2013 81	SeqID IDENTITY COVERAGE	10241 68% 89%	10597 59% 96%	10974 46% 90%	11387 44% 91%	11706 56% 89%	11833 57% 100%	12923 100% 104%	13387 52% 92%	13878 64% 89%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU2014 03	SeqID IDENTITY COVERAGE							12913 100% 100%		
SAU2014 69	SeqID IDENTITY COVERAGE							12967 100% 100%		
SAU2014 86	SeqID IDENTITY COVERAGE							13023 100% 100%		
SAU2015 06	SeqID IDENTITY COVERAGE	10145 49% 101%					11963 49% 102%	12946 100% 100%		13841 50% 100%
SAU2015 08	SeqID IDENTITY COVERAGE	10370 37% 73%					11874 42% 72%	12947 100% 100%		13805 36% 73%
SAU2015 13	SeqID IDENTITY COVERAGE	10229 29% 71%						12944 100% 101%		
SAU2015 39	SeqID IDENTITY COVERAGE	10109 33% 95%	11257 28% 96%				5099 34% 96%	12943 100% 100%	13625 32% 97%	13996 33% 95%
SAU2015 41	SeqID IDENTITY COVERAGE	10131 50% 71%	10500 39% 74%			11673 33% 77%	11951 41% 73%	12942 100% 100%	13474 41% 73%	
SAU2015 58	SeqID IDENTITY COVERAGE	10112 51% 96%	11258 51% 94%	11357 43% 94%			11875 49% 99%	12954 100% 101%	13598 46% 96%	14009 51% 96%
SAU2015 71	SeqID IDENTITY COVERAGE	10224 50% 98%	10951 61% 94%	11213 47% 99%	11357 50% 92%		11905 45% 103%	12997 100% 100%	13268 54% 70%	13957 49% 98%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU2016 11	SeqID IDENTITY COVERAGE				11539 38% 73%		11902 48% 99%	12973 100% 100%	13243 58% 95%	
SAU2016 15	SeqID IDENTITY COVERAGE						11962 40% 72%	12972 100% 100%		
SAU2016 21	SeqID IDENTITY COVERAGE	10038 49% 91%	10842 53% 91%		11392 42% 91%	11707 49% 91%	12047 47% 91%	12662 100% 101%		13902 46% 91%
SAU2016 54	SeqID IDENTITY COVERAGE							12982 100% 101%		
SAU2016 66	SeqID IDENTITY COVERAGE	10291 33% 71%	10900 29% 80%	11028 35% 71%	11557 31% 76%	11761 32% 79%	11811 34% 73%	12981 100% 100%		13743 33% 71%
SAU2017 52	SeqID IDENTITY COVERAGE		10623 45% 89%					12963 100% 100%	13689 40% 92%	
SAU2017 65	SeqID IDENTITY COVERAGE							12770 100% 100%		
SAU2017 73	SeqID IDENTITY COVERAGE							12996 100% 100%		
SAU2017 75	SeqID IDENTITY COVERAGE							12996 100% 100%		
SAU2018 10	SeqID IDENTITY COVERAGE							12769 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU201827	SeqID IDENTITY COVERAGE	10258 38% 108%	10783 46% 100%	11134 41% 100%	11310 41% 104%		11787 45% 88%	13002 100% 100%	13411 63% 101%	14088 39% 108%
SAU201929	SeqID IDENTITY COVERAGE							13008 100% 100%		
SAU201952	SeqID IDENTITY COVERAGE							13020 100% 100%		
SAU201971	SeqID IDENTITY COVERAGE							13015 100% 101%		
SAU202006	SeqID IDENTITY COVERAGE							13018 100% 100%		
SAU202039	SeqID IDENTITY COVERAGE				11359 44% 96%			13009 100% 101%	13374 48% 98%	
SAU202126	SeqID IDENTITY COVERAGE	10261 51% 94%	10874 50% 94%	10983 52% 91%	11561 33% 84%		11946 46% 93%	12714 100% 101%	13417 58% 94%	14085 52% 94%
SAU202174	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202176	SeqID IDENTITY COVERAGE							12895 100% 101%		
SAU202186	SeqID IDENTITY COVERAGE	10062 28% 73%						12731 100% 101%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU2022 67	SeqID IDENTITY COVERAGE							12727 100% 100%		
SAU2027 08	SeqID IDENTITY COVERAGE	10428 25% 86%	10913 28% 84%					12855 100% 100%		13735 25% 86%
SAU2027 36	SeqID IDENTITY COVERAGE	10148 39% 95%	10902 40% 93%	11181 37% 98%	11494 40% 91%	11677 37% 80%	11857 38% 93%	12927 100% 100%	13248 38% 103%	13844 39% 95%
SAU2027 56	SeqID IDENTITY COVERAGE	10436 44% 97%	10614 63% 92%	11071 47% 86%			5181 44% 92%	13027 100% 100%	13246 53% 91%	14045 40% 97%
SAU2027 81	SeqID IDENTITY COVERAGE							12718 100% 100%		
SAU2028 72	SeqID IDENTITY COVERAGE		10656 45% 101%					12866 100% 100%	13670 28% 98%	
SAU2028 82	SeqID IDENTITY COVERAGE							12848 100% 101%		
SAU2029 30	SeqID IDENTITY COVERAGE							12871 100% 100%		
SAU2029 45	SeqID IDENTITY COVERAGE							12868 100% 100%		
SAU2029 68	SeqID IDENTITY COVERAGE							12886 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU203001	SeqID IDENTITY COVERAGE							12894 100% 100%		
SAU203007	SeqID IDENTITY COVERAGE							12893 100% 100%		
SAU203196	SeqID IDENTITY COVERAGE							12945 100% 101%		
SAU203293	SeqID IDENTITY COVERAGE							12979 100% 101%		
SAU203296	SeqID IDENTITY COVERAGE				11330 29% 88%			12263 100% 101%		
SAU203524	SeqID IDENTITY COVERAGE							12957 100% 100%		
SAU300110	SeqID IDENTITY COVERAGE	10054 33% 82%	10544 38% 109%			11662 33% 73%		13031 100% 102%	13441 30% 109%	
SAU300131	SeqID IDENTITY COVERAGE	10344 45% 100%	10529 71% 99%	11112 44% 100%	11434 52% 99%		5164 47% 99%	13034 100% 101%	13213 60% 99%	14103 44% 100%
SAU300156	SeqID IDENTITY COVERAGE							13036 100% 100%		
SAU300191	SeqID IDENTITY COVERAGE		10562 43% 103%		11519 39% 91%		11844 32% 72%	12367 100% 101%	13522 41% 104%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU300572	SeqID IDENTITY COVERAGE				11522 32% 108%			12717 100% 100%		
SAU300617	SeqID IDENTITY COVERAGE		10851 50% 97%					12513 100% 100%	13289 49% 97%	
SAU300713	SeqID IDENTITY COVERAGE		10767 26% 83%				11823 30% 93%	13058 100% 100%		
SAU300719	SeqID IDENTITY COVERAGE	10468 46% 100%	10611 34% 87%	11246 34% 101%	11380 30% 94%	11644 30% 101%	11887 40% 100%	12987 100% 101%	13456 33% 96%	13726 34% 100%
SAU300732	SeqID IDENTITY COVERAGE	10282 26% 71%	10682 51% 88%					13061 100% 100%	13394 49% 86%	
SAU300825	SeqID IDENTITY COVERAGE		10655 52% 97%					13068 100% 100%	13671 41% 97%	
SAU300975	SeqID IDENTITY COVERAGE		10604 30% 72%					12203 100% 102%		
SAU300998	SeqID IDENTITY COVERAGE		10820 40% 99%					13077 100% 102%	13489 40% 99%	
SAU301004	SeqID IDENTITY COVERAGE		10744 40% 101%					13079 100% 100%		
SAU301030	SeqID IDENTITY COVERAGE							13080 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU301080	SeqID IDENTITY COVERAGE							13083 100% 100%		
SAU301118	SeqID IDENTITY COVERAGE	10242 47% 98%	10808 58% 98%	11092 48% 91%		11653 53% 78%		12904 100% 100%		13795 48% 96%
SAU301133	SeqID IDENTITY COVERAGE		10898 39% 96%					13087 100% 100%	13443 30% 93%	
SAU301223	SeqID IDENTITY COVERAGE	10297 31% 104%	10640 50% 99%	10964 31% 102%	11323 32% 90%		111783 34% 102%	13090 100% 100%	13664 48% 98%	13737 32% 104%
SAU301230	SeqID IDENTITY COVERAGE	10252 52% 95%	10877 52% 92%	11010 63% 74%		11669 52% 95%	11956 59% 77%	13092 100% 100%	13506 59% 92%	13704 52% 95%
SAU301268	SeqID IDENTITY COVERAGE							13102 100% 100%		
SAU301275	SeqID IDENTITY COVERAGE	10048 54% 99%	10926 47% 84%	11014 55% 97%	11511 50% 97%		11934 53% 97%	13103 100% 101%	13366 46% 84%	13897 54% 99%
SAU301357	SeqID IDENTITY COVERAGE		10696 74% 98%	11063 32% 80%		11766 33% 93%		12859 100% 101%	13354 76% 100%	
SAU301433	SeqID IDENTITY COVERAGE							12845 100% 100%	13393 26% 91%	
SAU301465	SeqID IDENTITY COVERAGE	10210 29% 100%	10663 54% 104%	11214 32% 104%	11554 37% 100%		11921 28% 101%	13013 100% 100%	13418 52% 103%	13925 29% 102%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU301472	SeqID IDENTITY COVERAGE	10157 36% 85%						12925 100% 100%		
SAU301592	SeqID IDENTITY COVERAGE							13137 100% 100%		
SAU301620	SeqID IDENTITY COVERAGE							13140 100% 100%		
SAU301758	SeqID IDENTITY COVERAGE							13156 100% 100%		
SAU301773	SeqID IDENTITY COVERAGE							12729 100% 100%		
SAU301829	SeqID IDENTITY COVERAGE	10107 45% 98%			11309 40% 97%		11857 42% 96%	13162 100% 100%	13248 38% 106%	13935 41% 99%
SAU301869	SeqID IDENTITY COVERAGE		10732 30% 80%		11373 36% 95%			12903 100% 100%		
SAU301898	SeqID IDENTITY COVERAGE		10932 27% 71%					13057 100% 100%		
SAU302060	SeqID IDENTITY COVERAGE							13042 100% 100%		
SAU302513	SeqID IDENTITY COVERAGE							12851 100% 100%		

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
SAU302626	SeqID IDENTITY COVERAGE							13105 100% 100%		
SAU302685	SeqID IDENTITY COVERAGE							13113 100% 100%		
SAU302698	SeqID IDENTITY COVERAGE							12725 100% 100%		
SAU302699	SeqID IDENTITY COVERAGE							13115 100% 100%		
SAU302805	SeqID IDENTITY COVERAGE				11345 33% 75%			13133 100% 101%		
SAU302901	SeqID IDENTITY COVERAGE							12872 100% 100%		
SAU302931	SeqID IDENTITY COVERAGE							13155 100% 100%		
SAU302950	SeqID IDENTITY COVERAGE							12664 100% 101%		
SAU302956	SeqID IDENTITY COVERAGE	10023 32% 88%		11256 28% 88%		11742 31% 88%	12044 26% 86%	12930 100% 101%	13372 31% 88%	14018 32% 88%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
ECO100078	Seq ID IDENTITY COVERAGE	10023 100% 100%		11256 66% 98%		11742 95% 100%	12044 65% 99%		13595 41% 97%	14018 97% 100%
ECO100252	Seq ID IDENTITY COVERAGE	10052 100% 100%			11503 41% 99%		12078 48% 96%	12626 38% 93%		13932 40% 93%
ECO100397	Seq ID IDENTITY COVERAGE	10064 100% 100%	10781 50% 96%	10993 71% 100%	11499 38% 97%		11959 71% 97%	12884 45% 97%	13614 47% 97%	13915 94% 99%
ECO100398	Seq ID IDENTITY COVERAGE	10065 100% 100%	10653 53% 95%	10992 81% 101%	11311 46% 98%		11958 71% 99%	12883 57% 95%	13177 50% 95%	13916 98% 100%
ECO100990	Seq ID IDENTITY COVERAGE	10120 100% 100%				11768 72% 82%				
ECO102108	Seq ID IDENTITY COVERAGE	10214 100% 100%	10608 36% 96%	11129 74% 100%		11757 94% 100%	11852 36% 97%		13627 36% 97%	13931 96% 73%
ECO102262	Seq ID IDENTITY COVERAGE	10228 100% 100%		11204 42% 100%		11631 86% 81%	12038 51% 100%	13132 35% 100%		13963 87% 100%
ECO102447	Seq ID IDENTITY COVERAGE	10247 100% 100%					11812 47% 93%			13948 99% 96%
ECO102539	Seq ID IDENTITY COVERAGE	10258 100% 100%	10628 46% 101%	11134 77% 100%	11489 48% 100%		5192 71% 100%	12526 52% 100%	13636 47% 82%	14088 97% 100%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
ECO102620	Seq ID IDENTITY COVERAGE	10266 100% 100%	10510 51% 93%	11269 26% 80%	11524 30% 94%		11819 28% 91%	12915 42% 96%	13279 49% 101%	14049 89% 99%
ECO103101	Seq ID IDENTITY COVERAGE	10315 100% 100%	10763 37% 74%	11215 73% 100%	11615 26% 76%	11716 96% 100%	12052 64% 100%		13662 33% 74%	13764 94% 101%
ECO104120	Seq ID IDENTITY COVERAGE	10462 100% 100%	10609 29% 79%	11034 34% 89%		11726 87% 100%	11853 28% 89%			13887 37% 92%
ECO104268	Seq ID IDENTITY COVERAGE	10475 100% 100%	10607 43% 92%					12370 43% 99%	13166 38% 92%	13707 95% 100%
KPN100432	Seq ID IDENTITY COVERAGE	10258 90% 100%	10736 37% 97%	11134 62% 100%	11310 37% 93%	11628 100% 101%	5192 62% 97%	12789 41% 86%	13636 47% 87%	14088 92% 101%
KPN100854	Seq ID IDENTITY COVERAGE	10086 35% 74%	10652 29% 72%	11197 26% 72%	11565 27% 85%	11630 100% 100%	11862 42% 77%		13389 32% 71%	14060 35% 74%
KPN101022	Seq ID IDENTITY COVERAGE	10475 90% 100%	10607 29% 77%			11642 100% 101%		12370 27% 101%	13166 26% 79%	13707 91% 101%
KPN101026	Seq ID IDENTITY COVERAGE	10228 86% 99%		11204 44% 97%		11631 100% 100%	12038 54% 98%	13132 37% 99%		13963 85% 99%
KPN101729	Seq ID IDENTITY COVERAGE			11045 50% 96%	11467 50% 96%	11647 100% 102%	12067 63% 96%	13032 63% 96%		
KPN101750	Seq ID	10052			11503	11652	12078	12626		13918

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
KPN10205 7	IDENTITY	94%			38%	100%	47%	37%		34%
	COVERAGE	100%			103%	100%	100%	96%		100%
KPN10263 8	Seq ID	10406	10892	11035		11661	11854	13153		13883
	IDENTITY	29%	30%	30%		100%	27%	28%		29%
KPN10388 2	COVERAGE	96%	96%	84%		100%	97%	85%		96%
	Seq ID	10266	10510		11524	11667		12915	13557	14049
KPN10418 3	IDENTITY	77%	51%		29%	100%		44%	50%	77%
	COVERAGE	79%	79%		83%	100%		80%	79%	79%
KPN10428 1	Seq ID	10315	10763	11215	11454	11716	12052		13662	13764
	IDENTITY	96%	38%	73%	26%	100%	65%		33%	93%
KPN10453 8	COVERAGE	100%	74%	100%	77%	100%	100%		74%	101%
	Seq ID	10065	10653	10992	11490	11650	11958	12883	13177	13916
KPN10471 6	IDENTITY	97%	56%	80%	46%	100%	80%	60%	55%	98%
	COVERAGE	85%	74%	89%	86%	100%	85%	74%	74%	85%
KPN10577 9	Seq ID	10023		11256		11742	12044		13595	14018
	IDENTITY	95%		68%		100%	66%		41%	95%
KPN10665 9	COVERAGE	94%		92%		101%	94%		91%	101%
	Seq ID	10462	10609	11034		11726	11853			13887
KPN10777 9	IDENTITY	87%	27%	35%		100%	29%			38%
	COVERAGE	100%	87%	89%		100%	89%			94%
KPN10887 9	Seq ID	10214	10608	11129		11757	11852		13627	13931
	IDENTITY	94%	36%	75%		100%	36%		35%	94%
KPN10993 9	COVERAGE	100%	96%	100%		100%	97%		97%	73%
	Seq ID					11770	12103			
KPN110665 9	IDENTITY					100%	28%			
	COVERAGE					101%	99%			
KPN111665 9	Seq ID	10064	10781	10993		11649	11959	12884	13614	13915
	IDENTITY	90%	58%	72%		100%	74%	51%	58%	91%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERAGE	80%	70%	75%		101%	74%	72%	70%	81%
KPN106840	Seq ID	10259	10857	10978		11664	12026	12182	13691	14087
	IDENTITY	91%	44%	74%		100%	55%	38%	42%	91%
	COVERAGE	100%	101%	98%		100%	99%	94%	92%	100%
KPN107776	Seq ID	10222		11132		11771	11810			13936
	IDENTITY	78%		37%		100%	35%			80%
	COVERAGE	98%		89%		102%	87%			98%
SAU100968	Seq ID	10064	10781	10993	11499		11959	12643	13614	13915
	IDENTITY	45%	62%	44%	36%		46%	100%	62%	46%
	COVERAGE	97%	97%	100%	99%		97%	100%	98%	97%
SAU201145	Seq ID	10064	10781	10993	11499		11959	12884	13614	13915
	IDENTITY	45%	62%	44%	36%		46%	100%	62%	46%
	COVERAGE	97%	97%	100%	99%		97%	100%	98%	97%
SPN101971	Seq ID	10064	10781	10993	11499		11959	12884	13287	13915
	IDENTITY	46%	77%	42%	36%		48%	62%	100%	46%
	COVERAGE	100%	99%	102%	100%		100%	99%	100%	100%
SPN201024	Seq ID	10064	10781	10993	11499		11959	12884	13614	13915
	IDENTITY	46%	77%	43%	36%		49%	62%	100%	46%
	COVERAGE	99%	99%	102%	101%		99%	99%	100%	99%
STY000277	Seq ID	10475	10607					12370	13166	13707
	IDENTITY	95%	44%					42%	38%	100%
	COVERAGE	100%	91%					99%	96%	100%
STY000625	Seq ID	10421								13784
	IDENTITY	93%								100%
	COVERAGE	100%								101%
STY000773	Seq ID	10315	10763	11215	11454	11716	12052		13662	13764
	IDENTITY	94%	36%	71%	26%	93%	62%		31%	100%
	COVERAGE	100%	74%	100%	77%	100%	100%		74%	100%

LOCUSID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
STY001430	Seq ID IDENTITY COVERAGE	10064 94% 100%	10781 49% 96%	10993 70% 101%	11499 37% 98%		11959 70% 98%	12884 46% 97%	13614 47% 98%	13915 100% 100%
STY001433	Seq ID IDENTITY COVERAGE	10065 98% 99%	10653 53% 94%	10992 82% 100%	11311 46% 97%		11958 72% 99%	12883 58% 94%	13177 50% 94%	13916 100% 100%
STY001867	Seq ID IDENTITY COVERAGE	10247 99% 98%					11812 47% 96%			13948 100% 100%
STY002995	Seq ID IDENTITY COVERAGE	10023 97% 94%		11256 67% 92%		11742 95% 101%	12044 65% 94%		13595 40% 91%	14018 100% 101%
STY003357	Seq ID IDENTITY COVERAGE	10228 87% 100%		11204 42% 100%		11631 85% 81%	12038 49% 101%	13132 36% 100%		13963 100% 100%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA0028	SeqID COVERAGE GE IDENTITY						5053 100% 100%			
PA0120	SeqID COVERAGE GE IDENTITY	10386 96% 28%		10959 94% 28%			5054 100% 100%		13899 95% 28%	
PA0129	SeqID COVERAGE GE IDENTITY	10265 93% 67%			11388 91% 32%		5055 100% 100%	12844 94% 36%		14048 91% 67%
PA0141	SeqID COVERAGE IDENTITY						5056 100% 100%			
PA0221	SeqID COVERAGE IDENTITY			11250 73% 32%	11386 77% 26%	11701 83% 28%	5057 100% 100%	12781 96% 28%		13778 77% 29%
PA0265	SeqID COVERAGE GE IDENTITY	10264 100% 81%	10550 97% 35%		11466 99% 26%		5058 100% 100%	12375 96% 38%	13316 91% 34%	14047 100% 80%
PA0321	SeqID COVERAGE IDENTITY						5059 100% 100%			
PA0337	SeqID	10278	10785	11275			5060	12351	13281	13880

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE IDENTITY	99% 43%	73% 35%	72% 37%			100% 100%	72% 36%	73% 35%	99% 42%
PA0353	SeqID COVERA GE IDENTITY	10408 97% 74%		11088 100% 75%	11397 88% 28%	11749 101% 74%	5061 100% 100%	12159 100% 45%	13511 96% 38%	14034 101% 74%
PA0378	SeqID COVERA GE IDENTITY	10324 94% 52%		11130 80% 49%			5062 100% 100%			13730 95% 53%
PA0401	SeqID COVERA GE IDENTITY	10078 99% 26%	10858 100% 31%				5063 100% 100%	12993 96% 33%	13560 100% 33%	13723 99% 26%
PA0413	SeqID COVERA GE IDENTITY						5064 100% 100%			
PA0414	SeqID COVERA GE IDENTITY						5065 100% 100%			
PA0419	SeqID COVERA GE IDENTITY	10296 100% 46%	10871 93% 29%	11003 102% 45%		11660 78% 47%	5066 100% 100%	12971 100% 27%	13461 91% 29%	13738 100% 47%
PA0423	SeqID COVERA GE IDENTITY	10123 99% 75%			11424 97% 32%		5067 100% 100%	12708 75% 32%		14038 99% 76%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA0469	SeqID COVERAGE IDENTITY						5068 100% 100%			
PA0472	SeqID COVERAGE IDENTITY	10471 88% 47%					5069 100% 100%			
PA0506	SeqID COVERAGE IDENTITY						5070 100% 100%			
PA0600	SeqID COVERAGE IDENTITY						5071 100% 100%			
PA0642	SeqID COVERAGE IDENTITY						5072 100% 100%			
PA0650	SeqID COVERAGE IDENTITY	10150 95% 38%	11237 83% 38%	11581 93% 35%			5073 100% 100%	12153 76% 34%	13459 95% 38%	13846 95% 39%
PA0715	SeqID COVERAGE IDENTITY						5074 100% 100%			
PA0788	SeqID COVERAGE IDENTITY						5075 100% 100%			
PA0882	SeqID COVERAGE IDENTITY	10233 85%					5076 100% 100%			14013 101%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA0934	IDENTITY		33%							28%
	SeqID	10276	10876	11006		11753	5077	12646	13483	
	COVERAGE	101%	93%	101%		80%	100%	92%	94%	
	GE									
	IDENTITY	47%	40%	46%		37%	100%	39%	38%	
PA0938	SeqID						5078			
	COVERAGE						100%			
	IDENTITY						100%			
PA1019	SeqID	10467	10592	11180			5079			
	COVERAGE	88%	84%	88%			100%			
	GE									
	IDENTITY	26%	25%	28%			100%			
PA1072	SeqID	10377					5080		13410	13813
	COVERAGE	100%					100%		71%	100%
	GE									
	IDENTITY	62%					100%		36%	61%
PA1115	SeqID						5081			
	COVERAGE						100%			
	IDENTITY						100%			
PA1270	SeqID	10328				11751	5082			13946
	COVERAGE	76%				79%	100%			76%
	GE									
	IDENTITY	26%				25%	100%			26%
PA1301	SeqID	10470					5083			
	COVERAGE	96%					100%			
	GE									
	IDENTITY	28%					100%			
PA1360	SeqID	10104					5084		13282	14000

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE IDENTITY	92% 63%					100% 100%		97% 25%	92% 63%
PA1365	SeqID COVERA IDENTITY						5085 100% 100%			
PA1398	SeqID COVERA IDENTITY						5086 100% 100%			
PA1462	SeqID COVERA IDENTITY		10915 98% 29%		11559 101% 30%		5087 100% 100%			
PA1493	SeqID COVERA GE IDENTITY	10423 92% 56%				11718 97% 49%	5088 100% 100%			13786 92% 56%
PA1547	SeqID COVERA IDENTITY				11377 88% 28%		5089 100% 100%			
PA1636	SeqID COVERA GE IDENTITY	10091 101% 37%					5090 100% 100%	12990 96% 26%		13890 81% 32%
PA1684	SeqID COVERA IDENTITY					11693 99% 59%	5091 100% 100%			
PA1868	SeqID COVERA GE	10361 82%					5092 100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA1876	IDENTITY	35%								
	SeqID					11746	5093			14036
	COVERAGE					76%	100%			93%
PA1918	IDENTITY					40%	100%			39%
	SeqID	10153		11033			5094			13745
	COVERAGE	79%		82%			100%			79%
PA1986	IDENTITY	31%		28%			100%			28%
	SeqID						5095			
	COVERAGE						100%			
PA2009	IDENTITY						100%			
	SeqID						5096			
	COVERAGE						100%			
PA2083	IDENTITY						100%			
	SeqID	10253				11692	5097			
	COVERAGE	87%				85%	100%			
PA2101	IDENTITY	31%				35%	100%			
	SeqID	10198					5098		13282	13861
	COVERAGE	92%					100%		88%	95%
PA2108	IDENTITY	30%					100%		25%	28%
	SeqID	10109		11257			5099	12943	13625	13996
	COVERAGE	96%		95%			100%	94%	90%	96%
PA2128	IDENTITY	37%		27%			100%	34%	29%	37%
	SeqID	10472	10865			11752	5100		13683	13893
	COVERAGE	97%	96%			86%	100%		80%	97%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA2147	IDENTITY	27%	26%			25%	100%		27%	33%
	SeqID	10181					5101			13985
	COVERAGE	98%					100%			98%
PA2196	GE						100%			59%
	IDENTITY	60%					100%			
	SeqID	10169					5102			13852
PA2197	COVERAGE	99%					100%			99%
	GE						100%			43%
	IDENTITY	43%					100%			
PA2197	SeqID	10160					5103	12917		13830
	COVERAGE	100%					100%	97%		100%
	GE						100%	44%		73%
PA2222	IDENTITY	74%					100%			
	SeqID						5104			
	COVERAGE						100%			
PA2313	IDENTITY						100%			
	SeqID						5105			
	COVERAGE						100%			
PA2398	IDENTITY						100%			
	SeqID	10132					5106			
	COVERAGE	86%					100%			
PA2424	GE						100%			
	IDENTITY	35%					100%			
	SeqID						5107			
PA2461	COVERAGE						100%			
	IDENTITY						100%			
	SeqID						5108			
	COVERAGE						100%			
	IDENTITY						100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA2470	SeqID COVERAGE IDENTITY						5109 100% 100%			13930 98% 60%
PA2488	SeqID COVERAGE GE IDENTITY	10189 89% 32%	11172 70% 28%				5110 100% 100%			13980 87% 29%
PA2494	SeqID COVERAGE GE IDENTITY	10331 99% 42%	11145 98% 31%	11516 100% 26%			5111 100% 100%			13719 98% 41%
PA2584	SeqID COVERAGE GE IDENTITY	10195 94% 60%	10967 94% 57%	11504 97% 38%			5112 100% 100%	12330 99% 41%	13442 92% 42%	14058 94% 58%
PA2594	SeqID COVERAGE GE IDENTITY	10116 97% 41%				11714 80% 45%	5113 100% 100%			
PA2634	SeqID COVERAGE GE IDENTITY	10441 74% 28%					5114 100% 100%			
PA2641	SeqID COVERAGE GE IDENTITY	10226 95% 80%	10566 89% 37%				5115 100% 100%			13959 95% 80%
PA2671	SeqID COVERAGE						5116 100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA2680	IDENTITY									
	SeqID	10444	10703			11730	5117			14029
	COVERA GE	101%	74%			90%	100%			101%
PA2684	IDENTITY		30%			43%	100%			42%
	SeqID	10384					5118			
	COVERA GE	99%					100%			
PA2726	IDENTITY						100%			
	SeqID						5119			
	COVERA GE						100%			
PA2742	IDENTITY									
	SeqID	10177	10660	11222	11296		5120	12628	13302	
	COVERA GE	91%	97%	84%	89%		100%	97%	97%	
PA3006	IDENTITY		50%	67%	47%		100%	55%	45%	
	SeqID						5121			
	COVERA GE						100%			
PA3011	IDENTITY									
	SeqID	10151	10695	11233	11293		5122	12339		13848
	COVERA GE	100%	79%	100%	86%		100%	75%		100%
PA3013	IDENTITY		40%	64%	39%		100%	42%		66%
	SeqID	10416	10494	11095	11525		5123	12461		13750
	COVERA GE	98%	80%	102%	102%		100%	102%		98%
PA3041	IDENTITY		39%	43%	41%		100%	40%		64%
	SeqID	10307					5124			13777

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE IDENTITY	88% 32%					100% 100%			88% 32%
PA3048	SeqID COVERA GE IDENTITY	10117 99% 47%	10966 75% 45%				5125 100% 100%			14005 99% 47%
PA3068	SeqID COVERA GE IDENTITY						5126 100% 100%			
PA3121	SeqID COVERA GE IDENTITY	10021 99% 63%	11164 99% 59%	11363 81% 26%			5127 100% 100%	12156 99% 56%		14017 99% 62%
PA3153	SeqID COVERA GE IDENTITY						5128 100% 100%			
PA3154	SeqID COVERA GE IDENTITY						5129 100% 100%			
PA3160	SeqID COVERA GE IDENTITY						5130 100% 100%			
PA3279	SeqID COVERA GE IDENTITY						5131 100% 100%			
PA3280	SeqID COVERA GE IDENTITY						5132 100% 100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA3374	SeqID COVERAGE GE IDENTITY	10452 99% 55%					5133 100% 100%			
PA3479	SeqID COVERAGE IDENTITY						5134 100% 100%			
PA3484	SeqID COVERAGE IDENTITY						5135 100% 100%			
PA3522	SeqID COVERAGE GE IDENTITY	10331 98% 41%		11145 99% 30%	11516 99% 26%		5136 100% 100%		13719 99% 40%	
PA3643	SeqID COVERAGE GE IDENTITY	10046 99% 53%		11173 100% 51%	11378 79% 30%		5137 100% 100%		13912 99% 52%	
PA3703	SeqID COVERAGE GE IDENTITY	10194 100% 30%					5138 100% 100%		13751 100% 31%	
PA3709	SeqID COVERAGE IDENTITY						5139 100% 100%			
PA3716	SeqID COVERAGE IDENTITY						5140 100% 100%			
PA3764	SeqID	10255		10991			5141			13793

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE	94%		91%			100%			82%
	IDENTITY	38%		41%			100%			39%
PA3845	SeqID	10277	11200				5142			13882
	COVERA GE	98%	98%				100%			98%
	IDENTITY	34%	30%				100%			35%
PA3866	SeqID						5143			
	COVERA GE						100%			
	IDENTITY						100%			
PA3876	SeqID	10144					5144			13840
	COVERA GE	97%					100%			97%
	IDENTITY	61%					100%			58%
PA3877	SeqID	10161					5145	12699		13831
	COVERA GE	98%					100%	92%		98%
	IDENTITY	28%					100%	27%		27%
PA3931	SeqID	10050	10833	11067	11460	11656	5146	12548	13173	13720
	COVERA GE	82%	92%	103%	92%	82%	100%	96%	109%	95%
	IDENTITY	50%	43%	41%	49%	48%	100%	44%	36%	35%
PA3984	SeqID	10087		11002		11674	5147			14061
	COVERA GE	97%		98%		91%	100%			99%
	IDENTITY	40%		37%		39%	100%			40%
PA4024	SeqID	10244	10700			11736	5148			13951
	COVERA GE	95%	95%			71%	100%			95%

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	IDENTITY	50%	50%	50%		72%	100%			50%
PA4027	SeqID COVERAGE IDENTITY						5149 100% 100%			
PA4037	SeqID COVERAGE GE IDENTITY	10102 72% 35%	10563 83% 30%	11194 72% 33%	11527 72% 34%	11725 72% 33%	5150 100% 100%	12958 70% 35%	13296 71% 31%	14002 72% 34%
PA4067	SeqID COVERAGE GE IDENTITY	10149 98% 44%					5151 100% 100%			13845 99% 43%
PA4070	SeqID COVERAGE GE IDENTITY	10159 96% 28%					5152 100% 100%			
PA4081	SeqID COVERAGE IDENTITY						5153 100% 100%			
PA4105	SeqID COVERAGE IDENTITY						5154 100% 100%			
PA4124	SeqID COVERAGE IDENTITY						5155 100% 100%			14023 93% 64%
PA4125	SeqID COVERAGE IDENTITY						5156 100% 100%			14024 94% 67%
PA4158	SeqID	10080	10610	11009	11379	11769	5157	12297		13725

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE IDENTITY	98% 61%	95% 38%	88% 31%	83% 28%	74% 61%	100% 100%	96% 50%	97% 61%	
PA4237	SeqID COVERA GE IDENTITY	10333 91% 79%	10542 97% 43%	11123 98% 76%	11582 90% 43%		5158 100% 100%	12232 92% 45%	13224 97% 42%	14093 91% 79%
PA4242	SeqID COVERA GE IDENTITY	10338 100% 87%	10538 100% 68%	11117 100% 76%	11428 100% 74%		5159 100% 100%			
PA4244	SeqID COVERA GE IDENTITY	10340 100% 65%	10534 100% 46%	11116 100% 63%			5160 100% 100%	12225 100% 42%	13217 100% 43%	14099 100% 65%
PA4245	SeqID COVERA GE IDENTITY	10341 95% 56%	10532 98% 42%	11115 95% 58%			5161 100% 100%	12223 98% 42%	13216 98% 40%	13812 78% 33%
PA4246	SeqID COVERA GE IDENTITY	10342 100% 77%	10531 92% 52%	11114 99% 74%	11432 88% 49%		5162 100% 100%	12222 99% 52%	13215 92% 53%	14101 100% 77%
PA4247	SeqID COVERA GE IDENTITY	10343 99% 59%	10530 98% 52%	11113 99% 63%	11433 97% 37%		5163 100% 100%	12221 98% 48%	13214 98% 54%	14102 99% 59%
PA4248	SeqID	10344	10529	11112	11434		5164	12220	13571	14103

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERA GE IDENTITY	100% 62%	99% 49%	100% 66%	99% 50%		100% 100%	99% 43%	99% 47%	100% 62%
PA4249	SeqID COVERA GE IDENTITY	10345 99% 64%	10528 102% 46%	11111 99% 64%	11435 100% 40%		5165 100% 100%	13033 102% 44%	13212 102% 47%	14104 99% 64%
PA4250	SeqID COVERA GE IDENTITY	10346 100% 69%	10599 100% 43%	11110 100% 63%			5166 100% 100%	12737 100% 46%	13211 100% 53%	14105 100% 67%
PA4251	SeqID COVERA GE IDENTITY	10347 99% 69%	10527 99% 58%	11109 99% 68%	11589 99% 48%	11654 99% 69%	5167 100% 100%	12218 90% 63%	13210 98% 61%	14106 99% 68%
PA4252	SeqID COVERA GE IDENTITY	10348 97% 65%	10526 92% 49%	11108 94% 62%			5168 100% 100%	12217 98% 49%	13209 92% 46%	14107 96% 64%
PA4253	SeqID COVERA GE IDENTITY	10349 101% 85%	10525 100% 66%	11107 101% 85%	11436 100% 65%		5169 100% 100%	12216 100% 66%	13208 100% 66%	14108 101% 84%
PA4254	SeqID COVERA GE IDENTITY	10350 90% 71%	10524 98% 53%	11106 90% 62%	11437 84% 45%		5170 100% 100%	12215 89% 55%	13207 89% 56%	

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA4256	SeqID COVERA GE IDENTITY	10352 100% 77%	10560 100% 54%	11104 100% 77%	11439 96% 65%		5171 100% 100%	12260 98% 58%	13204 98% 57%	13968 100% 77%
PA4257	SeqID COVERA GE IDENTITY	10353 99% 74%	10559 91% 61%	11103 100% 72%	11592 99% 55%		5172 100% 100%	12259 91% 57%	13203 93% 59%	13969 99% 74%
PA4258	SeqID COVERA GE IDENTITY	10354 100% 69%	10558 91% 57%	11102 100% 70%	11593 95% 41%		5173 100% 100%	12258 99% 48%	13202 91% 58%	13970 100% 69%
PA4259	SeqID COVERA GE IDENTITY	10355 100% 82%	10557 101% 70%	11101 100% 84%	11594 99% 61%		5174 100% 100%	12255 100% 63%	13201 100% 67%	
PA4262	SeqID COVERA GE IDENTITY	10358 100% 68%	10549 95% 45%	11098 100% 72%	11595 96% 36%		5175 100% 100%	12240 101% 46%	13198 97% 44%	13973 100% 68%
PA4263	SeqID COVERA GE IDENTITY	10359 99% 75%		11097 98% 73%	11442 91% 35%		5176 100% 100%	12235 103% 46%	13197 99% 51%	13974 99% 75%
PA4264	SeqID COVERA GE IDENTITY	10360 100% 90%	10533 75% 58%	11096 100% 92%	11443 95% 57%	11643 100% 92%	5177 100% 100%		13196 99% 61%	13975 100% 91%
PA4268	SeqID	10365	10479	11062	11409		5178	12445	13231	13967

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA4269	COVERA	100%	111%	100%	100%		100%	111%	111%	100%
	GE	89%	70%	89%	75%		100%	68%	70%	89%
	IDENTITY									
PA4271	SeqID	10439	10627	11036	11410		5179	12446	13646	14042
	COVERA	100%	100%	100%	109%		100%	101%	99%	100%
	GE	76%	46%	73%	47%		100%	46%	45%	75%
PA4272	IDENTITY									
	SeqID	10437	10615	11072	11572		5180	12449	13247	14044
	COVERA	100%	101%	101%	102%		100%	98%	100%	100%
PA4272	GE	66%	65%	66%	54%		100%	58%	58%	64%
	IDENTITY									
PA4272	SeqID	10436	10614	11071			5181	12450	13246	14045
	COVERA	99%	95%	100%			100%	99%	95%	99%
	GE	68%	40%	66%			100%	39%	42%	65%
PA4316	IDENTITY									
	SeqID	10200		11235			5182			13821
	COVERA	88%		90%			100%			91%
PA4332	GE	51%		47%			100%			51%
	IDENTITY									
PA4332	SeqID						5183			
	COVERA						100%			
	GE						100%			
PA4347	IDENTITY									
	SeqID					11699	5184			
	COVERA					86%	100%			
PA4363	IDENTITY					27%	100%			
	SeqID	10292				11740	5185			13742
	COVERA	95%				81%	100%			95%
PA4363	GE	40%				36%	100%			41%
	IDENTITY									

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA4375	SeqID	10072		11145	11516		5186			13719
	COVERAGE	101%		100%	100%		100%			101%
	IDENTITY	33%		45%	28%		100%			33%
PA4413	SeqID	10030	10805	11188	11458		5187	12360	13333	14077
	COVERAGE	90%	94%	92%	93%		100%	93%	98%	90%
	IDENTITY	45%	33%	41%	30%		100%	33%	32%	44%
PA4433	SeqID	10327	10602	11241	11289	11655	5188	12237	13356	13729
	COVERAGE	100%	99%	100%	94%	72%	100%	99%	99%	100%
	IDENTITY	75%	59%	73%	54%	76%	100%	55%	56%	72%
PA4473	SeqID	10463		11195			5189			13986
	COVERAGE	84%		81%			100%			84%
	IDENTITY	39%		37%			100%			39%
PA4506	SeqID	10381	10658	11198	11314	11717	5190	12850	13248	13800
	COVERAGE	99%	77%	98%	79%	91%	100%	99%	81%	99%
	IDENTITY	58%	48%	60%	51%	59%	100%	46%	42%	58%
PA4512	SeqID						5191			13815
	COVERAGE						100%			99%
	IDENTITY						100%			57%
PA4542	SeqID	10258	10628	11134	11489		5192	12526	13421	14088
	COVERAGE	100%	101%	100%	100%		100%	101%	80%	100%
	IDENTITY	71%	47%	70%	49%		100%	52%	46%	71%
PA4576	SeqID						5193			
	COVERAGE						100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA4598	IDENTITY									
	SeqID	10072		11145	11516		5194			13719
	COVERAGE	100%		100%	99%		100%			100%
PA4665	GE									
	IDENTITY	50%		29%	28%		100%			50%
	SeqID	10143	10826	11251	11287	11675	5195	12380	13336	13979
PA4681	COVERAGE	100%	97%	101%	97%	100%	100%	98%	99%	100%
	GE									
	IDENTITY	66%	54%	64%	52%	65%	100%	53%	50%	66%
PA4709	SeqID						5196			
	COVERAGE						100%			
	IDENTITY						100%			
PA4744	SeqID						5197			
	COVERAGE						100%			
	IDENTITY						100%			
PA4771	SeqID	10314		11216	11501		5198	12322	13663	13765
	COVERAGE	107%		98%	93%		100%	78%	91%	107%
	GE									
PA4888	IDENTITY	58%		58%	39%		100%	48%	43%	58%
	SeqID	10387		11280			5199		13402	13828
	COVERAGE	100%		99%			100%		96%	97%
PA4942	GE									
	IDENTITY	87%		75%			100%		33%	33%
	SeqID						5200			
PA4942	COVERAGE						100%			
	GE						100%			
	IDENTITY						100%			
PA4942	SeqID	10455		10972			5201			13856
	COVERAGE	93%		91%			100%			95%
	GE									

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA4997	IDENTITY									48%
	SeqID	10115	10619	10960	11394		5202	12501	13458	14006
	COVERAGE	86%	82%	97%	83%		100%	96%	97%	86%
	GE									
	IDENTITY	43%	36%	44%	31%		100%	37%	32%	44%
PA5030	SeqID	10165					5203			
	COVERAGE	90%					100%			
	GE									
	IDENTITY	64%					100%			
PA5076	SeqID	10197	10796	11176	11383	11694	5204		13292	14057
	COVERAGE	94%	82%	97%	97%	90%	100%		98%	94%
	GE									
	IDENTITY	29%	33%	27%	26%	29%	100%		30%	30%
PA5088	SeqID						5205			
	COVERAGE						100%			
	IDENTITY						100%			
PA5193	SeqID	10373		11126		11709	5206			13808
	COVERAGE	100%		96%		77%	100%			100%
	GE									
	IDENTITY	41%		39%		42%	100%			41%
PA5199	SeqID	10375	10596			11711	5207			13810
	COVERAGE	102%	71%			102%	100%			103%
	GE									
	IDENTITY	33%	26%			34%	100%			32%
PA5207	SeqID			11260	11612		5208	12730		
	COVERAGE			100%	88%		100%	100%		
	IDENTITY			54%	39%		100%	28%		
PA5209	SeqID	10302					5209			13758

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
	COVERAGE	90%					100%			89%
	IDENTITY	29%					100%			28%
PA5248	SeqID						5210			
	COVERAGE						100%			
	IDENTITY						100%			
PA5299	SeqID						5211			
	COVERAGE						100%			
	IDENTITY						100%			
PA5316	SeqID	10391		11158	11327		5212	12129		
	COVERAGE	100%		99%	78%		100%	73%		
	IDENTITY	82%		79%	39%		100%	40%		
PA5388	SeqID		10503				5213			
	COVERAGE		85%				100%			
	IDENTITY		28%				100%			
PA5393	SeqID						5214			
	COVERAGE						100%			
	IDENTITY						100%			
PA5436	SeqID	10330	10924	11160	11321		5215	13127	13617	13885
	COVERAGE	94%	94%	94%	94%		100%	94%	94%	94%
	IDENTITY	52%	51%	52%	46%		100%	55%	54%	52%
PA5443	SeqID	10413	10788	11199	11452		5216	12489	13643	13748
	COVERAGE	100%	103%	100%	96%		100%	100%	105%	100%
	IDENTITY	64%	38%	56%	35%		100%	38%	39%	64%
PA5490	SeqID						5217			
	COVERAGE						100%			

LOCUS ID	Data	<i>Escherichia coli</i>	<i>Enterococcus faecalis</i>	<i>Haemophilus influenzae</i>	<i>Helicobacter pylori</i>	<i>Klebsiella pneumoniae</i>	<i>Pseudomonas aeruginosa</i>	<i>Staphylococcus aureus</i>	<i>Streptococcus pneumoniae</i>	<i>Salmonella typhi</i>
PA5493	IDENTITY									
	SeqID	10417	10668	11133	11609		5218	12623	13236	
	COVERA GE	102%	102%	102%	102%		100%	100%	101%	
PA5507	IDENTITY									
	SeqID	10119					5219			
	COVERA GE	99%					100%			
PA5567	IDENTITY									
	SeqID	10397	10911	11169	11450		5220	12703	13338	13923
	COVERA GE	99%	103%	99%	100%		100%	102%	101%	99%
	IDENTITY									
			39%	64%	33%		100%	34%	37%	67%

TABLE IV

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
15	EFA102326	ECO101796	PAE100280	SAU102515
55	EFA100151	ECO104157	PAE100416	SAU100633
57	EFA100617	ECO102690	PAE105434	SAU100158
1443	EFA100689	ECO103692	PAE101987	SAU100952
1861	EFA101412	ECO103231	PAE104331	SAU101793
2286	EFA103268	ECO103265	PAE104314	SAU101756
2362	EFA101425	ECO100662	PAE101537	SAU101236
2367	EFA101417	ECO103226	PAE103206	SAU101798
2549	EFA101410	ECO103233	PAE104329	SAU101791
3816	EFA101159	ECO103243	PAE104319	SAU100546
3857	EFA101415	ECO103228	PAE103204	SAU101796
4322	EFA101165	ECO103237	PAE104325	SAU100141
4569	EFA100955	ECO103217	PAE103215	SAU101808
4948	EFA101160	ECO103242	PAE104320	SAU100547
5818	EFA100742	ECO103224	PAE103208	SAU101800
8159	EFA101163	ECO103239	PAE104323	SAU100139
8296	EFA101164	ECO103238	PAE104324	SAU100140
8316	EFA101409	ECO103234	PAE104328	SAU101790
8494	EFA103062	ECO103884	PAE104311	SAU100433
8498	EFA101411	ECO103232	PAE104330	SAU101792
8499	EFA101416	ECO103227	PAE103205	SAU101797
7		ECO100071	PAE100837	SAU102674
8	EFA101340		PAE106580	SAU100118
28	EFA101403		PAE102647	SAU100514
41	EFA101753	ECO100148		SAU101565
63	EFA101685		PAE103857	SAU100331
147		ECO100645	PAE100543	SAU100053
548		ECO100377	PAE100604	SAU100747
730		ECO103592	PAE103108	SAU100061
1721	EFA101686	ECO100663		SAU101996
1749	EFA101477	ECO102557		SAU100613
2153	EFA102656	ECO100184		SAU101869
2790	EFA102764	ECO100500		SAU101578
3164	EFA101162	ECO103240		SAU102602
3312	EFA103174		PAE105008	SAU100521
3926	EFA100194	ECO103220		SAU101806
4441	EFA102541		PAE105364	SAU101814
5685	EFA100190	ECO103264		SAU100157
7417	EFA102788	ECO101684		SAU102992
7437	EFA102351	ECO100084		SAU100056

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
7579		ECO102470	PAE102641	SAU100607
7726	EFA102551	ECO103221		SAU101805
7727	EFA100978	ECO103218		SAU101807
8092		ECO102035	PAE102964	SAU100794
8158	EFA103365		PAE104318	SAU102880
8161	EFA100210		PAE104326	SAU102527
8162	EFA101414		PAE103203	SAU101795
8164	EFA100741	ECO103223		SAU101801
8493	EFA101141		PAE104310	SAU100432
10185	EFA102728	ECO104092		SAU102578
35		ECO102870		SAU100497
44			PAE101061	SAU101143
54			PAE100225	SAU100123
85		ECO101104		SAU101262
184			PAE104901	SAU101366
362	EFA102736			SAU100414
575	EFA101790			SAU100133
579	EFA102110			SAU101624
911			PAE105432	SAU102054
941		ECO101365		SAU102162
952	EFA100615			SAU100964
1084	EFA100289	ECO102819		
1141		ECO102255		SAU102356
1232		ECO100703		SAU101346
1274			PAE103655	SAU102264
1337		ECO102562		SAU100567
1350		ECO100930	PAE103901	
1374		ECO103659		SAU101385
1427	EFA100394			SAU100714
1535		ECO101207		SAU101561
1653	EFA102655			SAU101868
1849	EFA100642			SAU101653
1932	EFA100919			SAU101365
2156	EFA101150			SAU101271
2189		ECO102827	PAE100476	
2238		ECO101436		SAU101092
2338	EFA103038			SAU100518
2411	EFA102802			SAU102246
2501	EFA101121			SAU100996
2974			PAE102537	SAU102125
3027		ECO103959		SAU200242
3239	EFA103021			SAU100300

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
3244	EFA100399			SAU101891
3386	EFA100426			SAU100886
3447	EFA102915			SAU102112
3460	EFA102023			SAU101399
3682	EFA100740			SAU101802
3771	EFA101540			SAU100275
4424	EFA102542			SAU101815
4654		ECO100488	PAE106184	
5148	EFA100065			SAU100658
7227	EFA100023			SAU100436
7240		ECO103672		SAU101682
7278			PAE101620	SAU301370
7374			PAE106765	SAU103042
7375	EFA102051			SAU103038
7402		ECO103572	PAE106044	
7419		ECO101686		SAU102693
7436	EFA101792			SAU101495
7504	EFA101670			SAU102603
7653	EFA100397			SAU100246
7660	EFA102352	ECO103698		
7719	EFA100756			SAU100496
7725	EFA100739			SAU101803
8040	EFA101736			SAU101197
8058	EFA103571			SAU101242
8077	EFA100200			SAU102231
8082	EFA101080			SAU100199
8116	EFA101963			SAU101028
8122	EFA101737			SAU101198
8141	EFA102780			SAU102433
8177	EFA103348			SAU202126
8178	EFA101022			SAU102283
8181	EFA101541			SAU102909
8191	EFA102022			SAU101398
8234	EFA103033			SAU100745
8237	EFA101682			SAU101266
8238	EFA103295			SAU100963
8251			PAE100662	SAU100596
8300	EFA101120			SAU100944
8539	EFA101339			SAU101400
8610		ECO103661		SAU102298
8874	EFA100748			SAU101155
9028	EFA103210			SAU100731

PathoSeq Cluster ID	Enterococcus faecalis	Escherichia coli	Pseudomonas aeruginosa	Staphylococcus aureus
9996	EFA102338			SAU100175
10234	EFA102186			SAU102933
10248		ECO102828		SAU101220
10297			PAE105229	SAU101381
10328	EFA101079			SAU101547
10345	EFA100295			SAU100659
10365	EFA100641			SAU101655
10393	EFA103504			SAU100961
10402	EFA101833			SAU100880
12426	EFA101413			SAU101794
14277	EFA103081			SAU200088
14330	EFA101161			SAU102881
14455	EFA101424			SAU101771
14520	EFA100211			SAU101789
15660	EFA103375			SAU102694

- Table VI A at the end of the present specification provides the SEQ ID NOs., clone names, and organisms for the sequences used in the above analysis. Table VI B at the end of the present specification provides the clone name, clone SEQ ID NO.,
- 5 PathoSeq locus, Gene SEQ ID NO. (protein) Genemarked gene and full length ORF protein SEQ ID NOs. for the sequences used in the above analysis. Table VI C at the end of the present specification provides the PathoSeq Gene Locus, nucleotide SEQ ID NOs. and Protein SEQ ID NOs. of the sequences used in the above analysis.

In some embodiments of the present invention, strains in which genes encoding gene products required for cellular proliferation under the control of a desired promoter, such as a constitutive or regulatable promoter which provides a desired level of expression, are constructed by replacing the natural promoter with the desired promoter through homologous recombination as described in Examples 9-13 below. It will be appreciated that although Examples 9-13 use *Candida albicans* as an exemplary organism, similar methods may be utilized in other organisms.

EXAMPLE 9

Construction of Strains which Overexpress or Underexpress Gene Products Required for Proliferation by Promoter Replacement

Strains which overexpress or underexpress gene products required for proliferation may also be constructed by replacing the promoters which naturally direct transcription of these gene products with promoters which provide the desired level of expression. As described above, such strains are useful in methods for identifying the targets of compounds which inhibit proliferation, as well as in methods for identifying genes encoding gene products required for proliferation.

For example, in some embodiments, the natural promoter may be replaced using techniques which employ homologous recombination to exchange a promoter present on the chromosome of the cell with the desired promoter. In such methodology, a nucleic acid comprising a promoter replacement cassette is introduced into the cell. As illustrated in Figure 5A, the promoter replacement cassette comprises a 5' region homologous to the sequence which is 5' of the natural promoter in the chromosome, the promoter which is to replace the chromosomal promoter and a 3' region which is homologous to sequences 3' of the natural promoter in the chromosome. In some embodiments, the promoter replacement cassette may also include a nucleic acid encoding an identifiable or selectable marker disposed between the 5' region which is homologous to the sequence 5' of the natural promoter and the promoter which is to replace the chromosomal promoter. If desired, the promoter replacement cassette may also contain a transcriptional terminator 3' of the gene encoding an identifiable or selectable marker, as illustrated in Figure 5B. As illustrated in Figure 5A and 5B, homologous recombination is allowed to occur between the chromosomal region

containing the natural promoter and the promoter replacement cassette. Cells in which the promoter replacement cassette has integrated into the chromosome are identified or selected. To confirm that homologous recombination has occurred, the chromosomal structure of the cells may be verified by Southern analysis or PCR.

5 In some embodiments, the promoter replacement cassette may be introduced into the cell as a linear nucleic acid, such a PCR product or a restriction fragment. Alternatively, the promoter replacement may be introduced into the cell on a plasmid. Figures 5A and 5B illustrates the replacement of a chromosomal promoter with a desired promoter through homologous recombination.

10 In some embodiments, the cell into which the promoter replacement cassette is introduced may carry mutations which enhance its ability to be transformed with linear DNA or which enhance the frequency of homologous recombination. For example, if the cell is an *Escherichia coli* cell it may have a mutation in the gene encoding Exonuclease V of the RecBCD recombination complex. If the cell is an *Escherichia*
15 *coli* cell it may have a mutation that activates the RecET recombinase of the Rac prophage and/or a mutation that enhances recombination through the RecF pathway. For example, the *Escherichia coli* cells may be RecB or RecC mutants carrying an sbcA or sbcB mutation. Alternatively, the *Escherichia coli* cells may be recD mutants. In other embodiments the *Escherichia coli* cells may express the λ Red recombination
20 genes. For example, *Escherichia coli* cells suitable for use in techniques employing homologous recombination have been described in Datsenko, K.A. and Wanner, B.L., PNAS 97:6640-6645 (2000); Murphy, K.C., J. Bact 180: 2053-2071 (1998); Zhang, Y., et al., Nature Genetics 20: 123-128 (1998); and Muyrers, J.P.P. et al., Genes & Development 14: 1971-1982 (2000), the disclosures of which are incorporated herein by
25 reference in their entirety. It will be appreciated that cells carrying mutations in similar genes may be constructed in organisms other than *Escherichia coli*.

 In some embodiments, the methods described in U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), the U.S. Patent Application Serial Number 10/032,585 filed
30 December 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), and U.S. Patent Application 09/948,993 (the disclosure of which is

incorporated herein by reference in its entirety), may be used to place the gene required for proliferation under the control of a regulatable promoter.

If the organism in which promoter replacement is to be performed is diploid, strains in which genes encoding gene products required for proliferation are under the control of a desired promoter may be constructed using the methods described in U.S. Patent Application Serial No. 09/792,024 filed February 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), and U.S. Patent Application Serial Number 10/032,585 filed December 20, 2001 (the disclosure of which is incorporated herein by reference in its entirety), disclose genes and gene products required for proliferation which may be used in any of the methods of the present invention.. In such methods, one chromosomal copy of a gene encoding a gene product required for proliferation is inactivated. For example, the gene may be inactivated by insertion of or replacement by a nucleotide sequence encoding a selectable or detectable gene product, such as a polypeptide which provides resistance to a drug or which allows growth under certain culture conditions. The other chromosomal copy of the gene encoding a gene product required for proliferation is placed under the control of a regulatable promoter by homologous recombination. The resultant strains may be used to identify genes which encode gene products required for proliferation and in the methods of the present invention.

For example, one method of constructing diploid cells in which a gene encoding a gene product required for proliferation is under the control of a regulated promoter is depicted in Figures 6A and 6B. In the method illustrated in Figures 6A and 6B, one chromosomal copy of the essential *Candida albicans* gene CaKRE9 is disrupted using a cassette in which nucleic acid sequences homologous to the CaKRE9 gene flank a nucleic acid comprising the SAT1 gene, which is under the control of the ACT-1 promoter and the PCK1 terminator sequence, which is at the 3' end of the SAT1 gene. The presence of the *Escherichia coli* SAT1 gene within *C. albicans* allows acetylation of the drug rendering it nontoxic and permitting the strain to grow in the presence of streptothricin at a concentration of 200 micrograms per milliliter. Expression of the SAT1 gene in *C. albicans* is made possible by engineering the gene so that its DNA sequence is altered to conform to the genetic code of this organism and by providing a

CaACT1 promoter (Morschhauser et al. (1998) Mol. Gen. Genet. 257:412-420) and a *CaPCK1* terminator sequence (Leuker et al. (1997) Gene 192: 235-40). This genetically modified marker is referred to as *CaSAT1* which is the subject of a copending United States Patent Application, Serial No 09/785,669, filed February 16, 2001, Publication
5 Number, US2001-0031724-A1, the disclosure of which is incorporated herein by reference in its entirety.

C. albicans is also sensitive to a second fungicidal compound, blasticidin, whose cognate resistance gene from *Bacillus cereus*, BSR, has similarly been genetically engineered for expression in *C. albicans* (*CaBSR1*), and has been shown to
10 confer a dominant drug resistance phenotype. PCR amplification of either dominant selectable marker so as to include about 65 bp of flanking sequence identical to the sequence 5' and 3' of the *C. albicans* gene to be disrupted, allows construction of a gene disruption cassette for any given *C. albicans* gene.

By employing the method of Baudin et al. (1993, Nucleic Acids Research
15 21:3329-30), a gene disruption event can be obtained following transformation of a *C. albicans* strain with the PCR-amplified gene disruption cassette and selection for drug resistant transformants that have precisely replaced the wild type gene with the dominant selectable marker. Such mutant strains can be selected for growth in the presence of a drug, such as but not limited to streptothricin. The resulting gene
20 disruptions are generally heterozygous in the diploid *C. albicans*, with one copy of the allelic pair on one homologous chromosome disrupted, and the other allele on the other homologous chromosome remaining as a wild type allele as found in the initial parental strain. The disrupted allele is non-functional, and expression from this allele of the gene is nil. By repeating this process for all the genes in the genome of an organism, a set of
25 gene disruptions can be obtained for every gene in the organism. The method can also be applied to a desired subset of genes.

In the method illustrated in Figures 6A and 6B, the second chromosomal copy of the *Candida albicans* CaKRE9 gene is placed under the control of a regulatable promoter using a promoter replacement cassette in which nucleic acid sequences
30 homologous to the promoter region to be replaced flank a nucleic acid comprising the

CaHIS3 gene (which encodes a selectable marker), the ADH terminator, which is at the 3' end of the CaHIS3 gene, and a tetracycline regulatable promoter (described below).

The tetracycline-regulatable promoter system was developed initially for *S. cerevisiae* but is modified for use in *C. albicans*. See Gari et al., 1997, *Yeast* 13:837-848; and Nagahashi et al., 1997, *Mol. Gen. Genet.* 255:372-375. Briefly, conditional expression is achieved by first constructing a transactivation fusion protein comprising the *E. coli* TetR tetracycline repressor domain or DNA binding domain (amino acids 1-207) fused to the transcription activation domain of *S. cerevisiae* GAL4 (amino acids 785-881) or HAP4 (amino acids 424-554). Multiple CTG codon corrections were introduced to comply with the *C. albicans* genetic code. The nucleotide sequences encoding the transactivation fusion proteins of *E. coli* TetR (amino acids 1-207) plus *S. cerevisiae* GAL4 (amino acids 785-881), and of *E. coli* TetR (amino acids 1-207) plus *S. cerevisiae* HAP4 (amino acids 424-554), both have been modified for proper expression in *C. albicans*.

Constitutive expression of the transactivation fusion protein in *C. albicans* can be achieved by providing a *CaACT1* promoter and *CaACT1* terminator sequence. However, it will be appreciated that any regulatory regions, promoters and terminators, that are functional in *C. albicans* can be used to express the fusion protein. Thus, a nucleic acid molecule comprising a promoter functional in *C. albicans*, the coding region of a transactivation fusion protein, and a terminator functional in *C. albicans* can be used to obtain cells in which a gene encoding a gene product required for proliferation is under the control of a regulatable promoter. Such a nucleic acid molecule can be a plasmid, a cosmid, a transposon, or a mobile genetic element. In a preferred embodiment, the TetR-Gal4 or TetR-Hap4 transactivators can be stably integrated into a *C. albicans* strain, by using either *ura3* and *his3* auxotrophic markers.

The heterologous tetracycline promoter initially developed for *S. cerevisiae* gene expression contains an *ADHI* 3' terminator sequence, variable number of copies of the tetracycline operator sequence (2, 4, or 7 copies), and the *CYC1* basal promoter. The tetracycline promoter has been subcloned adjacent to both *CaHIS3* and *CaSAT1* selectable markers in the orientation favoring tetracycline promoter-dependent regulation when placed immediately upstream the open reading frame of the gene of

interest. PCR amplification of the *CaHIS3*-Tet promoter cassette incorporates 65bp of flanking sequence homologous to the promoter sequence around nucleotide positions -200 and -1 (relative to the start codon) of the target gene, thereby producing a conditional promoter replacement fragment for transformation. When transformed into a *C. albicans* strain made heterozygous as described herein using the *CaSAT1* disruption cassette, homologous recombination between the promoter replacement fragment and the promoter of the wild type allele generates a strain in which the remaining wild type gene is conditionally regulated gene by the tetracycline promoter. Transformants are selected as His prototrophs and verified by Southern blot and PCR analysis.

In the method illustrated in Figures 6A and 6B, the promoter is induced in the absence of tetracycline, and repressed by the presence of tetracycline. Analogs of tetracycline, including but not limited to chlortetracycline, demeclocycline, doxycycline, meclocycline, methocycline, minocycline hydrochloride, anhydrotetracycline, and oxytetracycline, can also be used to repress the expression of the modified gene allele.

Alternative variants of the tetracycline promoter system, based upon a mutated tetracycline repressor (tetR) molecule, designated tetR', which is activated (*i.e.* binds to its cognate operator sequence) by binding of the antibiotic effector molecule to promote expression, and is repressed (*i.e.* does not bind to the operator sequence) in the absence of the antibiotic effectors, when the tetR' is used instead of, or in addition to, the wild-type tetR may also be used. For example, the method could be performed using tetR' instead of tetR in cases where repression is desired under conditions which lack the presence of tetracycline, such as shut off of a gene participating in drug transport (*e.g.* CaCDR1, CaPDR5, or CaMDR1). Also, the method could be adapted to incorporate both the tetR and tetR' molecules in a dual activator/repressor system where tetR is fused to an activator domain and tetR' is fused to a general repressor (*e.g.* CaSsr6 or CaTup1) to enhance or further repress expression in the presence of the antibiotic effector molecules (Belli et al., 1998, Nucl Acid Res 26:942-947 which is incorporated herein by reference). These methods of providing conditional expression are also contemplated.

The method may also be applied to haploid organisms by modifying the single allele of the gene via recombination of the allele with a promoter replacement fragment comprising a nucleotide sequence encoding a heterologous promoter, such that the expression of the gene is conditionally regulated by the heterologous promoter. By repeating this process for a preferred subset of genes in a haploid pathogenic organism, or its entire genome, a collection or a complete set of conditional mutant strains can be obtained. A preferred subset of genes comprises genes that share substantial nucleotide sequence homology with target genes of other organisms, e.g., *C. albicans* and *S. cerevisiae*. For example, the method may be applied to haploid fungal pathogens including, but not limited to, animal fungal pathogens such as *Aspergillus fumigatus*, *Aspergillus niger*, *Aspergillus flavus*, *Candida glabrata*, *Cryptococcus neoformans*, *Coccidioides immitis*, *Exophiala dermatitidis*, *Fusarium oxysporum*, *Histoplasma capsulatum*, *Pneumocystis carinii*, *Trichosporon beigeli*, *Rhizopus arrhizus*, *Mucor rouxii*, *Rhizomucor pusillus*, or *Absidia corymbigera*, or the plant fungal pathogens, such as *Botrytis cinerea*, *Erysiphe graminis*, *Magnaporthe grisea*, *Puccinia recodita*, *Septoria triticii*, *Tilletia controversa*, *Ustilago maydis*, or any species falling within the genera of any of the above species. Similarly, the method may be applied to bacteria, including the bacterial species and genera discussed above.

It will be appreciated that the means to achieve conditional expression are not restricted to the tetracycline promoter system and can be performed using other conditional promoters. Such conditional promoter may, for example, be regulated by a repressor which repress transcription from the promoter under particular condition or by a transactivator which increases transcription from the promoter, such as, when in the presence of an inducer. For example, the *C. albicans* *CaPCK1* promoter is not transcribed in the presence of glucose but has a high level of expression in cells grown on other carbon sources, such as succinate, and therefore could also be adopted for conditional expression of the modified allele. To this end, it has been shown that both *CaHIS1* and *CaSAT1* are essential for growth on glucose-containing medium using the *CaPCK1* promoter as an alternative to the tetracycline promoter in the above description. In this instance, the *CaPCK1* promoter is heterologous to the gene expressed and not to the organism, and such heterologous promoters are also

encompassed in the invention. Alternative promoters that could functionally replace the tetracycline promoter include but are not limited to other antibiotic-based regulatable promoter systems (e.g., pristinamycin-induced promoter or PIP) as well as *Candida albicans* conditionally-regulated promoters such as *MET25*, *MAL2*, *PHO5*, *GAL1,10*,
5 *STE2*, or *STE3*.

Although not mandatory, performing the gene disruption first enables heterozygous strains to be constructed and separately collected as a heterozygote strain collection during the process of drug target validation. Heterozygous strains for a given gene express approximately half the normal diploid level of a particular gene product.
10 Consequently, these strains provide constructions having a diminished level of the encoded gene product, and they may be used in the methods described herein. However, it is clear to those skilled in the art that the order of allele modification followed in this embodiment of the invention is not critical, and that it is feasible to perform these steps in a different order such that the conditional-expressing allele is
15 constructed first and the disruption of the remaining wild type gene allele be performed subsequently. However, where the promoter replacement step is carried out first, it is preferable to delete sequences homologous to those employed in the gene disruption step.

Alternatively, conditional expression could be achieved by means other than the
20 reliance of conditional promoters. For example, conditional expression could be achieved by the replacement of the wild type allele in haploid or heterozygous strains with temperature sensitive alleles derived *in vitro*, and their phenotype would then be analyzed at the nonpermissive temperature. In a related approach, in heterozygous strains, insertion of a ubiquitination signal into the remaining wild type allele to
25 destabilize the gene product during activation conditions can be adopted to examine phenotypic effects resulting from gene inactivation.

In another alternative, a constitutive promoter regulated by an excisable transactivator can be used. The promoter is placed upstream to a target gene to repress
30 expression to the basal level characteristic of the promoter. For example, if the strains are fungal organisms, a heterologous promoter containing *lexA* operator elements may be used in combination with a fusion protein composed of the *lexA* DNA binding

domain and any transcriptional activator domain (e.g. GAL4, HAP4, VP16) to provide constitutive expression of a target gene. Counterselection mediated by 5-FOA can be used to select those cells which have excised the gene encoding the fusion protein. This procedure enables an examination of the phenotype associated with repression of the target gene to the basal level of expression provided by the *lexA* heterologous promoter in the absence of a functional transcription activator. The strains generated by this approach may be used in the present invention.

Alternatively, conditional expression of a target gene can be achieved without the use of a transactivator containing a DNA binding, transcriptional activator domain. A cassette could be assembled to contain a heterologous constitutive promoter downstream of, for example, the *URA3* selectable marker, which is flanked with a direct repeat containing homologous sequences to the 5' portion of the target gene. Additional homologous sequences upstream of the target, when added to this cassette would facilitate homologous recombination and replacement of the native promoter with the above-described heterologous promoter cassette immediately upstream of the start codon of the target gene or open reading frame. Conditional expression is achieved by selecting strains, by using 5-FOA containing media, which have excised the heterologous constitutive promoter and *URA3* marker (and consequently lack those regulatory sequences upstream of the target gene required for expression of the gene) and examining the growth of the resulting strain *versus* a wild type strain grown under identical conditions.

A specific application of the above method as used to construct modified alleles of the target gene *CaKRE9* is provided in Example 10 below.

EXAMPLE 10

Construction of a *Candida albicans* Strain in which a Gene Encoding a Gene Product Required for Proliferation is Under the Control of a Regulatable Promoter

Oligonucleotide primers for PCR amplification of the SAT selectable marker used in Step 1 (*i.e.* gene replacement) contain 25 nucleotides complementary to the SAT disruption cassette in pRC18-ASP, and 65 nucleotides homologous to regions flanking the *CaKRE9* open reading frame. Figures 6A and 6B illustrate the procedure for constructing *Candida albicans* strains in which a gene encoding a gene product is under

the control of a regulatable promoter. As Figures 6A and 6B illustrate, the 2.2 kb *cakre9Δ::SAT* disruption fragment produced after PCR amplification and resulting gene replacement of the first wild type *CaKRE9* allele via homologous recombination following transformation. PCR conditions were as follows: 5-50 ng pRC18-ASP, 100 pmol of each primer, 200 μM dNTPs, 10 mM Tris- pH 8.3, 1.5 mM MgCl₂, 50 mM KCl, 1 unit Taq DNA polymerase (Gibco). PCR amplification times were: 5 min 94°C, 1 min 54°C, 2 min 72°C, for 1 cycle; 45 sec 94°C, 45 sec 54°C, 2 min 72°C, for 30 cycles. Transformation was performed using the lithium acetate method adapted for *C. albicans*, by Braun and Johnson, (Braun, B. R., and A. D. Johnson (1997), Control of filament formation in *Candida albicans* by the transcriptional repressor TUP1, Science 277:105-109), with minor modifications, including shorter incubation times at 30°C and 42°C (1 hr and 5 min respectively) and a greater amount of material transformed (50 μg of ethanol-precipitated *cakre9Δ::SAT* PCR product). Transformed cells were spread onto YPD plates and incubated overnight at 30°C, providing a preincubation period for expression of SAT prior to replica plating onto YPD medium containing streptothricin (400 μg/ml). Streptothricin-resistant colonies were detected after 36 hr and *cakre9Δ::SAT/CaKRE9* heterozygotes identified by PCR analysis using suitable primers which amplify both *CaKRE9* and *cakre9Δ::SAT* alleles.

Oligonucleotide primers for PCR amplification of the conditional promoter used in Step 2 (i.e. promoter replacement) contain 25 nucleotides complementary to the *CaHIS3*-marked tetracycline regulated promoter cassette in pBSK-HT4 and 65 nucleotides of homologous sequence corresponding to promoter regions -270 to -205, relative to the point of transcription initiation, and nucleotides 1-65 of the *CaKRE9* open reading frame. The resulting 2.2 kb PCR product was transformed into the *cakre9Δ::SAT/CaKRE9* heterozygous strain produced in step 1, and His⁺ transformants selected on YNB agar. Bonafide *CaKRE9* strains containing both a *cakre9Δ::SAT* allele and *CaHIS3-Tet-CaKRE9* allele were determined by PCR analysis. Typically, 2 independent strains are constructed and evaluated to provide a reliable determination of the terminal phenotype of any given drug target. Terminal phenotype is that phenotype caused by the absence of the gene product of an essential gene.

The phenotype of the resulting strain was evaluated as follows.

EXAMPLE 11

Evaluation of Phenotype of *Candida albicans* Strains in which a Gene Encoding
a Gene Product Required for Proliferation is Under the Control of a Regulatable
Promoter

5 Three independent methods were used to evaluate the phenotype of *Candida albicans* strains in which one copy of the CaKRE9 gene was disrupted and the other copy was under the control of a regulatable promoter. In the first, rapid determination of the strain's terminal phenotype was achieved by streaking approximately 1.0×10^6 cells onto both a YNB plate and YNB plate containing 100 µg/ml tetracycline and
10 comparing growth rate after 48 hr at room temperature. For essential genes, such as *CaKRE9*, no significant growth is detected in the presence of tetracycline. In the second approach, the essential nature of a gene may be determined by streaking the cells onto a casamino acid plate containing 625 µg/ml 5-fluororotic acid (5FOA) and 100 µg/ml uridine to select for ura⁻ cells which have excised (*via* recombination between *CaLEU2*
15 sequence duplications created during targeted integration) the transactivator gene that is normally required for expression of the tetracycline promoter-regulated target gene. Again, whereas strains in which one copy of a gene which is not required for proliferation is disrupted and the other copy is under control of a regulatable promoter demonstrate robust growth under such conditions, the CaKRE9 strains prepared as
20 described above fail to grow. Quantitative evaluation of the terminal phenotype associated with the CaKRE9 strain is performed using 2×10^3 cells/ml of overnight culture inoculated into 5.0 ml YNB either lacking or supplemented with 100 µg/ml tetracycline and measuring optical density (O.D.₆₀₀) after 24 and 48 hr incubation at 30°C. Typically, for strains in which a gene required for proliferation is under the
25 control of an inducible promoter, no significant increase in optical density is detected after 48 hrs in the absence of inducer. Discrimination between cell death (*cidal*) and growth inhibitory (*static*) terminal phenotypes for a demonstrated essential gene is achieved by determining the percentage of viable cells (as judged by the number of colony forming units (CFU) from an equivalent of 2×10^3 washed cells at T=0) from the
30 above tetracycline-treated cultures after 24 and 48 hours of incubation. Strains producing a *cidal* terminal phenotype are those which display a reduction in percent viable cells (i.e. $< 2 \times 10^3$ CFU) following incubation under repressing conditions.

To determine the variation in the level of a gene product under control of the tetracycline regulatable promoter the experiments described in Example 12 were performed.

EXAMPLE 12

5 Target Level Variation Under Induced and Repressed Conditions

Both a *CaHIS3* heterozygote strain and a tetracycline promoter-regulated *CaHIS3* strain in which one chromosomal copy of the *CaHIS3* gene was disrupted and the other was under the control of a regulatable promoter were compared against a wild type (diploid) *CaHIS3* strain for sensitivity towards the 3-aminotriazole (3-AT) (Figures 10 7A-7D). 3-AT is a competitive inhibitor of the enzyme encoded by *CaHIS3*, imidazoleglycerol phosphate dehydratase, and together serve as a model for a drug and drug target respectively. Overexpression, achieved by the constitutive expression level of *CaHIS3* maintained by the tetracycline promoter, confers 3-AT resistance at concentrations sufficient to completely inhibit growth of both wild type and *CaHIS3* 15 heterozygote strains (Fig 7A). The phenotype observed is consistent with that expected in light of the predicted 7.5 fold overexpression of *CaHIS3* determined by Northern blot analysis (see Fig 8). A heterozygous *CaHIS3* strain demonstrates enhanced sensitivity (i.e. haploinsufficient phenotype) to an intermediate 3-AT concentration unable to effect either wild type or tetracycline promoter-based overproducing *CaHIS3* strains noticeably (Fig 7B). A third *CaHIS3* expression level evaluated for differential 20 sensitivity to 3-AT was produced by partial repression of the tetracycline regulated strain using a threshold concentration of tetracycline 0.1% that normally is used to achieve complete shut-off.

This level of *CaHIS3* expression represents the minimum expression level 25 required for viability and as predicted, demonstrates an enhanced drug sensitivity relative the heterozygous *CaHIS3* strain at an intermediate 3-AT concentration (Fig 7C). Similarly, strain-specific drug resistance and sensitivity phenotypes to fluconazole and tunicamycin have been demonstrated by increasing and decreasing the level of expression of their respective known drug targets, *CaERG11* and *CaALG7*. Together 30 these results demonstrate that three different levels of expression are achieved using the *C. albicans* strain collection, and that they exhibit the predicted drug sensitivity phenotypes between known drugs and their known drug target.

EXAMPLE 13

Identification of *Candida albicans* Genes which Encode a Gene ProductRequired for Proliferation

Candida albicans genes which encode gene products required for proliferation were identified by constructing strains in which one chromosomal copy of a gene was disrupted and the other chromosomal copy of the gene was under the control of a regulatable promoter as described above. To identify genes which encode gene products required for proliferation, a strain containing the modified alleles of the gene was cultured under conditions wherein the second modified allele of the gene which is under conditional expression, was substantially underexpressed or not expressed. The viability and/or growth of the strain was compared with that of a wild type strain cultured under the same conditions. A loss or reduction of viability or growth indicated that the gene product encoded by the gene is required for proliferation. The level of expression of the gene in strains prepared as described above can be less than 50% of the non-modified allele, less than 30%, less than 20%, and preferably less than 10%. Depending on the heterologous promoter used, the level of expression can be controlled by, for example, antibiotics, metal ions, specific chemicals, nutrients, pH, temperature, etc.

For example, *C. albicans* conditional gene expression using the method described above was performed using *CaKRE1*, *CaKRE5*, *CaKRE6*, and *CaKRE9* (Fig. 9). *CaKRE5*, *CaKRE6*, and *CaKRE9* are predicted to be essential or conditionally essential (*CaKRE9* null strains are nonviable on glucose but viable on galactose), in *C. albicans* as demonstrated by gene disruption using the Ura blaster method. *CaKRE1* has been demonstrated as a nonessential gene using the Ura blaster method in *C. albicans*. Strains heterozygous for the above genes were constructed by PCR-based gene disruption method using the *CaSAT1* disruption cassette followed by tetracycline regulated promoter replacement of the native promoter of the wild type allele. Robust growth of each of these strains suggests expression proceeds normally in the absence of tetracycline. When tetracycline is added to the growth medium, expression of these tetracycline promoter-regulated genes is greatly reduced or abolished. In the presence of tetracycline, the strains in which each of the three essential *C. albicans* genes cited

above were under the control of a regulatable promoter stopped growing. As expected, only the *CaKRE1* strain demonstrates robust growth despite repression of *CaKRE1* expression.

5 To further examine the utility of the above method in target validation, growth of four additional strains in which expression of the known essential genes *CaTUB1*, *CaALG7*, *CaAUR1*, and *CaFKS1*, as well as the predicted essential gene *CaSAT2*, and *CaKRE1* were under the control of a regulatable promoter were compared under inducing versus repressing conditions (Fig. 10). As expected, strains in which *CaTUB1*, *CaALG7*, *CaAUR1* and *CaFKS1* were under the control of a regulatable promoter failed to grow under repressing conditions, unlike the strains in which the non-essential *CaKRE1* was under the control of a regulatable promoter. Furthermore, as predicted, the strain in which the *CaSAT2* gene was under the control of a regulatable promoter demonstrates essentiality of this gene in *C. albicans*. The *CaSAT2* gene, which has been engineered as a dominant selectable marker for use in *C. albicans*, is a
10 *C. albicans* gene that is homologous to a *S. cerevisiae* gene but is unrelated to the *Sat1* gene of *E. coli*.
15

In all cases based on other disruption data that have been generated, this is the expected response if the tetracycline regulated gene is repressed to a level where it is nonfunctional in the presence of tetracycline. Furthermore, in applying the above methodology of conditional gene disruption to two additional *C. albicans* genes (*CaYPD1*, and *CaYNL194c*) whose *S. cerevisiae* counterpart is known not to be essential, no inhibition of growth was observed when these strains were incubated in the presence of tetracycline. These results establish that the above method of conditional gene expression is a reliable indicator of gene essentiality.
20

25 Furthermore, the utility of the present method, as a rapid and accurate means to identifying the complete set of essential genes in *C. albicans*, has been demonstrated by an analysis of the null phenotype of a large number of genes using the above two-step method of gene disruption and conditional expression. Target genes were selected as being fungal specific and essential. Such genes are referred to as target essential genes
30 in the screening assays described below.

A literature search identified reports of URA blaster-based gene disruption experiments on a total of 89 genes, of which 13 genes were presumed to be essential, based on the inability to construct homozygous deletion strains. The 13 genes are *CaCCT8* (Rademacher et al., Microbiology, UK 144, 2951-2960 (1998)); *CaFKS1* (Mio et al., J. Bacteriol, 179, 4096-105 (1997); and Douglas, et al., Antimicrob Agents Chemother 41, 2471-9 (1997)); *CaHSP90* (Swoboda et al., Infect Immun 63, 4506-14 (1995)); *CaKRE6* (Mio et al., J. Bacteriol 179, 2363-72 (1997)); *CaNMT1* (Weinberg et al., Mol Microbiol 16, 241-50 (1995)); *CaPRS1* (Payne et al., J. Med. Vet. Mycol. 35, 305-12 (1997)); *CaPSA1* (Care et al., Mol Microbiol 34, 792-798 (1999)); *CaRAD6* (Care et al., Mol Microbiol 34, 792-798 (1999)); *CaSEC4* (Mao et al., J. Bacteriol 181, 7235-7242 (1999)); *CaSEC14* (Monteoliva et al., Yeast 12, 1097-105 (1996)); *CaSNF1* (Petter et al., Infect Immun. 65, 4909-17 (1997)); *CaTOP2* (Keller, et al., Biochem J., 329-39 (1997)); and *CaEFT2* (Mendoza et al., Gene 229, 183-1991 (1999)). These 13 putatively essential genes and *CaTUB1*, *CaALG1*, and *CaAUR1* of *C. albicans* are not initially identified by the above method. However, strains in which any one of these 17 genes are under the control of a regulatable promoter may be used in the methods of the present invention, for example, the *CaTUB1*, *CaALG1*, and *CaAUR1* strains in Fig. 10 and the *CaKRE6* strain in Fig. 9. Any of these 17 genes may be included as a control for comparisons in the methods described above, or as a positive control for essentiality in the collections of essential genes. The nucleic acid molecules comprising a nucleotide sequence corresponding to any of these 17 genes may be used in the methods of the present invention, as drug targets, or they may be included individually or in subgroups as controls in a kit or in a nucleic acid microarray.

Using methods such as those described above, the genes of SEQ ID NOs: 14111-14944, which encode the polypeptides of SEQ ID NOs.: 14945-15778 were identified as being required for proliferation. Table VII, provided at the end of the present specification, lists the SEQ ID NOs. of the identified genes along with their *Candida* designation. The *Candida* designations provided in Table VII were formulated by identifying the *Saccharomyces cerevisiae* gene which is homologous to the identified *Candida albicans* gene. The *Candida* designation also references the location of the homologous *Saccharomyces cerevisiae* gene in the *Saccharomyces cerevisiae* genom.

For example, the *Candida* designation CaYAL038W means that the homologous *Saccharomyces cerevisiae* gene was on yeast chromosome 1 (YB would mean yeast chromosome 2 etc), left arm of centromere (R means right arm of centromere), position 038; w for watson strand (c for crick strand). The homologous *Saccharomyces cerevisiae* gene was identified from genome-www.stanford.edu/saccharomyces. Homologous coding nucleic acids, homologous antisense nucleic acids and homologous polypeptides having homology to the genes of SEQ ID NOs: 14111-14944, nucleic acids complementary to SEQ ID NOs: 14111-14944, or the polypeptides of SEQ ID NOs: 14945-15778 may be identified using any of the methods described above.

An alternative method is available for assessing the essentiality of the modified gene in strains constructed as described above. Repression of expression of the modified gene allele within a strain constructed as described above may be achieved by homologous recombination-mediated excision of the gene encoding the transactivator protein. For example, where conditional expression of a target gene is achieved using the tetracycline-regulated promoter, constitutive expression (under nonrepressing conditions) may be repressed by homologous recombination-mediated excision of the transactivator gene (TetR-GAL4AD). In this way, an absolute achievable repression level is produced independently of that produced by tetracycline-mediated inactivation of the transactivator protein. Excision of the transactivator gene is made possible by virtue of the selectable marker and integration strategy used in strain construction. Stable integration of the *CaURA3*-marked plasmid containing the TetR-GAL4AD transactivator gene into the *CaLEU2* locus results in a tandem duplication of *CaLEU2* flanking the integrated plasmid. Counterselection on 5-FOA-containing medium can then be performed to select for excision of the *CaURA3*-marked transactivator gene and to directly examine whether this alternative repression strategy reveals the target gene to be essential.

Three examples of genes defined as essential on 5-FOA containing medium but lacking any detectable growth impairment on tetracycline supplemented medium are the genes, *CaYCL052c*, *CaYNL194c* and *CaYJR046c*. Presumably, this is due to the target gene exhibiting a lower basal level of expression under conditions where the transactivator gene has been completely eliminated than its gene product incompletely

inactivated by addition of tetracycline. Thus, the method described above offers two independent approaches for the determination of whether or not a given gene is essential for viability of the host strain.

EXAMPLE 14

5 Promoter Replacement to Generate Cells Capable of Overexpressing or
 Underexpressing a Gene Encoding a Gene Product Required for Proliferation

 A target for promoter replacement is selected. A promoter replacement cassette is obtained by inserting a nucleic acid comprising the *rrnBT1T2* transcriptional terminator followed by the *lac* promoter into pACYC184 such that the *rrnB* terminator and *lac* promoter are positioned 3' of the *CAT* gene. The promoter replacement cassette (CAT-*rrnBT1T2*-*plac*) is amplified by PCR. The PCR product is used as the template for another round of PCR using primers with 60-80 bp of homology to a target promoter (i.e. a promoter which directs expression of a gene encoding a gene product required for proliferation) and 20 bp of homology to the CAT/*rrnBT1T2*/*plac* template as described above. The region of homology is chosen such that upon homologous recombination, the CAT/*rrnBT1T2*/*plac* cassette replaces the promoter of the target gene but leaves its Shine-Delgarno motif untouched.

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 The promoter replacement cassette is transformed into competent JC8679. JC8679 is available from the *E. coli* genetics stock center. JC8679 allows recombination of short linear DNAs and also contains a *lacY* mutation which allows titratable regulation of the *lac* promoter. The transformed cells are plated onto LB/chloramphenicol plates containing various levels of IPTG to assure that the correct level of expression is achieved to allow survival. The correct integration of the promoter replacement cassette is confirmed by colony PCR. If desired, proper regulation of the target gene by the inserted promoter may be confirmed by testing the integrants for growth defects when inducer is absent or present at levels lower than that at which the original colonies were obtained. The inability to grow in the absence of inducer (IPTG) or in the presence of lower levels of the inducer than were used to obtain the clones confirms that the target gene is properly regulated by the inserted promoter. It will be appreciated that although the *lac* promoter and the strain JC8679 are used as examples, the method may be performed using any suitable regulatable

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promoter and organism or strain to generate cells which are capable of overexpressing or underexpressing a gene encoding a gene product required for proliferation.

EXAMPLE 15

Operator Insertion to Generate Cells Capable of Overexpressing or Underexpressing a Gene Encoding a Gene Product Required for Proliferation

5 An oligonucleotide comprising a lac operator flanked on each side by 40 nucleotides homologous to the target promoter is designed. The target promoter is the promoter which drives expression of a gene encoding a gene product required for proliferation, such as the *yabB yabC ftsL ftsI murE* genes in an operon. The sequence of the oligonucleotide (SEQ ID NO. 15810) and locations of the regions homologous to the promoter are illustrated in Figure 11. The sequence of the promoter is also shown with the locations of the -10 and -35 regions indicated (SEQ ID NO. 15811). The single stranded oligonucleotide is transformed into a bacterium expressing the λ Beta and Gam proteins. The cells in the transformation mixture are diluted and plated on medium containing IPTG. Colonies in which the lac operator has integrated into the target promoter are identified by colony PCR. If desired, proper regulation of the target promoter by the inserted operator is confirmed by growing the identified colonies in medium containing or lacking IPTG. The colonies proliferate on medium containing IPTG but fail to grow on medium lacking IPTG, thereby confirming that the target promoter is properly regulated by the inserted operator. It will be appreciated that the preceding method may be performed with any target promoter and any operator to generate cells which overexpress or underexpress a gene encoding a gene product required for proliferation.

25 In the methods of the present invention, strains which overexpress or under express gene products required for proliferation are used to identify the gene product on which a compound which inhibits proliferation of an organism acts or to profile a compound's activity. Examples 16-18 describe methods for identifying the gene product on which a compound which inhibits the proliferation of an organism acts using cells which overexpress or underexpress a gene product required for proliferation.

EXAMPLE 16**Strains in which a Gene Encoding a Gene Product Required for Proliferation is Overexpressed are able to Grow at Elevated Antibiotic Concentrations**

To confirm that cells which overexpress a gene product required for proliferation
5 are able to grow at elevated antibiotic concentrations, 11 such genes from
Staphylococcus aureus which are the targets of known antibiotics were operably linked
to the xylose inducible promoter XylT5 described above as follows. The genes and the
antibiotics which target the products of these genes are listed in Table V below.

PCR primer pairs were designed for each of the 11 genes encoding a gene
10 product required for proliferation of *Staphylococcus aureus* as shown in Table V. The
upstream primers for each gene included the native ribosomal binding sites (S-D
sequences). In addition, restriction sites for appropriate restriction enzymes were
designed into the primers to facilitate directional cloning of the genes. PCR reactions
were carried out using Pfu DNA polymerase (Stratagene, San Diego) under the
15 following conditions per 50 μ l reaction: Pfu polymerase 2U, dNTP 200 μ M, primers
400 nM each, *S. aureus* RN450 genomic DNA (template) 5-10 ng. The reaction
involved an initial heating at 94°C for 5 min, followed by 25 cycles of 30 sec at
94°C/30 sec at 55°C/5 min at 72°C, and ending with 7 min of extension at 72°C.

The amplified genes were operably linked to the XylT5 promoter as follows.
20 PCR products were cleaned using QIAGEN PCR Cleaning Kits and then were digested
with the proper restriction enzymes. The resulting fragments were ligated overnight at
16°C with precut vector DNA containing the XylT5 promoter. Ligation mixtures were
ethanol precipitated at -80°C for 20 min in the presence of 0.3 M sodium acetate. The
precipitated DNA was spun down at 14,000 rpm for 30 min at 4°C and washed with 1
25 ml of 70% EtoH. The DNA pellets were air-dried and dissolved in EB or sterile water.
To transform *Staphylococcus aureus* cells, the precipitated DNA was mixed with 45 μ l
of electroporation competent cells and incubated at room temperature for 30 min. The
DNA/cell mixtures were electroporated (settings: 2 volts, 25 μ F, 200 Ω) in 2 mm
cuvettes and mixed with 450 μ l B2 medium containing 0.2 μ g/ml chloramphenicol.
30 The cells were incubated at 37°C with shaking for 90 min. Transformed cells were
plated onto LB agar plates containing chloramphenicol (34 μ g/ml) for the selection of

plasmids. Several colonies for each cloning reaction were picked and streaked to obtain a pure culture. Colony PCR reactions using vector-specific primers were performed to verify the size and identity of the inserts.

5 155. Gene-walking sequencing was employed to completely sequence the entire insert for several clones of each cloned gene. This was carried out to avoid using a cloned gene whose DNA sequence was mutated during the PCR process.

To demonstrate that genes encoding gene products required for proliferation can confer resistance to their specific inhibitors upon induction at proper inducer levels, cells of each clone in which the genes were operably linked to the xylose inducible promoter were grown in LB medium with chloramphenicol (34 µg/ml) at a combination of differing antibiotic and inducer concentrations. This was accomplished by using microtitration plates (96 or 384 wells) which contained antibiotic and inducer at gradient concentrations in a matrix format in 10 times excess quantity (see Figure 12). Media containing inoculated cells (9 volume) was dispensed into the wells containing 10 15 volume of antibiotic/inducer for a final volume of 50 µl (for 384 well plates) or 200 µl (for 96 well plates). The plates were incubated at 37°C with periodic shaking and growth of cells was monitored by automatic measurement of optical density at OD600 using a Ultramark reader. A clone over-expressing a particular gene was considered resistant to its specific antibiotic (inhibitor) if significant growth was observed at appropriate inducer concentrations in the presence of a particular concentration of antibiotic but not in the absence of inducer at that concentration of antibiotic.

The results are indicated in Figure 13 and Figure 14. As illustrated in Figure 13, at appropriate concentrations of inducer cells which overexpress the defB gene product were able to grow at elevated concentrations of the antibiotic actinonin, which acts on 25 the defB gene product. Similarly, as illustrated in Figure 14, at appropriate concentrations of inducer cells which overexpress the folA gene product were able to grow at elevated concentrations of the antibiotic trimethoprim, which acts on the folA gene product.

Thus, elevated expression of a gene product required for proliferation enables 30 cells to grow in the presence of antibiotic concentrations which inhibit or prevent growth of wild type cells.

Table V - Essential Genes/Proteins and Specific Inhibitors

Gene	Target	Inhibitor	Primers
gyrB	β subunit of DNA gyrase or topoisomerase II	Novobiocin	GCGGATCCTTATAAAGTAACAGAAAGCGATGGTGACTGC; CAGGTCGACCGAGCTTAGAAGTCTAAGTTGCATAAACTG
murA	UDP-N-acetylglucosamine enolpyruvyl transferase	Fosfomycin	CTGGATCCTTCTAAGTGGAGGATTACG; CAGGTCGACGAAATTAATCGTTAATACGTT
fabI	Enoyl-acyl carrier protein reductase	Triclosan	GCCGGATCCATAAGGAGTTATCTTACATG; CGCGTCGACTTATTAATTGCGTGAATC
rpoB	RNA polymerase β subunit	Rifampicin	GCTGGATCCTGAGGGGTGAATCTGTTTGGC; CTGCTCGAGTGGTATTAATCAGTAACTT
fusA	Elongation factor G	Fusidic acid	GCTGGATCCCTGGAAAGGAGAAATAACATGGCTAGAG; CCGTCGACGGCTAGCTAGTCAAAACAAGTTATATTTCAC
folA	Dihydrofolate reductase	Trimethoprim	GCTGGATCCAGAAAGAGGAGGATAATTATG; CCGTCGACTTTTCCCCCTTATTTTTAC
ileS	Isoleucyl tRNA synthetase	Mupirocin (bactroban)*	GCTGGATCCTAAGGAGTGAAAAAATGGATTACAAAGAAACG; CCGTCGACCAATATACAAGTGATTTTACAACCTGTGGCATC
trpS	Tryptophanyl tRNA synthetase	Indolmycin*	GCGGGATCCCTAAGAAAGTAGGCATTTAAATGGAGAC; CCGTCGACGTTTATTTTATCTCTTACGTCCTAAACC
fabB	β keto-acyl carrier protein synthase	Cerulenin	GCTGGATCCAATAGGAGGATAACGAATGAG; CAGGTCGACAAATATGCTTCAAAATTTCTT
defB	Peptide deformylase	Actinonin	GCTGGATCCATAAGGAAGGTGCAATATATG; CAGGTCGACGTTTAAACTTCTACTGCAT
PBP-2a	Penicillin binding protein 2	Cloxacillin	GCCGGATCCCAATGTAGTCTTATATAAGGAGGATATTGATG; CAGGTCGACGCTTCACTGTTTTTGTATTCTATCTATATC

antibiotics unavailable commercially

*

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EXAMPLE 17

Overexpression of Genes Encoding Gene Products Required for Proliferation Confers Specific Resistance to Antibiotics which Target the Overexpressed Gene Product

To demonstrate that cells which overexpress a gene encoding a gene product
5 required for proliferation are specifically resistant to antibiotics which target that gene product, the following experiments were performed. Several identical compound plates were prepared as described in Example 14 above in which different antibiotics were present in different wells. Media containing cells overexpressing different genes were separately dispensed into each one of these plates. Plate incubation and growth
10 measurement were the same as described in Example 16 above. Growth was deemed specific if cells overexpressing one particular gene only gained resistance to antibiotics which target the product of the overexpressed gene but not to other antibiotics which target the products of genes which were not overexpressed.

As indicated in Figure 15 overexpression of the *fabI* gene conferred resistance
15 to triclosan, which acts on the gene product of the *fabI* gene, enoyl-acyl carrier protein reductase. However, overexpression of the *fabI* gene did not confer resistance to cerulenin, trimethoprim, or actinonin, each of which act on other gene products.

Similarly, as indicated in Figure 16 overexpression of the *folA* gene conferred
20 resistance to trimethoprim, which acts on the gene product of the *folA* gene, dihydrofolate reductase. However, overexpression of the *folA* gene did not confer resistance to triclosan, cerulenin, or actinonin, each of which act on other gene products.

As indicated in Figure 17 overexpression of the *defB* gene conferred resistance
25 to actinonin, which acts on the gene product of the *defB* gene, peptide deformylase. However, overexpression of the *defB* gene did not confer resistance to cerulenin, trimethoprim, or triclosan, each of which act on other gene products.

As indicated in Figure 18 overexpression of the *fabF* gene conferred resistance
to cerulenin, which acts on the gene product of the *fabF* gene, β keto-acyl carrier protein synthase II. However, overexpression of the *fabF* gene did not confer

resistance to triclosan, trimethoprim, or actinonin, each of which act on other gene products.

Thus, overexpression of a gene encoding a gene product required for proliferation confers specific resistance to antibiotics which target the overexpressed gene product.

EXAMPLE 18

Selection of a Strain Overexpressing a Gene Encoding a Target Gene Product from a Mixture of Strains Overexpressing Genes Required for Proliferation

To confirm that a strain expressing the gene product targeted by an antibiotic can be selected from a mixture of strains which each overexpress a different gene required for proliferation, the following experiment was performed. *S. aureus* strains overexpressing one of nine genes encoding a gene product required for proliferation were constructed as described above. The nine overexpressed genes were *fabF*, *defB*, *folA*, *fabI*, *ileS*, *fusA*, *gyrB*, *murA*, *rpoB*. A mixture of the nine strains was grown in 96 well plate in medium containing various concentrations of inducer and a sufficient concentration of actinonin, cerulenin, triclosan or trimethoprim to inhibit the growth of strains which do not overexpress the targets of these antibiotics.

Growth was observed in wells containing appropriate inducer concentrations and each one of the four antibiotics (See Figure 19). The cultures which grew in the presence of one of the antibiotics were analyzed as follows. The cultures were removed from the wells of the plate and single colonies were obtained by plating serial dilutions LB agar plates containing an appropriate antibiotic. Plasmids were isolated from at least 60 individual colonies for each culture and the genes which conferred antibiotic resistance were amplified by performing PCR reactions using vector-specific primers. The PCR products were then sequenced.

All of the plasmids obtained from the culture which grew in the presence of cerulenin contained the *fabF* sequence. Similarly, all of the plasmids obtained from clones which grew in the presence of triclosan contained the *fabI* gene. All of the plasmid obtained from colonies which grew in the presence of actinonin contained the *defB* gene. In addition, 81% of the plasmids obtained from colonies which grew in

the presence of trimethoprim contained the folA gene. Growth conditions could be further optimized to provide 100% recovery of plasmids containing the folA gene.

These results demonstrate that a strain expressing the gene product targetted by an antibiotic can be selected from a mixture of strains which each overexpress a different gene required for proliferation.

EXAMPLE 19

Identification of Amplification Products Having Distinguishable Lengths

As discussed above, plasmids in which antisense nucleic acids complementary to nucleotide sequences in the pbpC, secA, ylaO(Bs), yphC(Bs), trpS, polC, fabI, rpsR (Bs), fabF(yjaY), ileS, murC, fnhB, murA (Bs), murF(Bs), ftsZ, tufA, gyrA, rpoB, grlA or folA(dfrA) genes were transcribed from the XylT5 promoter were used to identify the foregoing genes as being required for proliferation. The sequences of the antisense nucleic acids are provided herein as follows:

15	tufA	SEQ ID NO: 1359
	ylaO	SEQ ID NO: 1380
	rpoB	SEQ ID NO: 1392
	polC	SEQ ID NO: 1409
	murC	SEQ ID NO: 1416
20	fnhB	SEQ ID NO: 1444
	yphC	SEQ ID NO 1463
	gyrA	SEQ ID NO 1483
	ileS	SEQ ID NO 1636
	secA	SEQ ID NO 1651
25	fabI	SEQ ID NO 1697
	murA	SEQ ID NO 2086
	grlA	SEQ ID NO 2331
	trpS	SEQ ID NO 2505
	folA	SEQ ID NO 2526
30	pbpC	SEQ ID NO 2634
	fabF	SEQ ID NO 2988
	murF	SEQ ID NO 3522
	rpsR	SEQ ID NO 3563
35	ftsZ	SEQ ID NO 3598

Amplification primers were designed which would yield amplification products of the following lengths if the plasmid encoding the corresponding antisense nucleic acid is present in a mixture of nucleic acids:

	yphC	260bp	secA	267bp
5	folA	230 bp	tufA	243bp
	fabI	220bp	gyrA	225bp
	trpS	208bp	ileS	215bp
	fabF	189bp	murF	203bp
	murA	176bp	fmhB	181bp
10	rpoB	159bp	ylaO	169bp
	grlA	151bp	pbpC	156bp
	murC	129bp	polC	145bp
	rpsR	109bp	ftsZ	117bp

The 5' primer of each pair was complementary to a nucleotide sequence within the xylT5 promoter while 3' primer was complementary to a nucleotide sequence within the antisense clone. The 5' primer of each pair was identical for each amplification reaction. The nucleotide sequence GTTTCTT was appended on the 5' end of the 3' primers. One primer in each pair was labeled with either VIC or 6FAM.

Two sets of ten plasmids containing the antisense nucleic acids complementary to the genes listed in each of the columns above were mixed in equal amounts in 11 tubes except that either the plasmid encoding antisense nucleic acids complementary to a nucleotide sequence in the *grlA* gene or the plasmid encoding antisense nucleic acids complementary to nucleotide sequences in the *fmhB* gene were serially diluted two fold in each of the 11 tubes (i.e. the first tube had 100pg of the *grlA* plasmid or the *fmhB* plasmid while the last tube had 0.10pg of the *grlA* plasmid or the *fmhB* plasmid). Amplification reactions were conducted on the mixtures and the amplification products were separated on a 5% NuSieve 3:1 agarose gel (BioWhittaker Molecular Applications Rockland, ME). The levels of the 151bp or 181 amplification products for the *grlA* or *fmhB* primer respectively were specifically reduced in a stepwise fashion with increasing dilutions while the levels of the

undiluted products remained constant. The assay readily detected a 10-fold decrease in template concentration reflected in the amplification products corresponding to the *grlA* or *fmhB* plasmids.

EXAMPLE 20

5 Selective Disappearance of Amplification Products Corresponding to Strains
 Underexpressing a Gene Product on which a Compound which Inhibits Proliferation
 Acts

 Strains of *Staphylococcus aureus* containing plasmids encoding antisense
nucleic acids complementary to nucleotide sequences within the *yphC*, *folA*, *fabI*,
10 *trpS*, *fabF*, *murA*, *rpoB*, *grlA*, *murC* or *rpsR* genes (described in Example 19 above)
were mixed together in identical cultures such that the number of cells of each strain
in the culture was identical. Each of the cultures containing the ten strains was
contacted with one of the following antibiotics at one of the following concentrations:
spectinomycin- 2.5, 5.0ug/ml
15 mupriocin- 4.3, 8.6, 17.2ug/ml.
cerulenin- 4.5, 9.0, 18.0ug/ml

 Spectinomycin acts on the product of the *rpsR* gene, mupriocin acts on the
product of the *ileS* gene and cerulenin acts on the product of the *FabF* gene. The
middle concentration for each antibiotic is its IC50.

20 The culture containing the ten strains were grown in rich medium (L-Broth; for
antisense LB + chloroamphenicol to maintain antisense plasmid) until the cells
reached early log phase then contacted with one of the above-stated compounds at
one of the concentrations listed above (preferably near IC50). The cultures were
grown for a sufficient length of time to permit the compounds to specifically inhibit
25 the growth of strains underexpressing their targets. Preferably the cultures were
grown at least 16 hr, more preferably between 24 and 48 hrs. It is desirable to avoid
allowing the culture to grow for time periods which might place selective pressure on
the strains which could lead to false positives.

30 The cells were harvested by centrifugation and plasmid DNA was isolated
from the cultures. PCR amplifications were performed as described in Example 19.

Amplification products were run on NuSieve agarose gels as described above. The amounts of the amplification products corresponding to each antisense nucleic acid were determined and compared to those in a control culture which was not contacted with the drug or to the amounts of the amplification products corresponding to the other antisense nucleic acids which were not complementary to nucleotide sequences in the genes encoding the gene products on which the compounds act. In each case, only the amplification product corresponding to the target on which the antibiotic acts was not detectable on the gel.

It is desirable, in embodiments in which the level or activity of gene products is regulated by transcribing antisense nucleic acids complementary to gene products required for proliferation or by replacing the native promoters of such genes with regulatable promoters, to perform dose-response curve for the inducer used to induce transcription of the antisense nucleic acids or induce transcription from the regulatable promoter. In such embodiments, it is desirable to use the lowest concentration of inducer which provides optimal transcription levels for detecting the effects of a particular test compound while interfering as little as possible with the growth of strains which do not overexpress or underexpress the target on which the compound acts. It also desirable contact the cultures with varying amounts of test compounds to determine the optimal amounts for obtaining differential growth of strains which overexpress or underexpress the targets on which the compounds act. Preferably, if the strains overexpress gene products required for proliferation, the level of the compound is preferably about IC_{90} or above. Preferably, if the strains underexpress gene products required for proliferation, the level of the compound is preferably about IC_{50} or below.

It will be appreciated that, if desired, the amplification products may be detected using the dyes described above. It will also be appreciated that amplification products may be detected using any desired amplification method including RT-PCR and PCR.

It will be appreciated that no matter how detailed the foregoing appears in text, the invention can be practiced in many ways. As is also stated above, it should further be

noted that the use of particular terminology when describing certain features or aspects of the present invention should not be taken to imply that the broadest reasonable meaning of such terminology is not intended, or that the terminology is being re-defined herein to be restricted to including any specific characteristics of the features or aspects of the invention with which that terminology is associated. Thus, although this invention has been described in terms of certain preferred embodiments, other embodiments which will be apparent to those of ordinary skill in the art in view of the disclosure herein are also within the scope of this invention. Accordingly, the scope of the invention is intended to be defined only by reference to the appended claims and any equivalents thereof. All documents cited herein are incorporated herein by reference in their entireties

TABLE VI A

SeqID	Clone name	Organism
8	E3M10000001A02	<i>Enterococcus faecalis</i>
9	E3M10000001A06	<i>Enterococcus faecalis</i>
10	E3M10000001B01	<i>Enterococcus faecalis</i>
11	E3M10000001B02	<i>Enterococcus faecalis</i>
12	E3M10000001B05	<i>Enterococcus faecalis</i>
13	E3M10000001B06	<i>Enterococcus faecalis</i>
14	E3M10000001B08	<i>Enterococcus faecalis</i>
15	E3M10000001B10	<i>Enterococcus faecalis</i>
16	E3M10000001C02	<i>Enterococcus faecalis</i>
17	E3M10000001C09	<i>Enterococcus faecalis</i>
18	E3M10000001D02	<i>Enterococcus faecalis</i>
19	E3M10000001D04	<i>Enterococcus faecalis</i>
20	E3M10000001D05	<i>Enterococcus faecalis</i>
21	E3M10000001D09	<i>Enterococcus faecalis</i>
22	E3M10000001E01	<i>Enterococcus faecalis</i>
23	E3M10000001E02	<i>Enterococcus faecalis</i>
24	E3M10000001E03	<i>Enterococcus faecalis</i>
25	E3M10000001E04	<i>Enterococcus faecalis</i>
26	E3M10000001E08	<i>Enterococcus faecalis</i>
27	E3M10000001E09	<i>Enterococcus faecalis</i>
28	E3M10000001F02	<i>Enterococcus faecalis</i>
29	E3M10000001F04	<i>Enterococcus faecalis</i>
30	E3M10000001F06	<i>Enterococcus faecalis</i>
31	E3M10000001F07	<i>Enterococcus faecalis</i>
32	E3M10000001G02	<i>Enterococcus faecalis</i>
33	E3M10000001G03	<i>Enterococcus faecalis</i>
34	E3M10000001G04	<i>Enterococcus faecalis</i>
35	E3M10000001G05	<i>Enterococcus faecalis</i>
36	E3M10000001H02	<i>Enterococcus faecalis</i>
37	E3M10000001H03	<i>Enterococcus faecalis</i>
38	E3M10000001H04	<i>Enterococcus faecalis</i>
39	E3M10000004A04	<i>Enterococcus faecalis</i>
40	E3M10000004C03	<i>Enterococcus faecalis</i>
41	E3M10000004D01	<i>Enterococcus faecalis</i>
42	E3M10000004D02	<i>Enterococcus faecalis</i>
43	E3M10000004D10	<i>Enterococcus faecalis</i>
44	E3M10000004E11	<i>Enterococcus faecalis</i>
45	E3M10000004F08	<i>Enterococcus faecalis</i>
46	E3M10000004F10	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
47	E3M10000004G01	<i>Enterococcus faecalis</i>
48	E3M10000004H11	<i>Enterococcus faecalis</i>
49	E3M10000005A07	<i>Enterococcus faecalis</i>
50	E3M10000005B01	<i>Enterococcus faecalis</i>
51	E3M10000005B08	<i>Enterococcus faecalis</i>
52	E3M10000005C01	<i>Enterococcus faecalis</i>
53	E3M10000005C03	<i>Enterococcus faecalis</i>
54	E3M10000005C04	<i>Enterococcus faecalis</i>
55	E3M10000005D03	<i>Enterococcus faecalis</i>
56	E3M10000005D04	<i>Enterococcus faecalis</i>
57	E3M10000005D10	<i>Enterococcus faecalis</i>
58	E3M10000005E01	<i>Enterococcus faecalis</i>
59	E3M10000005E02	<i>Enterococcus faecalis</i>
60	E3M10000005E03	<i>Enterococcus faecalis</i>
61	E3M10000005E08	<i>Enterococcus faecalis</i>
62	E3M10000005F07	<i>Enterococcus faecalis</i>
63	E3M10000005F10	<i>Enterococcus faecalis</i>
64	E3M10000005G05	<i>Enterococcus faecalis</i>
65	E3M10000005H04	<i>Enterococcus faecalis</i>
66	E3M10000006B03	<i>Enterococcus faecalis</i>
67	E3M10000006C01	<i>Enterococcus faecalis</i>
68	E3M10000006C12	<i>Enterococcus faecalis</i>
69	E3M10000006D03	<i>Enterococcus faecalis</i>
70	E3M10000006E11	<i>Enterococcus faecalis</i>
71	E3M10000006F04	<i>Enterococcus faecalis</i>
72	E3M10000006G04	<i>Enterococcus faecalis</i>
73	E3M10000006G12	<i>Enterococcus faecalis</i>
74	E3M10000006H09	<i>Enterococcus faecalis</i>
75	E3M10000007A02	<i>Enterococcus faecalis</i>
76	E3M10000007B02	<i>Enterococcus faecalis</i>
77	E3M10000007B03	<i>Enterococcus faecalis</i>
78	E3M10000007C03	<i>Enterococcus faecalis</i>
79	E3M10000007C04	<i>Enterococcus faecalis</i>
80	E3M10000007D03	<i>Enterococcus faecalis</i>
81	E3M10000007E05	<i>Enterococcus faecalis</i>
82	E3M10000007F01	<i>Enterococcus faecalis</i>
83	E3M10000007F06	<i>Enterococcus faecalis</i>
84	E3M10000007G01	<i>Enterococcus faecalis</i>
85	E3M10000008C03	<i>Enterococcus faecalis</i>
86	E3M10000008C08	<i>Enterococcus faecalis</i>
87	E3M10000008C09	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
88	E3M10000008D08	<i>Enterococcus faecalis</i>
89	E3M10000008E02	<i>Enterococcus faecalis</i>
90	E3M10000008G05	<i>Enterococcus faecalis</i>
91	E3M10000008G09	<i>Enterococcus faecalis</i>
92	E3M10000008H02	<i>Enterococcus faecalis</i>
93	E3M10000009C07	<i>Enterococcus faecalis</i>
94	E3M10000009C09	<i>Enterococcus faecalis</i>
95	E3M10000009D01	<i>Enterococcus faecalis</i>
96	E3M10000009E02	<i>Enterococcus faecalis</i>
97	E3M10000009E03	<i>Enterococcus faecalis</i>
98	E3M10000009E05	<i>Enterococcus faecalis</i>
99	E3M10000009G02	<i>Enterococcus faecalis</i>
100	E3M10000010C08	<i>Enterococcus faecalis</i>
101	E3M10000010D05	<i>Enterococcus faecalis</i>
102	E3M10000010F01	<i>Enterococcus faecalis</i>
103	E3M10000010G05	<i>Enterococcus faecalis</i>
104	E3M10000010G07	<i>Enterococcus faecalis</i>
105	E3M10000010G09	<i>Enterococcus faecalis</i>
106	E3M10000010G10	<i>Enterococcus faecalis</i>
107	E3M10000010H02	<i>Enterococcus faecalis</i>
108	E3M10000011A09	<i>Enterococcus faecalis</i>
109	E3M10000011B03	<i>Enterococcus faecalis</i>
110	E3M10000011B09	<i>Enterococcus faecalis</i>
111	E3M10000011C07	<i>Enterococcus faecalis</i>
112	E3M10000011D03	<i>Enterococcus faecalis</i>
113	E3M10000011H02	<i>Enterococcus faecalis</i>
114	E3M10000011H05	<i>Enterococcus faecalis</i>
115	E3M10000012B01	<i>Enterococcus faecalis</i>
116	E3M10000012B02	<i>Enterococcus faecalis</i>
117	E3M10000012B07	<i>Enterococcus faecalis</i>
118	E3M10000012B08	<i>Enterococcus faecalis</i>
119	E3M10000012C01	<i>Enterococcus faecalis</i>
120	E3M10000012D10	<i>Enterococcus faecalis</i>
121	E3M10000012E08	<i>Enterococcus faecalis</i>
122	E3M10000012F05	<i>Enterococcus faecalis</i>
123	E3M10000012F06	<i>Enterococcus faecalis</i>
124	E3M10000012F07	<i>Enterococcus faecalis</i>
125	E3M10000012F10	<i>Enterococcus faecalis</i>
126	E3M10000012G02	<i>Enterococcus faecalis</i>
127	E3M10000012G07	<i>Enterococcus faecalis</i>
128	E3M10000013A06	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
129	E3M10000013A07	<i>Enterococcus faecalis</i>
130	E3M10000013C05	<i>Enterococcus faecalis</i>
131	E3M10000013D02	<i>Enterococcus faecalis</i>
132	E3M10000013D08	<i>Enterococcus faecalis</i>
133	E3M10000013D10	<i>Enterococcus faecalis</i>
134	E3M10000013E02	<i>Enterococcus faecalis</i>
135	E3M10000013E08	<i>Enterococcus faecalis</i>
136	E3M10000013F05	<i>Enterococcus faecalis</i>
137	E3M10000013F12	<i>Enterococcus faecalis</i>
138	E3M10000013G10	<i>Enterococcus faecalis</i>
139	E3M10000013H03	<i>Enterococcus faecalis</i>
140	E3M10000013H05	<i>Enterococcus faecalis</i>
141	E3M10000013H10	<i>Enterococcus faecalis</i>
142	E3M10000014B12	<i>Enterococcus faecalis</i>
143	E3M10000014E12	<i>Enterococcus faecalis</i>
144	E3M10000014G09	<i>Enterococcus faecalis</i>
145	E3M10000015B04	<i>Enterococcus faecalis</i>
146	E3M10000015B12	<i>Enterococcus faecalis</i>
147	E3M10000015E12	<i>Enterococcus faecalis</i>
148	E3M10000016A03	<i>Enterococcus faecalis</i>
149	E3M10000016A04	<i>Enterococcus faecalis</i>
150	E3M10000016C11	<i>Enterococcus faecalis</i>
151	E3M10000016D03	<i>Enterococcus faecalis</i>
152	E3M10000016F06	<i>Enterococcus faecalis</i>
153	E3M10000016F10	<i>Enterococcus faecalis</i>
154	E3M10000016H05	<i>Enterococcus faecalis</i>
155	E3M10000016H10	<i>Enterococcus faecalis</i>
156	E3M10000017A09	<i>Enterococcus faecalis</i>
157	E3M10000017D09	<i>Enterococcus faecalis</i>
158	E3M10000018A07	<i>Enterococcus faecalis</i>
159	E3M10000018C02	<i>Enterococcus faecalis</i>
160	E3M10000018E01	<i>Enterococcus faecalis</i>
161	E3M10000018G09	<i>Enterococcus faecalis</i>
162	E3M10000018H06	<i>Enterococcus faecalis</i>
163	E3M10000019B06	<i>Enterococcus faecalis</i>
164	E3M10000019D02	<i>Enterococcus faecalis</i>
165	E3M10000019E03	<i>Enterococcus faecalis</i>
166	E3M10000019E04	<i>Enterococcus faecalis</i>
167	E3M10000020G04	<i>Enterococcus faecalis</i>
168	E3M10000020H05	<i>Enterococcus faecalis</i>
169	E3M10000021A08	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
170	E3M10000021A11	<i>Enterococcus faecalis</i>
171	E3M10000021B10	<i>Enterococcus faecalis</i>
172	E3M10000021C03	<i>Enterococcus faecalis</i>
173	E3M10000021C04	<i>Enterococcus faecalis</i>
174	E3M10000021C08	<i>Enterococcus faecalis</i>
175	E3M10000021D04	<i>Enterococcus faecalis</i>
176	E3M10000021E10	<i>Enterococcus faecalis</i>
177	E3M10000021G04	<i>Enterococcus faecalis</i>
178	E3M10000021G10	<i>Enterococcus faecalis</i>
179	E3M10000021G11	<i>Enterococcus faecalis</i>
180	E3M10000021H11	<i>Enterococcus faecalis</i>
181	E3M10000022A04	<i>Enterococcus faecalis</i>
182	E3M10000022A11	<i>Enterococcus faecalis</i>
183	E3M10000022B04	<i>Enterococcus faecalis</i>
184	E3M10000022B05	<i>Enterococcus faecalis</i>
185	E3M10000022B07	<i>Enterococcus faecalis</i>
186	E3M10000022C05	<i>Enterococcus faecalis</i>
187	E3M10000022C06	<i>Enterococcus faecalis</i>
188	E3M10000022C09	<i>Enterococcus faecalis</i>
189	E3M10000022D04	<i>Enterococcus faecalis</i>
190	E3M10000022F05	<i>Enterococcus faecalis</i>
191	E3M10000022F06	<i>Enterococcus faecalis</i>
192	E3M10000022F08	<i>Enterococcus faecalis</i>
193	E3M10000022G02	<i>Enterococcus faecalis</i>
194	E3M10000022G12	<i>Enterococcus faecalis</i>
195	E3M10000023A03	<i>Enterococcus faecalis</i>
196	E3M10000023A06	<i>Enterococcus faecalis</i>
197	E3M10000023A07	<i>Enterococcus faecalis</i>
198	E3M10000023A09	<i>Enterococcus faecalis</i>
199	E3M10000023B02	<i>Enterococcus faecalis</i>
200	E3M10000023B06	<i>Enterococcus faecalis</i>
201	E3M10000023C03	<i>Enterococcus faecalis</i>
202	E3M10000023C04	<i>Enterococcus faecalis</i>
203	E3M10000023C06	<i>Enterococcus faecalis</i>
204	E3M10000023C08	<i>Enterococcus faecalis</i>
205	E3M10000023C09	<i>Enterococcus faecalis</i>
206	E3M10000023D02	<i>Enterococcus faecalis</i>
207	E3M10000023D04	<i>Enterococcus faecalis</i>
208	E3M10000023D10	<i>Enterococcus faecalis</i>
209	E3M10000023E04	<i>Enterococcus faecalis</i>
210	E3M10000023E07	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
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212	E3M10000023F02	<i>Enterococcus faecalis</i>
213	E3M10000023F10	<i>Enterococcus faecalis</i>
214	E3M10000023G02	<i>Enterococcus faecalis</i>
215	E3M10000023G04	<i>Enterococcus faecalis</i>
216	E3M10000023G10	<i>Enterococcus faecalis</i>
217	E3M10000023H08	<i>Enterococcus faecalis</i>
218	E3M10000024A03	<i>Enterococcus faecalis</i>
219	E3M10000024A04	<i>Enterococcus faecalis</i>
220	E3M10000024A08	<i>Enterococcus faecalis</i>
221	E3M10000024C06	<i>Enterococcus faecalis</i>
222	E3M10000025A06	<i>Enterococcus faecalis</i>
223	E3M10000025B01	<i>Enterococcus faecalis</i>
224	E3M10000025B03	<i>Enterococcus faecalis</i>
225	E3M10000025B05	<i>Enterococcus faecalis</i>
226	E3M10000025B10	<i>Enterococcus faecalis</i>
227	E3M10000025C01	<i>Enterococcus faecalis</i>
228	E3M10000025C04	<i>Enterococcus faecalis</i>
229	E3M10000025C05	<i>Enterococcus faecalis</i>
230	E3M10000025C07	<i>Enterococcus faecalis</i>
231	E3M10000025C08	<i>Enterococcus faecalis</i>
232	E3M10000025C09	<i>Enterococcus faecalis</i>
233	E3M10000025C11	<i>Enterococcus faecalis</i>
234	E3M10000025D01	<i>Enterococcus faecalis</i>
235	E3M10000025D10	<i>Enterococcus faecalis</i>
236	E3M10000025E07	<i>Enterococcus faecalis</i>
237	E3M10000025E08	<i>Enterococcus faecalis</i>
238	E3M10000025E12	<i>Enterococcus faecalis</i>
239	E3M10000025F04	<i>Enterococcus faecalis</i>
240	E3M10000025F06	<i>Enterococcus faecalis</i>
241	E3M10000025F08	<i>Enterococcus faecalis</i>
242	E3M10000025F09	<i>Enterococcus faecalis</i>
243	E3M10000025F10	<i>Enterococcus faecalis</i>
244	E3M10000025F11	<i>Enterococcus faecalis</i>
245	E3M10000025F12	<i>Enterococcus faecalis</i>
246	E3M10000025G02	<i>Enterococcus faecalis</i>
247	E3M10000025G07	<i>Enterococcus faecalis</i>
248	E3M10000025G09	<i>Enterococcus faecalis</i>
249	E3M10000027A02	<i>Enterococcus faecalis</i>
250	E3M10000027A07	<i>Enterococcus faecalis</i>
251	E3M10000027A09	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
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253	E3M10000027B08	<i>Enterococcus faecalis</i>
254	E3M10000027B09	<i>Enterococcus faecalis</i>
255	E3M10000027C02	<i>Enterococcus faecalis</i>
256	E3M10000027C03	<i>Enterococcus faecalis</i>
257	E3M10000027C08	<i>Enterococcus faecalis</i>
258	E3M10000027D03	<i>Enterococcus faecalis</i>
259	E3M10000027D05	<i>Enterococcus faecalis</i>
260	E3M10000027D08	<i>Enterococcus faecalis</i>
261	E3M10000027D10	<i>Enterococcus faecalis</i>
262	E3M10000027G01	<i>Enterococcus faecalis</i>
263	E3M10000027G08	<i>Enterococcus faecalis</i>
264	E3M10000027H04	<i>Enterococcus faecalis</i>
265	E3M10000027H07	<i>Enterococcus faecalis</i>
266	E3M10000028A02	<i>Enterococcus faecalis</i>
267	E3M10000028A03	<i>Enterococcus faecalis</i>
268	E3M10000028A04	<i>Enterococcus faecalis</i>
269	E3M10000028A05	<i>Enterococcus faecalis</i>
270	E3M10000028A06	<i>Enterococcus faecalis</i>
271	E3M10000028A08	<i>Enterococcus faecalis</i>
272	E3M10000028B01	<i>Enterococcus faecalis</i>
273	E3M10000028B02	<i>Enterococcus faecalis</i>
274	E3M10000028B03	<i>Enterococcus faecalis</i>
275	E3M10000028B04	<i>Enterococcus faecalis</i>
276	E3M10000028B05	<i>Enterococcus faecalis</i>
277	E3M10000028B06	<i>Enterococcus faecalis</i>
278	E3M10000028B07	<i>Enterococcus faecalis</i>
279	E3M10000028B08	<i>Enterococcus faecalis</i>
280	E3M10000028C01	<i>Enterococcus faecalis</i>
281	E3M10000028C02	<i>Enterococcus faecalis</i>
282	E3M10000028C04	<i>Enterococcus faecalis</i>
283	E3M10000028C05	<i>Enterococcus faecalis</i>
284	E3M10000028C06	<i>Enterococcus faecalis</i>
285	E3M10000028C07	<i>Enterococcus faecalis</i>
286	E3M10000028C08	<i>Enterococcus faecalis</i>
287	E3M10000028D01	<i>Enterococcus faecalis</i>
288	E3M10000028D02	<i>Enterococcus faecalis</i>
289	E3M10000028D05	<i>Enterococcus faecalis</i>
290	E3M10000028D06	<i>Enterococcus faecalis</i>
291	E3M10000028D08	<i>Enterococcus faecalis</i>
292	E3M10000028E01	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
293	E3M10000028E04	<i>Enterococcus faecalis</i>
294	E3M10000028E07	<i>Enterococcus faecalis</i>
295	E3M10000028F02	<i>Enterococcus faecalis</i>
296	E3M10000028F03	<i>Enterococcus faecalis</i>
297	E3M10000028F04	<i>Enterococcus faecalis</i>
298	E3M10000028F05	<i>Enterococcus faecalis</i>
299	E3M10000028F06	<i>Enterococcus faecalis</i>
300	E3M10000028F07	<i>Enterococcus faecalis</i>
301	E3M10000028G05	<i>Enterococcus faecalis</i>
302	E3M10000028G06	<i>Enterococcus faecalis</i>
303	E3M10000028G07	<i>Enterococcus faecalis</i>
304	E3M10000028H04	<i>Enterococcus faecalis</i>
305	E3M10000028H07	<i>Enterococcus faecalis</i>
306	E3M10000029A02	<i>Enterococcus faecalis</i>
307	E3M10000029A04	<i>Enterococcus faecalis</i>
308	E3M10000029A05	<i>Enterococcus faecalis</i>
309	E3M10000029A10	<i>Enterococcus faecalis</i>
310	E3M10000029A11	<i>Enterococcus faecalis</i>
311	E3M10000029B01	<i>Enterococcus faecalis</i>
312	E3M10000029B02	<i>Enterococcus faecalis</i>
313	E3M10000029B05	<i>Enterococcus faecalis</i>
314	E3M10000029B06	<i>Enterococcus faecalis</i>
315	E3M10000029B08	<i>Enterococcus faecalis</i>
316	E3M10000029B11	<i>Enterococcus faecalis</i>
317	E3M10000029B12	<i>Enterococcus faecalis</i>
318	E3M10000029C01	<i>Enterococcus faecalis</i>
319	E3M10000029C02	<i>Enterococcus faecalis</i>
320	E3M10000029C03	<i>Enterococcus faecalis</i>
321	E3M10000029C04	<i>Enterococcus faecalis</i>
322	E3M10000029C05	<i>Enterococcus faecalis</i>
323	E3M10000029C06	<i>Enterococcus faecalis</i>
324	E3M10000029C07	<i>Enterococcus faecalis</i>
325	E3M10000029C08	<i>Enterococcus faecalis</i>
326	E3M10000029C09	<i>Enterococcus faecalis</i>
327	E3M10000029C10	<i>Enterococcus faecalis</i>
328	E3M10000029C12	<i>Enterococcus faecalis</i>
329	E3M10000029D01	<i>Enterococcus faecalis</i>
330	E3M10000029D03	<i>Enterococcus faecalis</i>
331	E3M10000029D04	<i>Enterococcus faecalis</i>
332	E3M10000029D05	<i>Enterococcus faecalis</i>
333	E3M10000029D06	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
334	E3M10000029D08	<i>Enterococcus faecalis</i>
335	E3M10000029D12	<i>Enterococcus faecalis</i>
336	E3M10000029E01	<i>Enterococcus faecalis</i>
337	E3M10000029E02	<i>Enterococcus faecalis</i>
338	E3M10000029E03	<i>Enterococcus faecalis</i>
339	E3M10000029E05	<i>Enterococcus faecalis</i>
340	E3M10000029E07	<i>Enterococcus faecalis</i>
341	E3M10000029E08	<i>Enterococcus faecalis</i>
342	E3M10000029E09	<i>Enterococcus faecalis</i>
343	E3M10000029E12	<i>Enterococcus faecalis</i>
344	E3M10000029F01	<i>Enterococcus faecalis</i>
345	E3M10000029F05	<i>Enterococcus faecalis</i>
346	E3M10000029F06	<i>Enterococcus faecalis</i>
347	E3M10000029F09	<i>Enterococcus faecalis</i>
348	E3M10000029F10	<i>Enterococcus faecalis</i>
349	E3M10000029F11	<i>Enterococcus faecalis</i>
350	E3M10000029F12	<i>Enterococcus faecalis</i>
351	E3M10000029G01	<i>Enterococcus faecalis</i>
352	E3M10000029G04	<i>Enterococcus faecalis</i>
353	E3M10000029G05	<i>Enterococcus faecalis</i>
354	E3M10000029G07	<i>Enterococcus faecalis</i>
355	E3M10000029G08	<i>Enterococcus faecalis</i>
356	E3M10000029G09	<i>Enterococcus faecalis</i>
357	E3M10000029G10	<i>Enterococcus faecalis</i>
358	E3M10000029G11	<i>Enterococcus faecalis</i>
359	E3M10000029G12	<i>Enterococcus faecalis</i>
360	E3M10000029H02	<i>Enterococcus faecalis</i>
361	E3M10000029H04	<i>Enterococcus faecalis</i>
362	E3M10000029H05	<i>Enterococcus faecalis</i>
363	E3M10000029H07	<i>Enterococcus faecalis</i>
364	E3M10000029H08	<i>Enterococcus faecalis</i>
365	E3M10000029H11	<i>Enterococcus faecalis</i>
366	E3M10000030A05	<i>Enterococcus faecalis</i>
367	E3M10000030A08	<i>Enterococcus faecalis</i>
368	E3M10000030A09	<i>Enterococcus faecalis</i>
369	E3M10000030A11	<i>Enterococcus faecalis</i>
370	E3M10000030B03	<i>Enterococcus faecalis</i>
371	E3M10000030B04	<i>Enterococcus faecalis</i>
372	E3M10000030B05	<i>Enterococcus faecalis</i>
373	E3M10000030B06	<i>Enterococcus faecalis</i>
374	E3M10000030B07	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
375	E3M10000030B08	<i>Enterococcus faecalis</i>
376	E3M10000030B10	<i>Enterococcus faecalis</i>
377	E3M10000030B11	<i>Enterococcus faecalis</i>
378	E3M10000030B12	<i>Enterococcus faecalis</i>
379	E3M10000030C03	<i>Enterococcus faecalis</i>
380	E3M10000030C04	<i>Enterococcus faecalis</i>
381	E3M10000030C12	<i>Enterococcus faecalis</i>
382	E3M10000030D02	<i>Enterococcus faecalis</i>
383	E3M10000030D05	<i>Enterococcus faecalis</i>
384	E3M10000030D08	<i>Enterococcus faecalis</i>
385	E3M10000030D09	<i>Enterococcus faecalis</i>
386	E3M10000030D10	<i>Enterococcus faecalis</i>
387	E3M10000030D12	<i>Enterococcus faecalis</i>
388	E3M10000030E01	<i>Enterococcus faecalis</i>
389	E3M10000030E02	<i>Enterococcus faecalis</i>
390	E3M10000030E04	<i>Enterococcus faecalis</i>
391	E3M10000030E08	<i>Enterococcus faecalis</i>
392	E3M10000030E09	<i>Enterococcus faecalis</i>
393	E3M10000030E10	<i>Enterococcus faecalis</i>
394	E3M10000030F01	<i>Enterococcus faecalis</i>
395	E3M10000030F04	<i>Enterococcus faecalis</i>
396	E3M10000030F06	<i>Enterococcus faecalis</i>
397	E3M10000030F07	<i>Enterococcus faecalis</i>
398	E3M10000030F10	<i>Enterococcus faecalis</i>
399	E3M10000030F12	<i>Enterococcus faecalis</i>
400	E3M10000030G01	<i>Enterococcus faecalis</i>
401	E3M10000030G03	<i>Enterococcus faecalis</i>
402	E3M10000030G06	<i>Enterococcus faecalis</i>
403	E3M10000030G08	<i>Enterococcus faecalis</i>
404	E3M10000030G09	<i>Enterococcus faecalis</i>
405	E3M10000030G12	<i>Enterococcus faecalis</i>
406	E3M10000030H03	<i>Enterococcus faecalis</i>
407	E3M10000030H04	<i>Enterococcus faecalis</i>
408	E3M10000030H06	<i>Enterococcus faecalis</i>
409	E3M10000030H07	<i>Enterococcus faecalis</i>
410	E3M10000030H08	<i>Enterococcus faecalis</i>
411	E3M10000030H10	<i>Enterococcus faecalis</i>
412	E3M10000030H11	<i>Enterococcus faecalis</i>
413	E3M10000031A02	<i>Enterococcus faecalis</i>
414	E3M10000031A06	<i>Enterococcus faecalis</i>
415	E3M10000031A07	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
416	E3M10000031A08	<i>Enterococcus faecalis</i>
417	E3M10000031B02	<i>Enterococcus faecalis</i>
418	E3M10000031B03	<i>Enterococcus faecalis</i>
419	E3M10000031B04	<i>Enterococcus faecalis</i>
420	E3M10000031B09	<i>Enterococcus faecalis</i>
421	E3M10000031B10	<i>Enterococcus faecalis</i>
422	E3M10000031B11	<i>Enterococcus faecalis</i>
423	E3M10000031B12	<i>Enterococcus faecalis</i>
424	E3M10000031C01	<i>Enterococcus faecalis</i>
425	E3M10000031C04	<i>Enterococcus faecalis</i>
426	E3M10000031C06	<i>Enterococcus faecalis</i>
427	E3M10000031C10	<i>Enterococcus faecalis</i>
428	E3M10000031C11	<i>Enterococcus faecalis</i>
429	E3M10000031C12	<i>Enterococcus faecalis</i>
430	E3M10000031D03	<i>Enterococcus faecalis</i>
431	E3M10000031D04	<i>Enterococcus faecalis</i>
432	E3M10000031D08	<i>Enterococcus faecalis</i>
433	E3M10000031E03	<i>Enterococcus faecalis</i>
434	E3M10000031E09	<i>Enterococcus faecalis</i>
435	E3M10000031F02	<i>Enterococcus faecalis</i>
436	E3M10000031F04	<i>Enterococcus faecalis</i>
437	E3M10000031F07	<i>Enterococcus faecalis</i>
438	E3M10000031F09	<i>Enterococcus faecalis</i>
439	E3M10000031F11	<i>Enterococcus faecalis</i>
440	E3M10000031G03	<i>Enterococcus faecalis</i>
441	E3M10000031G04	<i>Enterococcus faecalis</i>
442	E3M10000031G05	<i>Enterococcus faecalis</i>
443	E3M10000031G06	<i>Enterococcus faecalis</i>
444	E3M10000031G07	<i>Enterococcus faecalis</i>
445	E3M10000031G08	<i>Enterococcus faecalis</i>
446	E3M10000031G11	<i>Enterococcus faecalis</i>
447	E3M10000031H05	<i>Enterococcus faecalis</i>
448	E3M10000031H06	<i>Enterococcus faecalis</i>
449	E3M10000031H07	<i>Enterococcus faecalis</i>
450	E3M10000031H08	<i>Enterococcus faecalis</i>
451	E3M10000031H10	<i>Enterococcus faecalis</i>
452	E3M10000031H11	<i>Enterococcus faecalis</i>
453	E3M10000032A02	<i>Enterococcus faecalis</i>
454	E3M10000032A04	<i>Enterococcus faecalis</i>
455	E3M10000032A06	<i>Enterococcus faecalis</i>
456	E3M10000032A07	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
457	E3M10000032A08	<i>Enterococcus faecalis</i>
458	E3M10000032A09	<i>Enterococcus faecalis</i>
459	E3M10000032A10	<i>Enterococcus faecalis</i>
460	E3M10000032A11	<i>Enterococcus faecalis</i>
461	E3M10000032B03	<i>Enterococcus faecalis</i>
462	E3M10000032B04	<i>Enterococcus faecalis</i>
463	E3M10000032B07	<i>Enterococcus faecalis</i>
464	E3M10000032B08	<i>Enterococcus faecalis</i>
465	E3M10000032B09	<i>Enterococcus faecalis</i>
466	E3M10000032B11	<i>Enterococcus faecalis</i>
467	E3M10000032B12	<i>Enterococcus faecalis</i>
468	E3M10000032C01	<i>Enterococcus faecalis</i>
469	E3M10000032C02	<i>Enterococcus faecalis</i>
470	E3M10000032C03	<i>Enterococcus faecalis</i>
471	E3M10000032C04	<i>Enterococcus faecalis</i>
472	E3M10000032C06	<i>Enterococcus faecalis</i>
473	E3M10000032C09	<i>Enterococcus faecalis</i>
474	E3M10000032C11	<i>Enterococcus faecalis</i>
475	E3M10000032C12	<i>Enterococcus faecalis</i>
476	E3M10000032D01	<i>Enterococcus faecalis</i>
477	E3M10000032D02	<i>Enterococcus faecalis</i>
478	E3M10000032D03	<i>Enterococcus faecalis</i>
479	E3M10000032D06	<i>Enterococcus faecalis</i>
480	E3M10000032D09	<i>Enterococcus faecalis</i>
481	E3M10000032D12	<i>Enterococcus faecalis</i>
482	E3M10000032E04	<i>Enterococcus faecalis</i>
483	E3M10000032E05	<i>Enterococcus faecalis</i>
484	E3M10000032E08	<i>Enterococcus faecalis</i>
485	E3M10000032E10	<i>Enterococcus faecalis</i>
486	E3M10000032E11	<i>Enterococcus faecalis</i>
487	E3M10000032E12	<i>Enterococcus faecalis</i>
488	E3M10000032F02	<i>Enterococcus faecalis</i>
489	E3M10000032F03	<i>Enterococcus faecalis</i>
490	E3M10000032F05	<i>Enterococcus faecalis</i>
491	E3M10000032F07	<i>Enterococcus faecalis</i>
492	E3M10000032F08	<i>Enterococcus faecalis</i>
493	E3M10000032F11	<i>Enterococcus faecalis</i>
494	E3M10000032F12	<i>Enterococcus faecalis</i>
495	E3M10000032G01	<i>Enterococcus faecalis</i>
496	E3M10000032G02	<i>Enterococcus faecalis</i>
497	E3M10000032G04	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
498	E3M10000032G05	<i>Enterococcus faecalis</i>
499	E3M10000032G06	<i>Enterococcus faecalis</i>
500	E3M10000032G07	<i>Enterococcus faecalis</i>
501	E3M10000032H05	<i>Enterococcus faecalis</i>
502	E3M10000032H06	<i>Enterococcus faecalis</i>
503	E3M10000032H08	<i>Enterococcus faecalis</i>
504	E3M10000032H09	<i>Enterococcus faecalis</i>
505	E3M10000032H10	<i>Enterococcus faecalis</i>
506	E3M10000033A03	<i>Enterococcus faecalis</i>
507	E3M10000033A04	<i>Enterococcus faecalis</i>
508	E3M10000033A05	<i>Enterococcus faecalis</i>
509	E3M10000033A06	<i>Enterococcus faecalis</i>
510	E3M10000033A07	<i>Enterococcus faecalis</i>
511	E3M10000033A08	<i>Enterococcus faecalis</i>
512	E3M10000033A11	<i>Enterococcus faecalis</i>
513	E3M10000033B01	<i>Enterococcus faecalis</i>
514	E3M10000033B02	<i>Enterococcus faecalis</i>
515	E3M10000033B04	<i>Enterococcus faecalis</i>
516	E3M10000033B05	<i>Enterococcus faecalis</i>
517	E3M10000033B06	<i>Enterococcus faecalis</i>
518	E3M10000033B08	<i>Enterococcus faecalis</i>
519	E3M10000033B09	<i>Enterococcus faecalis</i>
520	E3M10000033C01	<i>Enterococcus faecalis</i>
521	E3M10000033C02	<i>Enterococcus faecalis</i>
522	E3M10000033C05	<i>Enterococcus faecalis</i>
523	E3M10000033C09	<i>Enterococcus faecalis</i>
524	E3M10000033C10	<i>Enterococcus faecalis</i>
525	E3M10000033C11	<i>Enterococcus faecalis</i>
526	E3M10000033C12	<i>Enterococcus faecalis</i>
527	E3M10000033D01	<i>Enterococcus faecalis</i>
528	E3M10000033D04	<i>Enterococcus faecalis</i>
529	E3M10000033D05	<i>Enterococcus faecalis</i>
530	E3M10000033D06	<i>Enterococcus faecalis</i>
531	E3M10000033D09	<i>Enterococcus faecalis</i>
532	E3M10000033D10	<i>Enterococcus faecalis</i>
533	E3M10000033D11	<i>Enterococcus faecalis</i>
534	E3M10000033E02	<i>Enterococcus faecalis</i>
535	E3M10000033E03	<i>Enterococcus faecalis</i>
536	E3M10000033E04	<i>Enterococcus faecalis</i>
537	E3M10000033E05	<i>Enterococcus faecalis</i>
538	E3M10000033E07	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
539	E3M10000033E08	<i>Enterococcus faecalis</i>
540	E3M10000033E09	<i>Enterococcus faecalis</i>
541	E3M10000033E11	<i>Enterococcus faecalis</i>
542	E3M10000033F01	<i>Enterococcus faecalis</i>
543	E3M10000033F03	<i>Enterococcus faecalis</i>
544	E3M10000033F04	<i>Enterococcus faecalis</i>
545	E3M10000033F05	<i>Enterococcus faecalis</i>
546	E3M10000033F07	<i>Enterococcus faecalis</i>
547	E3M10000033F08	<i>Enterococcus faecalis</i>
548	E3M10000033F10	<i>Enterococcus faecalis</i>
549	E3M10000033F12	<i>Enterococcus faecalis</i>
550	E3M10000033G01	<i>Enterococcus faecalis</i>
551	E3M10000033G02	<i>Enterococcus faecalis</i>
552	E3M10000033G03	<i>Enterococcus faecalis</i>
553	E3M10000033G04	<i>Enterococcus faecalis</i>
554	E3M10000033G06	<i>Enterococcus faecalis</i>
555	E3M10000033G07	<i>Enterococcus faecalis</i>
556	E3M10000033G08	<i>Enterococcus faecalis</i>
557	E3M10000033G09	<i>Enterococcus faecalis</i>
558	E3M10000033G12	<i>Enterococcus faecalis</i>
559	E3M10000033H02	<i>Enterococcus faecalis</i>
560	E3M10000033H04	<i>Enterococcus faecalis</i>
561	E3M10000033H05	<i>Enterococcus faecalis</i>
562	E3M10000033H07	<i>Enterococcus faecalis</i>
563	E3M10000033H08	<i>Enterococcus faecalis</i>
564	E3M10000033H09	<i>Enterococcus faecalis</i>
565	E3M10000033H10	<i>Enterococcus faecalis</i>
566	E3M10000033H11	<i>Enterococcus faecalis</i>
567	E3M10000034A02	<i>Enterococcus faecalis</i>
568	E3M10000034A03	<i>Enterococcus faecalis</i>
569	E3M10000034A04	<i>Enterococcus faecalis</i>
570	E3M10000034B02	<i>Enterococcus faecalis</i>
571	E3M10000034B04	<i>Enterococcus faecalis</i>
572	E3M10000034C04	<i>Enterococcus faecalis</i>
573	E3M10000034D01	<i>Enterococcus faecalis</i>
574	E3M10000034D02	<i>Enterococcus faecalis</i>
575	E3M10000034E01	<i>Enterococcus faecalis</i>
576	E3M10000034E04	<i>Enterococcus faecalis</i>
577	E3M10000034F02	<i>Enterococcus faecalis</i>
578	E3M10000034F03	<i>Enterococcus faecalis</i>
579	E3M10000034F04	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
580	E3M10000034G02	<i>Enterococcus faecalis</i>
581	E3M10000034G03	<i>Enterococcus faecalis</i>
582	E3M10000034H02	<i>Enterococcus faecalis</i>
583	E3M10000034H03	<i>Enterococcus faecalis</i>
584	E3M10000035A02	<i>Enterococcus faecalis</i>
585	E3M10000035A04	<i>Enterococcus faecalis</i>
586	E3M10000035A05	<i>Enterococcus faecalis</i>
587	E3M10000035A06	<i>Enterococcus faecalis</i>
588	E3M10000035A08	<i>Enterococcus faecalis</i>
589	E3M10000035A09	<i>Enterococcus faecalis</i>
590	E3M10000035A11	<i>Enterococcus faecalis</i>
591	E3M10000035B01	<i>Enterococcus faecalis</i>
592	E3M10000035B03	<i>Enterococcus faecalis</i>
593	E3M10000035B06	<i>Enterococcus faecalis</i>
594	E3M10000035B07	<i>Enterococcus faecalis</i>
595	E3M10000035B08	<i>Enterococcus faecalis</i>
596	E3M10000035B10	<i>Enterococcus faecalis</i>
597	E3M10000035B11	<i>Enterococcus faecalis</i>
598	E3M10000035B12	<i>Enterococcus faecalis</i>
599	E3M10000035C01	<i>Enterococcus faecalis</i>
600	E3M10000035C03	<i>Enterococcus faecalis</i>
601	E3M10000035C04	<i>Enterococcus faecalis</i>
602	E3M10000035C05	<i>Enterococcus faecalis</i>
603	E3M10000035C06	<i>Enterococcus faecalis</i>
604	E3M10000035C07	<i>Enterococcus faecalis</i>
605	E3M10000035C08	<i>Enterococcus faecalis</i>
606	E3M10000035C09	<i>Enterococcus faecalis</i>
607	E3M10000035C11	<i>Enterococcus faecalis</i>
608	E3M10000035C12	<i>Enterococcus faecalis</i>
609	E3M10000035D02	<i>Enterococcus faecalis</i>
610	E3M10000035D03	<i>Enterococcus faecalis</i>
611	E3M10000035D04	<i>Enterococcus faecalis</i>
612	E3M10000035D05	<i>Enterococcus faecalis</i>
613	E3M10000035D10	<i>Enterococcus faecalis</i>
614	E3M10000035D11	<i>Enterococcus faecalis</i>
615	E3M10000035E03	<i>Enterococcus faecalis</i>
616	E3M10000035E04	<i>Enterococcus faecalis</i>
617	E3M10000035E05	<i>Enterococcus faecalis</i>
618	E3M10000035E07	<i>Enterococcus faecalis</i>
619	E3M10000035E08	<i>Enterococcus faecalis</i>
620	E3M10000035E09	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
621	E3M10000035E10	<i>Enterococcus faecalis</i>
622	E3M10000035E11	<i>Enterococcus faecalis</i>
623	E3M10000035E12	<i>Enterococcus faecalis</i>
624	E3M10000035F01	<i>Enterococcus faecalis</i>
625	E3M10000035F02	<i>Enterococcus faecalis</i>
626	E3M10000035F03	<i>Enterococcus faecalis</i>
627	E3M10000035F06	<i>Enterococcus faecalis</i>
628	E3M10000035F07	<i>Enterococcus faecalis</i>
629	E3M10000035F08	<i>Enterococcus faecalis</i>
630	E3M10000035F09	<i>Enterococcus faecalis</i>
631	E3M10000035F11	<i>Enterococcus faecalis</i>
632	E3M10000035F12	<i>Enterococcus faecalis</i>
633	E3M10000035G02	<i>Enterococcus faecalis</i>
634	E3M10000035G04	<i>Enterococcus faecalis</i>
635	E3M10000035G05	<i>Enterococcus faecalis</i>
636	E3M10000035G08	<i>Enterococcus faecalis</i>
637	E3M10000035G09	<i>Enterococcus faecalis</i>
638	E3M10000035G10	<i>Enterococcus faecalis</i>
639	E3M10000035G11	<i>Enterococcus faecalis</i>
640	E3M10000035H03	<i>Enterococcus faecalis</i>
641	E3M10000035H06	<i>Enterococcus faecalis</i>
642	E3M10000035H09	<i>Enterococcus faecalis</i>
643	E3M10000035H11	<i>Enterococcus faecalis</i>
644	E3M10000036A03	<i>Enterococcus faecalis</i>
645	E3M10000036A04	<i>Enterococcus faecalis</i>
646	E3M10000036A05	<i>Enterococcus faecalis</i>
647	E3M10000036A06	<i>Enterococcus faecalis</i>
648	E3M10000036A07	<i>Enterococcus faecalis</i>
649	E3M10000036A08	<i>Enterococcus faecalis</i>
650	E3M10000036A09	<i>Enterococcus faecalis</i>
651	E3M10000036A10	<i>Enterococcus faecalis</i>
652	E3M10000036B01	<i>Enterococcus faecalis</i>
653	E3M10000036B03	<i>Enterococcus faecalis</i>
654	E3M10000036B06	<i>Enterococcus faecalis</i>
655	E3M10000036B07	<i>Enterococcus faecalis</i>
656	E3M10000036B08	<i>Enterococcus faecalis</i>
657	E3M10000036B09	<i>Enterococcus faecalis</i>
658	E3M10000036B11	<i>Enterococcus faecalis</i>
659	E3M10000036B12	<i>Enterococcus faecalis</i>
660	E3M10000036C01	<i>Enterococcus faecalis</i>
661	E3M10000036C03	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
662	E3M10000036C06	<i>Enterococcus faecalis</i>
663	E3M10000036C07	<i>Enterococcus faecalis</i>
664	E3M10000036C08	<i>Enterococcus faecalis</i>
665	E3M10000036C09	<i>Enterococcus faecalis</i>
666	E3M10000036C10	<i>Enterococcus faecalis</i>
667	E3M10000036C11	<i>Enterococcus faecalis</i>
668	E3M10000036D03	<i>Enterococcus faecalis</i>
669	E3M10000036D04	<i>Enterococcus faecalis</i>
670	E3M10000036D06	<i>Enterococcus faecalis</i>
671	E3M10000036D08	<i>Enterococcus faecalis</i>
672	E3M10000036D09	<i>Enterococcus faecalis</i>
673	E3M10000036D10	<i>Enterococcus faecalis</i>
674	E3M10000036D11	<i>Enterococcus faecalis</i>
675	E3M10000036D12	<i>Enterococcus faecalis</i>
676	E3M10000036E01	<i>Enterococcus faecalis</i>
677	E3M10000036E04	<i>Enterococcus faecalis</i>
678	E3M10000036E05	<i>Enterococcus faecalis</i>
679	E3M10000036E07	<i>Enterococcus faecalis</i>
680	E3M10000036E08	<i>Enterococcus faecalis</i>
681	E3M10000036F03	<i>Enterococcus faecalis</i>
682	E3M10000036F04	<i>Enterococcus faecalis</i>
683	E3M10000036F05	<i>Enterococcus faecalis</i>
684	E3M10000036F08	<i>Enterococcus faecalis</i>
685	E3M10000036F09	<i>Enterococcus faecalis</i>
686	E3M10000036F10	<i>Enterococcus faecalis</i>
687	E3M10000036F12	<i>Enterococcus faecalis</i>
688	E3M10000036G01	<i>Enterococcus faecalis</i>
689	E3M10000036G02	<i>Enterococcus faecalis</i>
690	E3M10000036G03	<i>Enterococcus faecalis</i>
691	E3M10000036G04	<i>Enterococcus faecalis</i>
692	E3M10000036G06	<i>Enterococcus faecalis</i>
693	E3M10000036G10	<i>Enterococcus faecalis</i>
694	E3M10000036H02	<i>Enterococcus faecalis</i>
695	E3M10000036H03	<i>Enterococcus faecalis</i>
696	E3M10000036H04	<i>Enterococcus faecalis</i>
697	E3M10000036H05	<i>Enterococcus faecalis</i>
698	E3M10000036H06	<i>Enterococcus faecalis</i>
699	E3M10000036H07	<i>Enterococcus faecalis</i>
700	E3M10000036H08	<i>Enterococcus faecalis</i>
701	E3M10000036H09	<i>Enterococcus faecalis</i>
702	E3M10000036H10	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
703	E3M10000037A03	<i>Enterococcus faecalis</i>
704	E3M10000037A06	<i>Enterococcus faecalis</i>
705	E3M10000037A08	<i>Enterococcus faecalis</i>
706	E3M10000037A09	<i>Enterococcus faecalis</i>
707	E3M10000037A10	<i>Enterococcus faecalis</i>
708	E3M10000037B02	<i>Enterococcus faecalis</i>
709	E3M10000037B07	<i>Enterococcus faecalis</i>
710	E3M10000037B08	<i>Enterococcus faecalis</i>
711	E3M10000037B11	<i>Enterococcus faecalis</i>
712	E3M10000037C01	<i>Enterococcus faecalis</i>
713	E3M10000037C02	<i>Enterococcus faecalis</i>
714	E3M10000037C04	<i>Enterococcus faecalis</i>
715	E3M10000037C05	<i>Enterococcus faecalis</i>
716	E3M10000037C07	<i>Enterococcus faecalis</i>
717	E3M10000037C11	<i>Enterococcus faecalis</i>
718	E3M10000037C12	<i>Enterococcus faecalis</i>
719	E3M10000037D02	<i>Enterococcus faecalis</i>
720	E3M10000037D03	<i>Enterococcus faecalis</i>
721	E3M10000037D04	<i>Enterococcus faecalis</i>
722	E3M10000037D05	<i>Enterococcus faecalis</i>
723	E3M10000037D06	<i>Enterococcus faecalis</i>
724	E3M10000037D09	<i>Enterococcus faecalis</i>
725	E3M10000037D11	<i>Enterococcus faecalis</i>
726	E3M10000037E01	<i>Enterococcus faecalis</i>
727	E3M10000037E02	<i>Enterococcus faecalis</i>
728	E3M10000037E03	<i>Enterococcus faecalis</i>
729	E3M10000037E05	<i>Enterococcus faecalis</i>
730	E3M10000037E07	<i>Enterococcus faecalis</i>
731	E3M10000037E08	<i>Enterococcus faecalis</i>
732	E3M10000037E10	<i>Enterococcus faecalis</i>
733	E3M10000037E12	<i>Enterococcus faecalis</i>
734	E3M10000037F01	<i>Enterococcus faecalis</i>
735	E3M10000037F02	<i>Enterococcus faecalis</i>
736	E3M10000037F06	<i>Enterococcus faecalis</i>
737	E3M10000037F07	<i>Enterococcus faecalis</i>
738	E3M10000037F12	<i>Enterococcus faecalis</i>
739	E3M10000037G01	<i>Enterococcus faecalis</i>
740	E3M10000037G02	<i>Enterococcus faecalis</i>
741	E3M10000037G03	<i>Enterococcus faecalis</i>
742	E3M10000037G05	<i>Enterococcus faecalis</i>
743	E3M10000037G06	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
744	E3M10000037G07	<i>Enterococcus faecalis</i>
745	E3M10000037G08	<i>Enterococcus faecalis</i>
746	E3M10000037G10	<i>Enterococcus faecalis</i>
747	E3M10000037G11	<i>Enterococcus faecalis</i>
748	E3M10000037H02	<i>Enterococcus faecalis</i>
749	E3M10000037H05	<i>Enterococcus faecalis</i>
750	E3M10000037H07	<i>Enterococcus faecalis</i>
751	E3M10000037H10	<i>Enterococcus faecalis</i>
752	E3M10000037H11	<i>Enterococcus faecalis</i>
753	E3M10000038A02	<i>Enterococcus faecalis</i>
754	E3M10000038A03	<i>Enterococcus faecalis</i>
755	E3M10000038A05	<i>Enterococcus faecalis</i>
756	E3M10000038A06	<i>Enterococcus faecalis</i>
757	E3M10000038A07	<i>Enterococcus faecalis</i>
758	E3M10000038A09	<i>Enterococcus faecalis</i>
759	E3M10000038A10	<i>Enterococcus faecalis</i>
760	E3M10000038A11	<i>Enterococcus faecalis</i>
761	E3M10000038B02	<i>Enterococcus faecalis</i>
762	E3M10000038B03	<i>Enterococcus faecalis</i>
763	E3M10000038B04	<i>Enterococcus faecalis</i>
764	E3M10000038B05	<i>Enterococcus faecalis</i>
765	E3M10000038B07	<i>Enterococcus faecalis</i>
766	E3M10000038B08	<i>Enterococcus faecalis</i>
767	E3M10000038B09	<i>Enterococcus faecalis</i>
768	E3M10000038B11	<i>Enterococcus faecalis</i>
769	E3M10000038C02	<i>Enterococcus faecalis</i>
770	E3M10000038C03	<i>Enterococcus faecalis</i>
771	E3M10000038C05	<i>Enterococcus faecalis</i>
772	E3M10000038C07	<i>Enterococcus faecalis</i>
773	E3M10000038C10	<i>Enterococcus faecalis</i>
774	E3M10000038C12	<i>Enterococcus faecalis</i>
775	E3M10000038D01	<i>Enterococcus faecalis</i>
776	E3M10000038D02	<i>Enterococcus faecalis</i>
777	E3M10000038D04	<i>Enterococcus faecalis</i>
778	E3M10000038D08	<i>Enterococcus faecalis</i>
779	E3M10000038D10	<i>Enterococcus faecalis</i>
780	E3M10000038D11	<i>Enterococcus faecalis</i>
781	E3M10000038D12	<i>Enterococcus faecalis</i>
782	E3M10000038E02	<i>Enterococcus faecalis</i>
783	E3M10000038E03	<i>Enterococcus faecalis</i>
784	E3M10000038E04	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
785	E3M10000038E05	<i>Enterococcus faecalis</i>
786	E3M10000038E07	<i>Enterococcus faecalis</i>
787	E3M10000038E08	<i>Enterococcus faecalis</i>
788	E3M10000038E11	<i>Enterococcus faecalis</i>
789	E3M10000038F02	<i>Enterococcus faecalis</i>
790	E3M10000038F04	<i>Enterococcus faecalis</i>
791	E3M10000038F05	<i>Enterococcus faecalis</i>
792	E3M10000038F06	<i>Enterococcus faecalis</i>
793	E3M10000038F07	<i>Enterococcus faecalis</i>
794	E3M10000038F09	<i>Enterococcus faecalis</i>
795	E3M10000038F10	<i>Enterococcus faecalis</i>
796	E3M10000038F11	<i>Enterococcus faecalis</i>
797	E3M10000038G02	<i>Enterococcus faecalis</i>
798	E3M10000038G03	<i>Enterococcus faecalis</i>
799	E3M10000038G06	<i>Enterococcus faecalis</i>
800	E3M10000038G07	<i>Enterococcus faecalis</i>
801	E3M10000038G11	<i>Enterococcus faecalis</i>
802	E3M10000038H02	<i>Enterococcus faecalis</i>
803	E3M10000038H05	<i>Enterococcus faecalis</i>
804	E3M10000038H06	<i>Enterococcus faecalis</i>
805	E3M10000038H07	<i>Enterococcus faecalis</i>
806	E3M10000038H08	<i>Enterococcus faecalis</i>
807	E3M10000038H09	<i>Enterococcus faecalis</i>
808	E3M10000038H10	<i>Enterococcus faecalis</i>
809	E3M10000039A02	<i>Enterococcus faecalis</i>
810	E3M10000039A06	<i>Enterococcus faecalis</i>
811	E3M10000039A07	<i>Enterococcus faecalis</i>
812	E3M10000039A08	<i>Enterococcus faecalis</i>
813	E3M10000039A10	<i>Enterococcus faecalis</i>
814	E3M10000039A11	<i>Enterococcus faecalis</i>
815	E3M10000039B01	<i>Enterococcus faecalis</i>
816	E3M10000039B03	<i>Enterococcus faecalis</i>
817	E3M10000039B04	<i>Enterococcus faecalis</i>
818	E3M10000039B06	<i>Enterococcus faecalis</i>
819	E3M10000039B07	<i>Enterococcus faecalis</i>
820	E3M10000039B08	<i>Enterococcus faecalis</i>
821	E3M10000039B09	<i>Enterococcus faecalis</i>
822	E3M10000039B11	<i>Enterococcus faecalis</i>
823	E3M10000039C02	<i>Enterococcus faecalis</i>
824	E3M10000039C04	<i>Enterococcus faecalis</i>
825	E3M10000039C05	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
826	E3M10000039C06	<i>Enterococcus faecalis</i>
827	E3M10000039C07	<i>Enterococcus faecalis</i>
828	E3M10000039C08	<i>Enterococcus faecalis</i>
829	E3M10000039C09	<i>Enterococcus faecalis</i>
830	E3M10000039C10	<i>Enterococcus faecalis</i>
831	E3M10000039D02	<i>Enterococcus faecalis</i>
832	E3M10000039D03	<i>Enterococcus faecalis</i>
833	E3M10000039D04	<i>Enterococcus faecalis</i>
834	E3M10000039D06	<i>Enterococcus faecalis</i>
835	E3M10000039E01	<i>Enterococcus faecalis</i>
836	E3M10000039E02	<i>Enterococcus faecalis</i>
837	E3M10000039E03	<i>Enterococcus faecalis</i>
838	E3M10000039E05	<i>Enterococcus faecalis</i>
839	E3M10000039E07	<i>Enterococcus faecalis</i>
840	E3M10000039E08	<i>Enterococcus faecalis</i>
841	E3M10000039F01	<i>Enterococcus faecalis</i>
842	E3M10000039F02	<i>Enterococcus faecalis</i>
843	E3M10000039F03	<i>Enterococcus faecalis</i>
844	E3M10000039F06	<i>Enterococcus faecalis</i>
845	E3M10000039F07	<i>Enterococcus faecalis</i>
846	E3M10000039F08	<i>Enterococcus faecalis</i>
847	E3M10000039G01	<i>Enterococcus faecalis</i>
848	E3M10000039G02	<i>Enterococcus faecalis</i>
849	E3M10000039G05	<i>Enterococcus faecalis</i>
850	E3M10000039G07	<i>Enterococcus faecalis</i>
851	E3M10000039G09	<i>Enterococcus faecalis</i>
852	E3M10000039G10	<i>Enterococcus faecalis</i>
853	E3M10000039H02	<i>Enterococcus faecalis</i>
854	E3M10000039H07	<i>Enterococcus faecalis</i>
855	E3M10000039H08	<i>Enterococcus faecalis</i>
856	E3M10000039H10	<i>Enterococcus faecalis</i>
857	E3M10000039H11	<i>Enterococcus faecalis</i>
858	E3M10000040A03	<i>Enterococcus faecalis</i>
859	E3M10000040A05	<i>Enterococcus faecalis</i>
860	E3M10000040A07	<i>Enterococcus faecalis</i>
861	E3M10000040A09	<i>Enterococcus faecalis</i>
862	E3M10000040A10	<i>Enterococcus faecalis</i>
863	E3M10000040A11	<i>Enterococcus faecalis</i>
864	E3M10000040B01	<i>Enterococcus faecalis</i>
865	E3M10000040B02	<i>Enterococcus faecalis</i>
866	E3M10000040B05	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
867	E3M10000040B06	<i>Enterococcus faecalis</i>
868	E3M10000040B08	<i>Enterococcus faecalis</i>
869	E3M10000040B09	<i>Enterococcus faecalis</i>
870	E3M10000040B10	<i>Enterococcus faecalis</i>
871	E3M10000040B11	<i>Enterococcus faecalis</i>
872	E3M10000040B12	<i>Enterococcus faecalis</i>
873	E3M10000040C02	<i>Enterococcus faecalis</i>
874	E3M10000040C05	<i>Enterococcus faecalis</i>
875	E3M10000040C06	<i>Enterococcus faecalis</i>
876	E3M10000040C07	<i>Enterococcus faecalis</i>
877	E3M10000040C08	<i>Enterococcus faecalis</i>
878	E3M10000040C09	<i>Enterococcus faecalis</i>
879	E3M10000040C10	<i>Enterococcus faecalis</i>
880	E3M10000040C11	<i>Enterococcus faecalis</i>
881	E3M10000040C12	<i>Enterococcus faecalis</i>
882	E3M10000040D03	<i>Enterococcus faecalis</i>
883	E3M10000040D04	<i>Enterococcus faecalis</i>
884	E3M10000040D08	<i>Enterococcus faecalis</i>
885	E3M10000040D12	<i>Enterococcus faecalis</i>
886	E3M10000040E02	<i>Enterococcus faecalis</i>
887	E3M10000040E10	<i>Enterococcus faecalis</i>
888	E3M10000040E11	<i>Enterococcus faecalis</i>
889	E3M10000040E12	<i>Enterococcus faecalis</i>
890	E3M10000040F01	<i>Enterococcus faecalis</i>
891	E3M10000040F03	<i>Enterococcus faecalis</i>
892	E3M10000040F08	<i>Enterococcus faecalis</i>
893	E3M10000040F09	<i>Enterococcus faecalis</i>
894	E3M10000040F10	<i>Enterococcus faecalis</i>
895	E3M10000040G01	<i>Enterococcus faecalis</i>
896	E3M10000040G02	<i>Enterococcus faecalis</i>
897	E3M10000040G04	<i>Enterococcus faecalis</i>
898	E3M10000040G05	<i>Enterococcus faecalis</i>
899	E3M10000040G07	<i>Enterococcus faecalis</i>
900	E3M10000040G08	<i>Enterococcus faecalis</i>
901	E3M10000040G09	<i>Enterococcus faecalis</i>
902	E3M10000040G11	<i>Enterococcus faecalis</i>
903	E3M10000040H02	<i>Enterococcus faecalis</i>
904	E3M10000040H03	<i>Enterococcus faecalis</i>
905	E3M10000040H04	<i>Enterococcus faecalis</i>
906	E3M10000040H05	<i>Enterococcus faecalis</i>
907	E3M10000040H09	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
908	E3M10000041A03	<i>Enterococcus faecalis</i>
909	E3M10000041A05	<i>Enterococcus faecalis</i>
910	E3M10000041A08	<i>Enterococcus faecalis</i>
911	E3M10000041A09	<i>Enterococcus faecalis</i>
912	E3M10000041A10	<i>Enterococcus faecalis</i>
913	E3M10000041A11	<i>Enterococcus faecalis</i>
914	E3M10000041B02	<i>Enterococcus faecalis</i>
915	E3M10000041B03	<i>Enterococcus faecalis</i>
916	E3M10000041B05	<i>Enterococcus faecalis</i>
917	E3M10000041B06	<i>Enterococcus faecalis</i>
918	E3M10000041B08	<i>Enterococcus faecalis</i>
919	E3M10000041B09	<i>Enterococcus faecalis</i>
920	E3M10000041B10	<i>Enterococcus faecalis</i>
921	E3M10000041B11	<i>Enterococcus faecalis</i>
922	E3M10000041B12	<i>Enterococcus faecalis</i>
923	E3M10000041C01	<i>Enterococcus faecalis</i>
924	E3M10000041C07	<i>Enterococcus faecalis</i>
925	E3M10000041C08	<i>Enterococcus faecalis</i>
926	E3M10000041C09	<i>Enterococcus faecalis</i>
927	E3M10000041C10	<i>Enterococcus faecalis</i>
928	E3M10000041C11	<i>Enterococcus faecalis</i>
929	E3M10000041C12	<i>Enterococcus faecalis</i>
930	E3M10000041D02	<i>Enterococcus faecalis</i>
931	E3M10000041D03	<i>Enterococcus faecalis</i>
932	E3M10000041D04	<i>Enterococcus faecalis</i>
933	E3M10000041D05	<i>Enterococcus faecalis</i>
934	E3M10000041D06	<i>Enterococcus faecalis</i>
935	E3M10000041D08	<i>Enterococcus faecalis</i>
936	E3M10000041D09	<i>Enterococcus faecalis</i>
937	E3M10000041D10	<i>Enterococcus faecalis</i>
938	E3M10000041D11	<i>Enterococcus faecalis</i>
939	E3M10000041D12	<i>Enterococcus faecalis</i>
940	E3M10000041E02	<i>Enterococcus faecalis</i>
941	E3M10000041E03	<i>Enterococcus faecalis</i>
942	E3M10000041E05	<i>Enterococcus faecalis</i>
943	E3M10000041E07	<i>Enterococcus faecalis</i>
944	E3M10000041E10	<i>Enterococcus faecalis</i>
945	E3M10000041E11	<i>Enterococcus faecalis</i>
946	E3M10000041F03	<i>Enterococcus faecalis</i>
947	E3M10000041F05	<i>Enterococcus faecalis</i>
948	E3M10000041F06	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
949	E3M10000041F07	<i>Enterococcus faecalis</i>
950	E3M10000041F08	<i>Enterococcus faecalis</i>
951	E3M10000041F09	<i>Enterococcus faecalis</i>
952	E3M10000041F10	<i>Enterococcus faecalis</i>
953	E3M10000041F11	<i>Enterococcus faecalis</i>
954	E3M10000041G02	<i>Enterococcus faecalis</i>
955	E3M10000041G03	<i>Enterococcus faecalis</i>
956	E3M10000041G04	<i>Enterococcus faecalis</i>
957	E3M10000041G06	<i>Enterococcus faecalis</i>
958	E3M10000041G07	<i>Enterococcus faecalis</i>
959	E3M10000041G08	<i>Enterococcus faecalis</i>
960	E3M10000041G09	<i>Enterococcus faecalis</i>
961	E3M10000041G10	<i>Enterococcus faecalis</i>
962	E3M10000041G12	<i>Enterococcus faecalis</i>
963	E3M10000041H04	<i>Enterococcus faecalis</i>
964	E3M10000041H05	<i>Enterococcus faecalis</i>
965	E3M10000041H06	<i>Enterococcus faecalis</i>
966	E3M10000041H07	<i>Enterococcus faecalis</i>
967	E3M10000041H08	<i>Enterococcus faecalis</i>
968	E3M10000041H09	<i>Enterococcus faecalis</i>
969	E3M10000041H10	<i>Enterococcus faecalis</i>
970	E3M10000041H11	<i>Enterococcus faecalis</i>
971	E3M10000042A03	<i>Enterococcus faecalis</i>
972	E3M10000042A08	<i>Enterococcus faecalis</i>
973	E3M10000042A10	<i>Enterococcus faecalis</i>
974	E3M10000042B01	<i>Enterococcus faecalis</i>
975	E3M10000042B02	<i>Enterococcus faecalis</i>
976	E3M10000042B04	<i>Enterococcus faecalis</i>
977	E3M10000042B08	<i>Enterococcus faecalis</i>
978	E3M10000042B09	<i>Enterococcus faecalis</i>
979	E3M10000042B10	<i>Enterococcus faecalis</i>
980	E3M10000042B11	<i>Enterococcus faecalis</i>
981	E3M10000042C02	<i>Enterococcus faecalis</i>
982	E3M10000042C03	<i>Enterococcus faecalis</i>
983	E3M10000042C04	<i>Enterococcus faecalis</i>
984	E3M10000042C10	<i>Enterococcus faecalis</i>
985	E3M10000042D01	<i>Enterococcus faecalis</i>
986	E3M10000042D02	<i>Enterococcus faecalis</i>
987	E3M10000042D03	<i>Enterococcus faecalis</i>
988	E3M10000042D06	<i>Enterococcus faecalis</i>
989	E3M10000042D09	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
990	E3M10000042D11	<i>Enterococcus faecalis</i>
991	E3M10000042D12	<i>Enterococcus faecalis</i>
992	E3M10000042E05	<i>Enterococcus faecalis</i>
993	E3M10000042E12	<i>Enterococcus faecalis</i>
994	E3M10000042F11	<i>Enterococcus faecalis</i>
995	E3M10000042G01	<i>Enterococcus faecalis</i>
996	E3M10000042G05	<i>Enterococcus faecalis</i>
997	E3M10000042G07	<i>Enterococcus faecalis</i>
998	E3M10000042G08	<i>Enterococcus faecalis</i>
999	E3M10000042G11	<i>Enterococcus faecalis</i>
1000	E3M10000042G12	<i>Enterococcus faecalis</i>
1001	E3M10000042H06	<i>Enterococcus faecalis</i>
1002	E3M10000042H08	<i>Enterococcus faecalis</i>
1003	E3M10000042H11	<i>Enterococcus faecalis</i>
1004	E3M10000043A02	<i>Enterococcus faecalis</i>
1005	E3M10000043A03	<i>Enterococcus faecalis</i>
1006	E3M10000043A05	<i>Enterococcus faecalis</i>
1007	E3M10000043A08	<i>Enterococcus faecalis</i>
1008	E3M10000043A09	<i>Enterococcus faecalis</i>
1009	E3M10000043A10	<i>Enterococcus faecalis</i>
1010	E3M10000043A11	<i>Enterococcus faecalis</i>
1011	E3M10000043B01	<i>Enterococcus faecalis</i>
1012	E3M10000043B02	<i>Enterococcus faecalis</i>
1013	E3M10000043B03	<i>Enterococcus faecalis</i>
1014	E3M10000043B06	<i>Enterococcus faecalis</i>
1015	E3M10000043B08	<i>Enterococcus faecalis</i>
1016	E3M10000043B09	<i>Enterococcus faecalis</i>
1017	E3M10000043B10	<i>Enterococcus faecalis</i>
1018	E3M10000043B11	<i>Enterococcus faecalis</i>
1019	E3M10000043B12	<i>Enterococcus faecalis</i>
1020	E3M10000043C01	<i>Enterococcus faecalis</i>
1021	E3M10000043C08	<i>Enterococcus faecalis</i>
1022	E3M10000043C09	<i>Enterococcus faecalis</i>
1023	E3M10000043D01	<i>Enterococcus faecalis</i>
1024	E3M10000043D02	<i>Enterococcus faecalis</i>
1025	E3M10000043D09	<i>Enterococcus faecalis</i>
1026	E3M10000043D10	<i>Enterococcus faecalis</i>
1027	E3M10000043D12	<i>Enterococcus faecalis</i>
1028	E3M10000043E03	<i>Enterococcus faecalis</i>
1029	E3M10000043E07	<i>Enterococcus faecalis</i>
1030	E3M10000043E08	<i>Enterococcus faecalis</i>

SeqID	Clone name	Organism
1031	E3M10000043E10	<i>Enterococcus faecalis</i>
1032	E3M10000043E11	<i>Enterococcus faecalis</i>
1033	E3M10000043F03	<i>Enterococcus faecalis</i>
1034	E3M10000043F04	<i>Enterococcus faecalis</i>
1035	E3M10000043F06	<i>Enterococcus faecalis</i>
1036	E3M10000043F08	<i>Enterococcus faecalis</i>
1037	E3M10000043F10	<i>Enterococcus faecalis</i>
1038	E3M10000043F12	<i>Enterococcus faecalis</i>
1039	E3M10000043G03	<i>Enterococcus faecalis</i>
1040	E3M10000043G04	<i>Enterococcus faecalis</i>
1041	E3M10000043G05	<i>Enterococcus faecalis</i>
1042	E3M10000043G07	<i>Enterococcus faecalis</i>
1043	E3M10000043G08	<i>Enterococcus faecalis</i>
1044	E3M10000043G10	<i>Enterococcus faecalis</i>
1045	E3M10000043G11	<i>Enterococcus faecalis</i>
1046	E3M10000043G12	<i>Enterococcus faecalis</i>
1047	E3M10000043H02	<i>Enterococcus faecalis</i>
1048	E3M10000043H05	<i>Enterococcus faecalis</i>
1049	E3M10000043H08	<i>Enterococcus faecalis</i>
1050	E3M10000043H09	<i>Enterococcus faecalis</i>
1051	E3M10000043H11	<i>Enterococcus faecalis</i>
1052	E3M10000044C02	<i>Enterococcus faecalis</i>
1053	E3M10000044E01	<i>Enterococcus faecalis</i>
1054	K1M10000002F02	<i>Klebsiella pneumoniae</i>
1055	K1M10000003C01	<i>Klebsiella pneumoniae</i>
1056	K1M10000004F06	<i>Klebsiella pneumoniae</i>
1057	K1M10000007F01	<i>Klebsiella pneumoniae</i>
1058	K1M10000008C02	<i>Klebsiella pneumoniae</i>
1059	K1M10000008C10	<i>Klebsiella pneumoniae</i>
1060	K1M10000008G10	<i>Klebsiella pneumoniae</i>
1061	K1M10000009D04	<i>Klebsiella pneumoniae</i>
1062	K1M10000013E04	<i>Klebsiella pneumoniae</i>
1063	K1M10000013E06	<i>Klebsiella pneumoniae</i>
1064	K1M10000019D06	<i>Klebsiella pneumoniae</i>
1065	K1M10000020B02	<i>Klebsiella pneumoniae</i>
1066	K1M10000021H06	<i>Klebsiella pneumoniae</i>
1067	K1M10000022C10	<i>Klebsiella pneumoniae</i>
1068	K1M10000023E09	<i>Klebsiella pneumoniae</i>
1069	K1M10000023E10	<i>Klebsiella pneumoniae</i>
1070	K1M10000030C07	<i>Klebsiella pneumoniae</i>
1071	K1M10000030E07	<i>Klebsiella pneumoniae</i>

SeqID	Clone name	Organism
1072	K1M10000031B11	<i>Klebsiella pneumoniae</i>
1073	K1M10000032E11	<i>Klebsiella pneumoniae</i>
1074	K1M10000033B02	<i>Klebsiella pneumoniae</i>
1075	K1M10000033E01	<i>Klebsiella pneumoniae</i>
1076	K1M10000036G08	<i>Klebsiella pneumoniae</i>
1077	K1M10000037D10	<i>Klebsiella pneumoniae</i>
1078	K1M10000038H09	<i>Klebsiella pneumoniae</i>
1079	K1M10000039H03	<i>Klebsiella pneumoniae</i>
1080	K1M10000043C01	<i>Klebsiella pneumoniae</i>
1081	K1M10000043D05	<i>Klebsiella pneumoniae</i>
1082	K1M10000043H10	<i>Klebsiella pneumoniae</i>
1083	K1M10000044D05	<i>Klebsiella pneumoniae</i>
1084	K1M10000044D08	<i>Klebsiella pneumoniae</i>
1085	K1M10000044E05	<i>Klebsiella pneumoniae</i>
1086	K1M10000044G05	<i>Klebsiella pneumoniae</i>
1087	K1M10000045A07	<i>Klebsiella pneumoniae</i>
1088	K1M10000045D10	<i>Klebsiella pneumoniae</i>
1089	K1M10000003D03	<i>Klebsiella pneumoniae</i>
1090	K1M10000010C02	<i>Klebsiella pneumoniae</i>
1091	K1M10000021H10	<i>Klebsiella pneumoniae</i>
1092	P1M10000008C06	<i>Pseudomonas aeruginosa</i>
1093	P1M10000008G04	<i>Pseudomonas aeruginosa</i>
1094	P1M10000010C03	<i>Pseudomonas aeruginosa</i>
1095	P1M10000014H10	<i>Pseudomonas aeruginosa</i>
1096	P1M10000015C06	<i>Pseudomonas aeruginosa</i>
1097	P1M10000015C09	<i>Pseudomonas aeruginosa</i>
1098	P1M10000016C04	<i>Pseudomonas aeruginosa</i>
1099	P1M10000018B01	<i>Pseudomonas aeruginosa</i>
1100	P1M10000018C01	<i>Pseudomonas aeruginosa</i>
1101	P1M10000018E01	<i>Pseudomonas aeruginosa</i>
1102	P1M10000018G01	<i>Pseudomonas aeruginosa</i>
1103	P1M10000019F01	<i>Pseudomonas aeruginosa</i>
1104	P1M10000021G03	<i>Pseudomonas aeruginosa</i>
1105	P1M10000021G05	<i>Pseudomonas aeruginosa</i>
1106	P1M10000022D09	<i>Pseudomonas aeruginosa</i>
1107	P1M10000024D06	<i>Pseudomonas aeruginosa</i>
1108	P1M10000024E06	<i>Pseudomonas aeruginosa</i>
1109	P1M10000024H03	<i>Pseudomonas aeruginosa</i>
1110	P1M10000025A06	<i>Pseudomonas aeruginosa</i>
1111	P1M10000025G07	<i>Pseudomonas aeruginosa</i>
1112	P1M10000025H07	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
1113	P1M10000026E06	<i>Pseudomonas aeruginosa</i>
1114	P1M10000026F04	<i>Pseudomonas aeruginosa</i>
1115	P1M10000026G09	<i>Pseudomonas aeruginosa</i>
1116	P1M10000026H02	<i>Pseudomonas aeruginosa</i>
1117	P1M10000026H05	<i>Pseudomonas aeruginosa</i>
1118	P1M10000027A06	<i>Pseudomonas aeruginosa</i>
1119	P1M10000027B02	<i>Pseudomonas aeruginosa</i>
1120	P1M10000027G05	<i>Pseudomonas aeruginosa</i>
1121	P1M10000028A08	<i>Pseudomonas aeruginosa</i>
1122	P1M10000028B01	<i>Pseudomonas aeruginosa</i>
1123	P1M10000028E02	<i>Pseudomonas aeruginosa</i>
1124	P1M10000029A09	<i>Pseudomonas aeruginosa</i>
1125	P1M10000029G03	<i>Pseudomonas aeruginosa</i>
1126	P1M10000029H05	<i>Pseudomonas aeruginosa</i>
1127	P1M10000032F04	<i>Pseudomonas aeruginosa</i>
1128	P1M10000033A02	<i>Pseudomonas aeruginosa</i>
1129	P1M10000033B08	<i>Pseudomonas aeruginosa</i>
1130	P1M10000033E03	<i>Pseudomonas aeruginosa</i>
1131	P1M10000033F01	<i>Pseudomonas aeruginosa</i>
1132	P1M10000033G08	<i>Pseudomonas aeruginosa</i>
1133	P1M10000035A06	<i>Pseudomonas aeruginosa</i>
1134	P1M10000037B12	<i>Pseudomonas aeruginosa</i>
1135	P1M10000037G12	<i>Pseudomonas aeruginosa</i>
1136	P1M10000038B08	<i>Pseudomonas aeruginosa</i>
1137	P1M10000038C03	<i>Pseudomonas aeruginosa</i>
1138	P1M10000038C06	<i>Pseudomonas aeruginosa</i>
1139	P1M10000038F04	<i>Pseudomonas aeruginosa</i>
1140	P1M10000038G02	<i>Pseudomonas aeruginosa</i>
1141	P1M10000039G05	<i>Pseudomonas aeruginosa</i>
1142	P1M10000039G12	<i>Pseudomonas aeruginosa</i>
1143	P1M10000040C01	<i>Pseudomonas aeruginosa</i>
1144	P1M10000040C04	<i>Pseudomonas aeruginosa</i>
1145	P1M10000040D04	<i>Pseudomonas aeruginosa</i>
1146	P1M10000040D05	<i>Pseudomonas aeruginosa</i>
1147	P1M10000040E10	<i>Pseudomonas aeruginosa</i>
1148	P1M10000040H03	<i>Pseudomonas aeruginosa</i>
1149	P1M10000041A12	<i>Pseudomonas aeruginosa</i>
1150	P1M10000041B02	<i>Pseudomonas aeruginosa</i>
1151	P1M10000041E01	<i>Pseudomonas aeruginosa</i>
1152	P1M10000041F01	<i>Pseudomonas aeruginosa</i>
1153	P1M10000042B12	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
1154	P1M10000042E08	<i>Pseudomonas aeruginosa</i>
1155	P1M10000043A03	<i>Pseudomonas aeruginosa</i>
1156	P1M10000043D06	<i>Pseudomonas aeruginosa</i>
1157	P1M10000044F07	<i>Pseudomonas aeruginosa</i>
1158	P1M10000046B03	<i>Pseudomonas aeruginosa</i>
1159	P1M10000046C07	<i>Pseudomonas aeruginosa</i>
1160	P1M10000046C08	<i>Pseudomonas aeruginosa</i>
1161	P1M10000046C09	<i>Pseudomonas aeruginosa</i>
1162	P1M10000046G11	<i>Pseudomonas aeruginosa</i>
1163	P1M10000047B04	<i>Pseudomonas aeruginosa</i>
1164	P1M10000047E11	<i>Pseudomonas aeruginosa</i>
1165	P1M10000047F07	<i>Pseudomonas aeruginosa</i>
1166	P1M10000047G10	<i>Pseudomonas aeruginosa</i>
1167	P1M10000048A03	<i>Pseudomonas aeruginosa</i>
1168	P1M10000049E08	<i>Pseudomonas aeruginosa</i>
1169	P1M10000049G10	<i>Pseudomonas aeruginosa</i>
1170	P1M10000050G11	<i>Pseudomonas aeruginosa</i>
1171	P1M10000051D11	<i>Pseudomonas aeruginosa</i>
1172	P1M10000051F01	<i>Pseudomonas aeruginosa</i>
1173	P1M10000052C03	<i>Pseudomonas aeruginosa</i>
1174	P1M10000052C12	<i>Pseudomonas aeruginosa</i>
1175	P1M10000052E04	<i>Pseudomonas aeruginosa</i>
1176	P1M10000053B12	<i>Pseudomonas aeruginosa</i>
1177	P1M10000053C02	<i>Pseudomonas aeruginosa</i>
1178	P1M10000053E07	<i>Pseudomonas aeruginosa</i>
1179	P1M10000053F08	<i>Pseudomonas aeruginosa</i>
1180	P1M10000055A11	<i>Pseudomonas aeruginosa</i>
1181	P1M10000055C08	<i>Pseudomonas aeruginosa</i>
1182	P1M10000055E05	<i>Pseudomonas aeruginosa</i>
1183	P1M10000056C07	<i>Pseudomonas aeruginosa</i>
1184	P1M10000056F05	<i>Pseudomonas aeruginosa</i>
1185	P1M10000056F06	<i>Pseudomonas aeruginosa</i>
1186	P1M10000056G01	<i>Pseudomonas aeruginosa</i>
1187	P1M10000058B07	<i>Pseudomonas aeruginosa</i>
1188	P1M10000059B04	<i>Pseudomonas aeruginosa</i>
1189	P1M10000059B10	<i>Pseudomonas aeruginosa</i>
1190	P1M10000059B11	<i>Pseudomonas aeruginosa</i>
1191	P1M10000059D11	<i>Pseudomonas aeruginosa</i>
1192	P1M10000059H08	<i>Pseudomonas aeruginosa</i>
1193	P1M10000059H09	<i>Pseudomonas aeruginosa</i>
1194	P1M10000060E03	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
1195	P1M10000060H02	<i>Pseudomonas aeruginosa</i>
1196	P1M10000060H04	<i>Pseudomonas aeruginosa</i>
1197	P1M10000061B04	<i>Pseudomonas aeruginosa</i>
1198	P1M10000061E04	<i>Pseudomonas aeruginosa</i>
1199	P1M10000061F04	<i>Pseudomonas aeruginosa</i>
1200	P1M10000062A12	<i>Pseudomonas aeruginosa</i>
1201	P1M10000062C03	<i>Pseudomonas aeruginosa</i>
1202	P1M10000062C04	<i>Pseudomonas aeruginosa</i>
1203	P1M10000062C07	<i>Pseudomonas aeruginosa</i>
1204	P1M10000062C12	<i>Pseudomonas aeruginosa</i>
1205	P1M10000062D07	<i>Pseudomonas aeruginosa</i>
1206	P1M10000062D08	<i>Pseudomonas aeruginosa</i>
1207	P1M10000062E08	<i>Pseudomonas aeruginosa</i>
1208	P1M10000062F06	<i>Pseudomonas aeruginosa</i>
1209	P1M10000062G11	<i>Pseudomonas aeruginosa</i>
1210	P1M10000062H01	<i>Pseudomonas aeruginosa</i>
1211	P1M10000062H04	<i>Pseudomonas aeruginosa</i>
1212	P1M10000063F02	<i>Pseudomonas aeruginosa</i>
1213	P1M10000063G02	<i>Pseudomonas aeruginosa</i>
1214	P1M10000063H02	<i>Pseudomonas aeruginosa</i>
1215	P1M10000064A10	<i>Pseudomonas aeruginosa</i>
1216	P1M10000064C02	<i>Pseudomonas aeruginosa</i>
1217	P1M10000064C03	<i>Pseudomonas aeruginosa</i>
1218	P1M10000064D03	<i>Pseudomonas aeruginosa</i>
1219	P1M10000064E05	<i>Pseudomonas aeruginosa</i>
1220	P1M10000064G12	<i>Pseudomonas aeruginosa</i>
1221	P1M10000064H07	<i>Pseudomonas aeruginosa</i>
1222	P1M10000065A04	<i>Pseudomonas aeruginosa</i>
1223	P1M10000065B07	<i>Pseudomonas aeruginosa</i>
1224	P1M10000065C03	<i>Pseudomonas aeruginosa</i>
1225	P1M10000065C05	<i>Pseudomonas aeruginosa</i>
1226	P1M10000065D06	<i>Pseudomonas aeruginosa</i>
1227	P1M10000065F01	<i>Pseudomonas aeruginosa</i>
1228	P1M10000065G06	<i>Pseudomonas aeruginosa</i>
1229	P1M10000065H07	<i>Pseudomonas aeruginosa</i>
1230	P1M10000066A10	<i>Pseudomonas aeruginosa</i>
1231	P1M10000066A11	<i>Pseudomonas aeruginosa</i>
1232	P1M10000066F04	<i>Pseudomonas aeruginosa</i>
1233	P1M10000067A05	<i>Pseudomonas aeruginosa</i>
1234	P1M10000067A06	<i>Pseudomonas aeruginosa</i>
1235	P1M10000067A08	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
1236	P1M10000067C04	<i>Pseudomonas aeruginosa</i>
1237	P1M10000067C06	<i>Pseudomonas aeruginosa</i>
1238	P1M10000067D05	<i>Pseudomonas aeruginosa</i>
1239	P1M10000067F05	<i>Pseudomonas aeruginosa</i>
1240	P1M10000067G05	<i>Pseudomonas aeruginosa</i>
1241	P1M10000068A09	<i>Pseudomonas aeruginosa</i>
1242	P1M10000068D04	<i>Pseudomonas aeruginosa</i>
1243	P1M10000068F04	<i>Pseudomonas aeruginosa</i>
1244	P1M10000068F08	<i>Pseudomonas aeruginosa</i>
1245	P1M10000068G01	<i>Pseudomonas aeruginosa</i>
1246	P1M10000068H05	<i>Pseudomonas aeruginosa</i>
1247	P1M10000069D09	<i>Pseudomonas aeruginosa</i>
1248	P1M10000069G06	<i>Pseudomonas aeruginosa</i>
1249	P1M10000069H02	<i>Pseudomonas aeruginosa</i>
1250	P1M10000070A05	<i>Pseudomonas aeruginosa</i>
1251	P1M10000070B10	<i>Pseudomonas aeruginosa</i>
1252	P1M10000070C06	<i>Pseudomonas aeruginosa</i>
1253	P1M10000070D08	<i>Pseudomonas aeruginosa</i>
1254	P1M10000070E03	<i>Pseudomonas aeruginosa</i>
1255	P1M10000070G06	<i>Pseudomonas aeruginosa</i>
1256	P1M10000070G12	<i>Pseudomonas aeruginosa</i>
1257	P1M10000070H06	<i>Pseudomonas aeruginosa</i>
1258	P1M10000071A03	<i>Pseudomonas aeruginosa</i>
1259	P1M10000071C01	<i>Pseudomonas aeruginosa</i>
1260	P1M10000071E04	<i>Pseudomonas aeruginosa</i>
1261	P1M10000071F01	<i>Pseudomonas aeruginosa</i>
1262	P1M10000073A06	<i>Pseudomonas aeruginosa</i>
1263	P1M10000073B10	<i>Pseudomonas aeruginosa</i>
1264	P1M10000073D04	<i>Pseudomonas aeruginosa</i>
1265	P1M10000073D09	<i>Pseudomonas aeruginosa</i>
1266	P1M10000073G03	<i>Pseudomonas aeruginosa</i>
1267	P1M10000074B01	<i>Pseudomonas aeruginosa</i>
1268	P1M10000074B04	<i>Pseudomonas aeruginosa</i>
1269	P1M10000074E04	<i>Pseudomonas aeruginosa</i>
1270	P1M10000074E09	<i>Pseudomonas aeruginosa</i>
1271	P1M10000074F10	<i>Pseudomonas aeruginosa</i>
1272	P1M10000074G12	<i>Pseudomonas aeruginosa</i>
1273	P1M10000075A04	<i>Pseudomonas aeruginosa</i>
1274	P1M10000075B03	<i>Pseudomonas aeruginosa</i>
1275	P1M10000075F02	<i>Pseudomonas aeruginosa</i>
1276	P1M10000075G05	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
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1278	P1M10000076D10	<i>Pseudomonas aeruginosa</i>
1279	P1M10000077A08	<i>Pseudomonas aeruginosa</i>
1280	P1M10000077C08	<i>Pseudomonas aeruginosa</i>
1281	P1M10000077E04	<i>Pseudomonas aeruginosa</i>
1282	P1M10000077H05	<i>Pseudomonas aeruginosa</i>
1283	P1M10000079A10	<i>Pseudomonas aeruginosa</i>
1284	P1M10000079B10	<i>Pseudomonas aeruginosa</i>
1285	P1M10000079C10	<i>Pseudomonas aeruginosa</i>
1286	P1M10000079D01	<i>Pseudomonas aeruginosa</i>
1287	P1M10000079D10	<i>Pseudomonas aeruginosa</i>
1288	P1M10000079F06	<i>Pseudomonas aeruginosa</i>
1289	P1M10000080B01	<i>Pseudomonas aeruginosa</i>
1290	P1M10000080B06	<i>Pseudomonas aeruginosa</i>
1291	P1M10000080C01	<i>Pseudomonas aeruginosa</i>
1292	P1M10000080C06	<i>Pseudomonas aeruginosa</i>
1293	P1M10000080E04	<i>Pseudomonas aeruginosa</i>
1294	P1M10000081D12	<i>Pseudomonas aeruginosa</i>
1295	P1M10000081G05	<i>Pseudomonas aeruginosa</i>
1296	P1M10000081H05	<i>Pseudomonas aeruginosa</i>
1297	P1M10000082A05	<i>Pseudomonas aeruginosa</i>
1298	P1M10000082B04	<i>Pseudomonas aeruginosa</i>
1299	P1M10000082C05	<i>Pseudomonas aeruginosa</i>
1300	P1M10000082D05	<i>Pseudomonas aeruginosa</i>
1301	P1M10000082E05	<i>Pseudomonas aeruginosa</i>
1302	P1M10000083A11	<i>Pseudomonas aeruginosa</i>
1303	P1M10000083B01	<i>Pseudomonas aeruginosa</i>
1304	P1M10000083B12	<i>Pseudomonas aeruginosa</i>
1305	P1M10000083C11	<i>Pseudomonas aeruginosa</i>
1306	P1M10000083C12	<i>Pseudomonas aeruginosa</i>
1307	P1M10000084A04	<i>Pseudomonas aeruginosa</i>
1308	P1M10000084D03	<i>Pseudomonas aeruginosa</i>
1309	P1M10000084E04	<i>Pseudomonas aeruginosa</i>
1310	P1M10000084E11	<i>Pseudomonas aeruginosa</i>
1311	P1M10000084F08	<i>Pseudomonas aeruginosa</i>
1312	P1M10000085D06	<i>Pseudomonas aeruginosa</i>
1313	P1M10000086A02	<i>Pseudomonas aeruginosa</i>
1314	P1M10000086B01	<i>Pseudomonas aeruginosa</i>
1315	P1M10000086D02	<i>Pseudomonas aeruginosa</i>
1316	P1M10000086E05	<i>Pseudomonas aeruginosa</i>
1317	P1M10000087A11	<i>Pseudomonas aeruginosa</i>

SeqID	Clone name	Organism
1318	P1M10000087C09	<i>Pseudomonas aeruginosa</i>
1319	P1M10000087E04	<i>Pseudomonas aeruginosa</i>
1320	P1M10000087F04	<i>Pseudomonas aeruginosa</i>
1321	P1M10000087F09	<i>Pseudomonas aeruginosa</i>
1322	P1M10000088A07	<i>Pseudomonas aeruginosa</i>
1323	P1M10000088D06	<i>Pseudomonas aeruginosa</i>
1324	P1M10000089C08	<i>Pseudomonas aeruginosa</i>
1325	P1M10000089D11	<i>Pseudomonas aeruginosa</i>
1326	P1M10000089G08	<i>Pseudomonas aeruginosa</i>
1327	P1M10000090B11	<i>Pseudomonas aeruginosa</i>
1328	P1M10000090F06	<i>Pseudomonas aeruginosa</i>
1329	P1M10000090F08	<i>Pseudomonas aeruginosa</i>
1330	P1M10000091D02	<i>Pseudomonas aeruginosa</i>
1331	P1M10000091E09	<i>Pseudomonas aeruginosa</i>
1332	P1M10000091G10	<i>Pseudomonas aeruginosa</i>
1333	P1M10000092B02	<i>Pseudomonas aeruginosa</i>
1334	P1M10000092B10	<i>Pseudomonas aeruginosa</i>
1335	P1M10000092D09	<i>Pseudomonas aeruginosa</i>
1336	P1M10000092E02	<i>Pseudomonas aeruginosa</i>
1337	P1M10000092F05	<i>Pseudomonas aeruginosa</i>
1338	P1M10000093A03	<i>Pseudomonas aeruginosa</i>
1339	P1M10000093B09	<i>Pseudomonas aeruginosa</i>
1340	P1M10000093C08	<i>Pseudomonas aeruginosa</i>
1341	P1M10000093E09	<i>Pseudomonas aeruginosa</i>
1342	P1M10000093F03	<i>Pseudomonas aeruginosa</i>
1343	P1M10000093H07	<i>Pseudomonas aeruginosa</i>
1344	P1M10000094F04	<i>Pseudomonas aeruginosa</i>
1345	P1M10000094H03	<i>Pseudomonas aeruginosa</i>
1346	P1M10000095C01	<i>Pseudomonas aeruginosa</i>
1347	P1M10000095C09	<i>Pseudomonas aeruginosa</i>
1348	P1M10000095E04	<i>Pseudomonas aeruginosa</i>
1349	P1M10000095G04	<i>Pseudomonas aeruginosa</i>
1350	P1M10000096E04	<i>Pseudomonas aeruginosa</i>
1351	P1M10000096E12	<i>Pseudomonas aeruginosa</i>
1352	ID2	<i>Pseudomonas aeruginosa</i>
1353	4.1	<i>Pseudomonas aeruginosa</i>
1354	S1M10000001A05	<i>Staphylococcus aureus</i>
1355	S1M10000001A08	<i>Staphylococcus aureus</i>
1356	S1M10000001A09	<i>Staphylococcus aureus</i>
1357	S1M10000001A10	<i>Staphylococcus aureus</i>
1358	S1M10000001C06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1359	S1M10000001D01	<i>Staphylococcus aureus</i>
1360	S1M10000001D02	<i>Staphylococcus aureus</i>
1361	S1M10000001D06	<i>Staphylococcus aureus</i>
1362	S1M10000001D07	<i>Staphylococcus aureus</i>
1363	S1M10000001E02	<i>Staphylococcus aureus</i>
1364	S1M10000001E04	<i>Staphylococcus aureus</i>
1365	S1M10000001E05	<i>Staphylococcus aureus</i>
1366	S1M10000001E09	<i>Staphylococcus aureus</i>
1367	S1M10000001E10	<i>Staphylococcus aureus</i>
1368	S1M10000001E11	<i>Staphylococcus aureus</i>
1369	S1M10000001F02	<i>Staphylococcus aureus</i>
1370	S1M10000001F04	<i>Staphylococcus aureus</i>
1371	S1M10000001F08	<i>Staphylococcus aureus</i>
1372	S1M10000001F09	<i>Staphylococcus aureus</i>
1373	S1M10000001F10	<i>Staphylococcus aureus</i>
1374	S1M10000001F11	<i>Staphylococcus aureus</i>
1375	S1M10000001G01	<i>Staphylococcus aureus</i>
1376	S1M10000001G07	<i>Staphylococcus aureus</i>
1377	S1M10000001G08	<i>Staphylococcus aureus</i>
1378	S1M10000001G10	<i>Staphylococcus aureus</i>
1379	S1M10000002A02	<i>Staphylococcus aureus</i>
1380	S1M10000002A09	<i>Staphylococcus aureus</i>
1381	S1M10000002A10	<i>Staphylococcus aureus</i>
1382	S1M10000002A12	<i>Staphylococcus aureus</i>
1383	S1M10000002B01	<i>Staphylococcus aureus</i>
1384	S1M10000002B03	<i>Staphylococcus aureus</i>
1385	S1M10000002B04	<i>Staphylococcus aureus</i>
1386	S1M10000002B05	<i>Staphylococcus aureus</i>
1387	S1M10000002B06	<i>Staphylococcus aureus</i>
1388	S1M10000002B07	<i>Staphylococcus aureus</i>
1389	S1M10000002B09	<i>Staphylococcus aureus</i>
1390	S1M10000002B11	<i>Staphylococcus aureus</i>
1391	S1M10000002C02	<i>Staphylococcus aureus</i>
1392	S1M10000002C09	<i>Staphylococcus aureus</i>
1393	S1M10000002C10	<i>Staphylococcus aureus</i>
1394	S1M10000002C11	<i>Staphylococcus aureus</i>
1395	S1M10000002C12	<i>Staphylococcus aureus</i>
1396	S1M10000002D01	<i>Staphylococcus aureus</i>
1397	S1M10000002D02	<i>Staphylococcus aureus</i>
1398	S1M10000002D03	<i>Staphylococcus aureus</i>
1399	S1M10000002D05	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1400	S1M10000002D07	<i>Staphylococcus aureus</i>
1401	S1M10000002D08	<i>Staphylococcus aureus</i>
1402	S1M10000002D10	<i>Staphylococcus aureus</i>
1403	S1M10000002D12	<i>Staphylococcus aureus</i>
1404	S1M10000002E01	<i>Staphylococcus aureus</i>
1405	S1M10000002E02	<i>Staphylococcus aureus</i>
1406	S1M10000002E07	<i>Staphylococcus aureus</i>
1407	S1M10000002E09	<i>Staphylococcus aureus</i>
1408	S1M10000002E11	<i>Staphylococcus aureus</i>
1409	S1M10000002E12	<i>Staphylococcus aureus</i>
1410	S1M10000002F01	<i>Staphylococcus aureus</i>
1411	S1M10000002F02	<i>Staphylococcus aureus</i>
1412	S1M10000002F04	<i>Staphylococcus aureus</i>
1413	S1M10000002F09	<i>Staphylococcus aureus</i>
1414	S1M10000002F12	<i>Staphylococcus aureus</i>
1415	S1M10000002G01	<i>Staphylococcus aureus</i>
1416	S1M10000002G03	<i>Staphylococcus aureus</i>
1417	S1M10000002G05	<i>Staphylococcus aureus</i>
1418	S1M10000002G06	<i>Staphylococcus aureus</i>
1419	S1M10000002G07	<i>Staphylococcus aureus</i>
1420	S1M10000002G08	<i>Staphylococcus aureus</i>
1421	S1M10000002G09	<i>Staphylococcus aureus</i>
1422	S1M10000002G10	<i>Staphylococcus aureus</i>
1423	S1M10000002G11	<i>Staphylococcus aureus</i>
1424	S1M10000002G12	<i>Staphylococcus aureus</i>
1425	S1M10000003A01	<i>Staphylococcus aureus</i>
1426	S1M10000003A02	<i>Staphylococcus aureus</i>
1427	S1M10000003A03	<i>Staphylococcus aureus</i>
1428	S1M10000003A04	<i>Staphylococcus aureus</i>
1429	S1M10000003A06	<i>Staphylococcus aureus</i>
1430	S1M10000003A07	<i>Staphylococcus aureus</i>
1431	S1M10000003A08	<i>Staphylococcus aureus</i>
1432	S1M10000003A10	<i>Staphylococcus aureus</i>
1433	S1M10000003A11	<i>Staphylococcus aureus</i>
1434	S1M10000003B06	<i>Staphylococcus aureus</i>
1435	S1M10000003B08	<i>Staphylococcus aureus</i>
1436	S1M10000003B09	<i>Staphylococcus aureus</i>
1437	S1M10000003B12	<i>Staphylococcus aureus</i>
1438	S1M10000003C06	<i>Staphylococcus aureus</i>
1439	S1M10000003C07	<i>Staphylococcus aureus</i>
1440	S1M10000003C10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1441	S1M10000003C12	<i>Staphylococcus aureus</i>
1442	S1M10000003D05	<i>Staphylococcus aureus</i>
1443	S1M10000003D06	<i>Staphylococcus aureus</i>
1444	S1M10000003D08	<i>Staphylococcus aureus</i>
1445	S1M10000003D10	<i>Staphylococcus aureus</i>
1446	S1M10000003E07	<i>Staphylococcus aureus</i>
1447	S1M10000003E09	<i>Staphylococcus aureus</i>
1448	S1M10000003E10	<i>Staphylococcus aureus</i>
1449	S1M10000003E11	<i>Staphylococcus aureus</i>
1450	S1M10000003F02	<i>Staphylococcus aureus</i>
1451	S1M10000003F05	<i>Staphylococcus aureus</i>
1452	S1M10000003F06	<i>Staphylococcus aureus</i>
1453	S1M10000003F07	<i>Staphylococcus aureus</i>
1454	S1M10000003F08	<i>Staphylococcus aureus</i>
1455	S1M10000003F12	<i>Staphylococcus aureus</i>
1456	S1M10000003G03	<i>Staphylococcus aureus</i>
1457	S1M10000003G04	<i>Staphylococcus aureus</i>
1458	S1M10000003G08	<i>Staphylococcus aureus</i>
1459	S1M10000003G10	<i>Staphylococcus aureus</i>
1460	S1M10000004A04	<i>Staphylococcus aureus</i>
1461	S1M10000004A06	<i>Staphylococcus aureus</i>
1462	S1M10000004A07	<i>Staphylococcus aureus</i>
1463	S1M10000004A11	<i>Staphylococcus aureus</i>
1464	S1M10000004A12	<i>Staphylococcus aureus</i>
1465	S1M10000004B03	<i>Staphylococcus aureus</i>
1466	S1M10000004B04	<i>Staphylococcus aureus</i>
1467	S1M10000004B06	<i>Staphylococcus aureus</i>
1468	S1M10000004B08	<i>Staphylococcus aureus</i>
1469	S1M10000004B09	<i>Staphylococcus aureus</i>
1470	S1M10000004B11	<i>Staphylococcus aureus</i>
1471	S1M10000004C01	<i>Staphylococcus aureus</i>
1472	S1M10000004C02	<i>Staphylococcus aureus</i>
1473	S1M10000004C03	<i>Staphylococcus aureus</i>
1474	S1M10000004C06	<i>Staphylococcus aureus</i>
1475	S1M10000004C07	<i>Staphylococcus aureus</i>
1476	S1M10000004C08	<i>Staphylococcus aureus</i>
1477	S1M10000004C09	<i>Staphylococcus aureus</i>
1478	S1M10000004C10	<i>Staphylococcus aureus</i>
1479	S1M10000004C12	<i>Staphylococcus aureus</i>
1480	S1M10000004D01	<i>Staphylococcus aureus</i>
1481	S1M10000004D03	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1482	S1M10000004D04	<i>Staphylococcus aureus</i>
1483	S1M10000004D06	<i>Staphylococcus aureus</i>
1484	S1M10000004D07	<i>Staphylococcus aureus</i>
1485	S1M10000004D08	<i>Staphylococcus aureus</i>
1486	S1M10000004D10	<i>Staphylococcus aureus</i>
1487	S1M10000004D12	<i>Staphylococcus aureus</i>
1488	S1M10000004E03	<i>Staphylococcus aureus</i>
1489	S1M10000004E04	<i>Staphylococcus aureus</i>
1490	S1M10000004E06	<i>Staphylococcus aureus</i>
1491	S1M10000004E07	<i>Staphylococcus aureus</i>
1492	S1M10000004E11	<i>Staphylococcus aureus</i>
1493	S1M10000004E12	<i>Staphylococcus aureus</i>
1494	S1M10000004F01	<i>Staphylococcus aureus</i>
1495	S1M10000004F02	<i>Staphylococcus aureus</i>
1496	S1M10000004F06	<i>Staphylococcus aureus</i>
1497	S1M10000004F07	<i>Staphylococcus aureus</i>
1498	S1M10000004F08	<i>Staphylococcus aureus</i>
1499	S1M10000004F09	<i>Staphylococcus aureus</i>
1500	S1M10000004F12	<i>Staphylococcus aureus</i>
1501	S1M10000004G01	<i>Staphylococcus aureus</i>
1502	S1M10000004G02	<i>Staphylococcus aureus</i>
1503	S1M10000004G03	<i>Staphylococcus aureus</i>
1504	S1M10000004G05	<i>Staphylococcus aureus</i>
1505	S1M10000004G06	<i>Staphylococcus aureus</i>
1506	S1M10000004G07	<i>Staphylococcus aureus</i>
1507	S1M10000004G09	<i>Staphylococcus aureus</i>
1508	S1M10000004G12	<i>Staphylococcus aureus</i>
1509	S1M10000005A01	<i>Staphylococcus aureus</i>
1510	S1M10000005A03	<i>Staphylococcus aureus</i>
1511	S1M10000005A05	<i>Staphylococcus aureus</i>
1512	S1M10000005A06	<i>Staphylococcus aureus</i>
1513	S1M10000005A07	<i>Staphylococcus aureus</i>
1514	S1M10000005A08	<i>Staphylococcus aureus</i>
1515	S1M10000005A09	<i>Staphylococcus aureus</i>
1516	S1M10000005A10	<i>Staphylococcus aureus</i>
1517	S1M10000005A11	<i>Staphylococcus aureus</i>
1518	S1M10000005B02	<i>Staphylococcus aureus</i>
1519	S1M10000005B04	<i>Staphylococcus aureus</i>
1520	S1M10000005B07	<i>Staphylococcus aureus</i>
1521	S1M10000005B08	<i>Staphylococcus aureus</i>
1522	S1M10000005B09	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1523	S1M10000005B12	<i>Staphylococcus aureus</i>
1524	S1M10000005C01	<i>Staphylococcus aureus</i>
1525	S1M10000005C05	<i>Staphylococcus aureus</i>
1526	S1M10000005C06	<i>Staphylococcus aureus</i>
1527	S1M10000005C09	<i>Staphylococcus aureus</i>
1528	S1M10000005C11	<i>Staphylococcus aureus</i>
1529	S1M10000005D01	<i>Staphylococcus aureus</i>
1530	S1M10000005D02	<i>Staphylococcus aureus</i>
1531	S1M10000005D03	<i>Staphylococcus aureus</i>
1532	S1M10000005D04	<i>Staphylococcus aureus</i>
1533	S1M10000005D05	<i>Staphylococcus aureus</i>
1534	S1M10000005D06	<i>Staphylococcus aureus</i>
1535	S1M10000005D07	<i>Staphylococcus aureus</i>
1536	S1M10000005D08	<i>Staphylococcus aureus</i>
1537	S1M10000005D09	<i>Staphylococcus aureus</i>
1538	S1M10000005D11	<i>Staphylococcus aureus</i>
1539	S1M10000005D12	<i>Staphylococcus aureus</i>
1540	S1M10000005E01	<i>Staphylococcus aureus</i>
1541	S1M10000005E02	<i>Staphylococcus aureus</i>
1542	S1M10000005E05	<i>Staphylococcus aureus</i>
1543	S1M10000005E06	<i>Staphylococcus aureus</i>
1544	S1M10000005E07	<i>Staphylococcus aureus</i>
1545	S1M10000005E08	<i>Staphylococcus aureus</i>
1546	S1M10000005E10	<i>Staphylococcus aureus</i>
1547	S1M10000005E11	<i>Staphylococcus aureus</i>
1548	S1M10000005E12	<i>Staphylococcus aureus</i>
1549	S1M10000005F02	<i>Staphylococcus aureus</i>
1550	S1M10000005F03	<i>Staphylococcus aureus</i>
1551	S1M10000005F04	<i>Staphylococcus aureus</i>
1552	S1M10000006A03	<i>Staphylococcus aureus</i>
1553	S1M10000006A04	<i>Staphylococcus aureus</i>
1554	S1M10000006A05	<i>Staphylococcus aureus</i>
1555	S1M10000006A07	<i>Staphylococcus aureus</i>
1556	S1M10000006A08	<i>Staphylococcus aureus</i>
1557	S1M10000006A10	<i>Staphylococcus aureus</i>
1558	S1M10000006A12	<i>Staphylococcus aureus</i>
1559	S1M10000006B02	<i>Staphylococcus aureus</i>
1560	S1M10000006B03	<i>Staphylococcus aureus</i>
1561	S1M10000006B04	<i>Staphylococcus aureus</i>
1562	S1M10000006B07	<i>Staphylococcus aureus</i>
1563	S1M10000006B10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1564	S1M10000006B11	<i>Staphylococcus aureus</i>
1565	S1M10000006C02	<i>Staphylococcus aureus</i>
1566	S1M10000006C04	<i>Staphylococcus aureus</i>
1567	S1M10000006C06	<i>Staphylococcus aureus</i>
1568	S1M10000006C07	<i>Staphylococcus aureus</i>
1569	S1M10000006C08	<i>Staphylococcus aureus</i>
1570	S1M10000006C10	<i>Staphylococcus aureus</i>
1571	S1M10000006D03	<i>Staphylococcus aureus</i>
1572	S1M10000006D05	<i>Staphylococcus aureus</i>
1573	S1M10000006D06	<i>Staphylococcus aureus</i>
1574	S1M10000006D07	<i>Staphylococcus aureus</i>
1575	S1M10000006D08	<i>Staphylococcus aureus</i>
1576	S1M10000006E02	<i>Staphylococcus aureus</i>
1577	S1M10000006E03	<i>Staphylococcus aureus</i>
1578	S1M10000006E04	<i>Staphylococcus aureus</i>
1579	S1M10000006E07	<i>Staphylococcus aureus</i>
1580	S1M10000006E08	<i>Staphylococcus aureus</i>
1581	S1M10000006F01	<i>Staphylococcus aureus</i>
1582	S1M10000006F02	<i>Staphylococcus aureus</i>
1583	S1M10000006F03	<i>Staphylococcus aureus</i>
1584	S1M10000006F04	<i>Staphylococcus aureus</i>
1585	S1M10000006F06	<i>Staphylococcus aureus</i>
1586	S1M10000006G02	<i>Staphylococcus aureus</i>
1587	S1M10000006G03	<i>Staphylococcus aureus</i>
1588	S1M10000006G05	<i>Staphylococcus aureus</i>
1589	S1M10000006G06	<i>Staphylococcus aureus</i>
1590	S1M10000006G07	<i>Staphylococcus aureus</i>
1591	S1M10000006G09	<i>Staphylococcus aureus</i>
1592	S1M10000006G10	<i>Staphylococcus aureus</i>
1593	S1M10000006G11	<i>Staphylococcus aureus</i>
1594	S1M10000007A02	<i>Staphylococcus aureus</i>
1595	S1M10000007A03	<i>Staphylococcus aureus</i>
1596	S1M10000007B02	<i>Staphylococcus aureus</i>
1597	S1M10000007B11	<i>Staphylococcus aureus</i>
1598	S1M10000007C02	<i>Staphylococcus aureus</i>
1599	S1M10000007C04	<i>Staphylococcus aureus</i>
1600	S1M10000007C05	<i>Staphylococcus aureus</i>
1601	S1M10000007C06	<i>Staphylococcus aureus</i>
1602	S1M10000007C07	<i>Staphylococcus aureus</i>
1603	S1M10000007C08	<i>Staphylococcus aureus</i>
1604	S1M10000007C09	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1605	S1M10000007D03	<i>Staphylococcus aureus</i>
1606	S1M10000007D06	<i>Staphylococcus aureus</i>
1607	S1M10000007D08	<i>Staphylococcus aureus</i>
1608	S1M10000007D10	<i>Staphylococcus aureus</i>
1609	S1M10000007D11	<i>Staphylococcus aureus</i>
1610	S1M10000007E04	<i>Staphylococcus aureus</i>
1611	S1M10000007E06	<i>Staphylococcus aureus</i>
1612	S1M10000007E07	<i>Staphylococcus aureus</i>
1613	S1M10000007F01	<i>Staphylococcus aureus</i>
1614	S1M10000007F02	<i>Staphylococcus aureus</i>
1615	S1M10000007F04	<i>Staphylococcus aureus</i>
1616	S1M10000007F08	<i>Staphylococcus aureus</i>
1617	S1M10000007F09	<i>Staphylococcus aureus</i>
1618	S1M10000007F10	<i>Staphylococcus aureus</i>
1619	S1M10000007F11	<i>Staphylococcus aureus</i>
1620	S1M10000007F12	<i>Staphylococcus aureus</i>
1621	S1M10000007G02	<i>Staphylococcus aureus</i>
1622	S1M10000007G03	<i>Staphylococcus aureus</i>
1623	S1M10000007G05	<i>Staphylococcus aureus</i>
1624	S1M10000007G07	<i>Staphylococcus aureus</i>
1625	S1M10000007G08	<i>Staphylococcus aureus</i>
1626	S1M10000008A03	<i>Staphylococcus aureus</i>
1627	S1M10000008A04	<i>Staphylococcus aureus</i>
1628	S1M10000008A05	<i>Staphylococcus aureus</i>
1629	S1M10000008A08	<i>Staphylococcus aureus</i>
1630	S1M10000008A09	<i>Staphylococcus aureus</i>
1631	S1M10000008A12	<i>Staphylococcus aureus</i>
1632	S1M10000008B03	<i>Staphylococcus aureus</i>
1633	S1M10000008B04	<i>Staphylococcus aureus</i>
1634	S1M10000008B06	<i>Staphylococcus aureus</i>
1635	S1M10000008B08	<i>Staphylococcus aureus</i>
1636	S1M10000008B09	<i>Staphylococcus aureus</i>
1637	S1M10000008B10	<i>Staphylococcus aureus</i>
1638	S1M10000008C05	<i>Staphylococcus aureus</i>
1639	S1M10000008C06	<i>Staphylococcus aureus</i>
1640	S1M10000008C07	<i>Staphylococcus aureus</i>
1641	S1M10000008C08	<i>Staphylococcus aureus</i>
1642	S1M10000008C09	<i>Staphylococcus aureus</i>
1643	S1M10000008D05	<i>Staphylococcus aureus</i>
1644	S1M10000008D09	<i>Staphylococcus aureus</i>
1645	S1M10000008E05	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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1647	S1M10000008E09	<i>Staphylococcus aureus</i>
1648	S1M10000008E10	<i>Staphylococcus aureus</i>
1649	S1M10000008F01	<i>Staphylococcus aureus</i>
1650	S1M10000008F02	<i>Staphylococcus aureus</i>
1651	S1M10000008F03	<i>Staphylococcus aureus</i>
1652	S1M10000008F06	<i>Staphylococcus aureus</i>
1653	S1M10000008F08	<i>Staphylococcus aureus</i>
1654	S1M10000008F09	<i>Staphylococcus aureus</i>
1655	S1M10000008F10	<i>Staphylococcus aureus</i>
1656	S1M10000008F11	<i>Staphylococcus aureus</i>
1657	S1M10000008G02	<i>Staphylococcus aureus</i>
1658	S1M10000008G03	<i>Staphylococcus aureus</i>
1659	S1M10000008G05	<i>Staphylococcus aureus</i>
1660	S1M10000009A02	<i>Staphylococcus aureus</i>
1661	S1M10000009A04	<i>Staphylococcus aureus</i>
1662	S1M10000009A07	<i>Staphylococcus aureus</i>
1663	S1M10000009A08	<i>Staphylococcus aureus</i>
1664	S1M10000009A09	<i>Staphylococcus aureus</i>
1665	S1M10000009A10	<i>Staphylococcus aureus</i>
1666	S1M10000009A11	<i>Staphylococcus aureus</i>
1667	S1M10000009B01	<i>Staphylococcus aureus</i>
1668	S1M10000009B02	<i>Staphylococcus aureus</i>
1669	S1M10000009B03	<i>Staphylococcus aureus</i>
1670	S1M10000009B04	<i>Staphylococcus aureus</i>
1671	S1M10000009B05	<i>Staphylococcus aureus</i>
1672	S1M10000009B06	<i>Staphylococcus aureus</i>
1673	S1M10000009B07	<i>Staphylococcus aureus</i>
1674	S1M10000009B10	<i>Staphylococcus aureus</i>
1675	S1M10000009B11	<i>Staphylococcus aureus</i>
1676	S1M10000009B12	<i>Staphylococcus aureus</i>
1677	S1M10000009C01	<i>Staphylococcus aureus</i>
1678	S1M10000009C02	<i>Staphylococcus aureus</i>
1679	S1M10000009C05	<i>Staphylococcus aureus</i>
1680	S1M10000009C06	<i>Staphylococcus aureus</i>
1681	S1M10000009C07	<i>Staphylococcus aureus</i>
1682	S1M10000009C08	<i>Staphylococcus aureus</i>
1683	S1M10000009C09	<i>Staphylococcus aureus</i>
1684	S1M10000009C10	<i>Staphylococcus aureus</i>
1685	S1M10000009C11	<i>Staphylococcus aureus</i>
1686	S1M10000009D01	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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1688	S1M10000009D03	<i>Staphylococcus aureus</i>
1689	S1M10000009D04	<i>Staphylococcus aureus</i>
1690	S1M10000009D05	<i>Staphylococcus aureus</i>
1691	S1M10000009D07	<i>Staphylococcus aureus</i>
1692	S1M10000009D09	<i>Staphylococcus aureus</i>
1693	S1M10000009D11	<i>Staphylococcus aureus</i>
1694	S1M10000009E02	<i>Staphylococcus aureus</i>
1695	S1M10000009E06	<i>Staphylococcus aureus</i>
1696	S1M10000009E08	<i>Staphylococcus aureus</i>
1697	S1M10000009E09	<i>Staphylococcus aureus</i>
1698	S1M10000009E11	<i>Staphylococcus aureus</i>
1699	S1M10000009E12	<i>Staphylococcus aureus</i>
1700	S1M10000009F01	<i>Staphylococcus aureus</i>
1701	S1M10000009F02	<i>Staphylococcus aureus</i>
1702	S1M10000009F03	<i>Staphylococcus aureus</i>
1703	S1M10000009F05	<i>Staphylococcus aureus</i>
1704	S1M10000009F06	<i>Staphylococcus aureus</i>
1705	S1M10000009F07	<i>Staphylococcus aureus</i>
1706	S1M10000009F09	<i>Staphylococcus aureus</i>
1707	S1M10000009F10	<i>Staphylococcus aureus</i>
1708	S1M10000009G02	<i>Staphylococcus aureus</i>
1709	S1M10000009G03	<i>Staphylococcus aureus</i>
1710	S1M10000009G05	<i>Staphylococcus aureus</i>
1711	S1M10000009G06	<i>Staphylococcus aureus</i>
1712	S1M10000009G07	<i>Staphylococcus aureus</i>
1713	S1M10000009G09	<i>Staphylococcus aureus</i>
1714	S1M10000009G10	<i>Staphylococcus aureus</i>
1715	S1M10000009G11	<i>Staphylococcus aureus</i>
1716	S1M10000009H01	<i>Staphylococcus aureus</i>
1717	S1M10000009H02	<i>Staphylococcus aureus</i>
1718	S1M10000009H03	<i>Staphylococcus aureus</i>
1719	S1M10000009H05	<i>Staphylococcus aureus</i>
1720	S1M10000009H07	<i>Staphylococcus aureus</i>
1721	S1M10000009H09	<i>Staphylococcus aureus</i>
1722	S1M10000009H11	<i>Staphylococcus aureus</i>
1723	S1M10000011A02	<i>Staphylococcus aureus</i>
1724	S1M10000011A03	<i>Staphylococcus aureus</i>
1725	S1M10000011A04	<i>Staphylococcus aureus</i>
1726	S1M10000011A06	<i>Staphylococcus aureus</i>
1727	S1M10000011B01	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1728	S1M10000011B02	<i>Staphylococcus aureus</i>
1729	S1M10000011B03	<i>Staphylococcus aureus</i>
1730	S1M10000011B04	<i>Staphylococcus aureus</i>
1731	S1M10000011B05	<i>Staphylococcus aureus</i>
1732	S1M10000011C01	<i>Staphylococcus aureus</i>
1733	S1M10000011C05	<i>Staphylococcus aureus</i>
1734	S1M10000011C06	<i>Staphylococcus aureus</i>
1735	S1M10000011D01	<i>Staphylococcus aureus</i>
1736	S1M10000011D02	<i>Staphylococcus aureus</i>
1737	S1M10000011D04	<i>Staphylococcus aureus</i>
1738	S1M10000011D06	<i>Staphylococcus aureus</i>
1739	S1M10000011E02	<i>Staphylococcus aureus</i>
1740	S1M10000011E03	<i>Staphylococcus aureus</i>
1741	S1M10000011E04	<i>Staphylococcus aureus</i>
1742	S1M10000011F01	<i>Staphylococcus aureus</i>
1743	S1M10000011F03	<i>Staphylococcus aureus</i>
1744	S1M10000011F04	<i>Staphylococcus aureus</i>
1745	S1M10000011F06	<i>Staphylococcus aureus</i>
1746	S1M10000011G01	<i>Staphylococcus aureus</i>
1747	S1M10000011G03	<i>Staphylococcus aureus</i>
1748	S1M10000011G04	<i>Staphylococcus aureus</i>
1749	S1M10000011G05	<i>Staphylococcus aureus</i>
1750	S1M10000011G06	<i>Staphylococcus aureus</i>
1751	S1M10000011H01	<i>Staphylococcus aureus</i>
1752	S1M10000011H03	<i>Staphylococcus aureus</i>
1753	S1M10000011H04	<i>Staphylococcus aureus</i>
1754	S1M10000012A02	<i>Staphylococcus aureus</i>
1755	S1M10000012A06	<i>Staphylococcus aureus</i>
1756	S1M10000012A08	<i>Staphylococcus aureus</i>
1757	S1M10000012A09	<i>Staphylococcus aureus</i>
1758	S1M10000012A10	<i>Staphylococcus aureus</i>
1759	S1M10000012A11	<i>Staphylococcus aureus</i>
1760	S1M10000012B01	<i>Staphylococcus aureus</i>
1761	S1M10000012B05	<i>Staphylococcus aureus</i>
1762	S1M10000012B06	<i>Staphylococcus aureus</i>
1763	S1M10000012B07	<i>Staphylococcus aureus</i>
1764	S1M10000012B11	<i>Staphylococcus aureus</i>
1765	S1M10000012C01	<i>Staphylococcus aureus</i>
1766	S1M10000012C03	<i>Staphylococcus aureus</i>
1767	S1M10000012C04	<i>Staphylococcus aureus</i>
1768	S1M10000012C05	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1769	S1M10000012C06	<i>Staphylococcus aureus</i>
1770	S1M10000012C11	<i>Staphylococcus aureus</i>
1771	S1M10000012C12	<i>Staphylococcus aureus</i>
1772	S1M10000012D04	<i>Staphylococcus aureus</i>
1773	S1M10000012D06	<i>Staphylococcus aureus</i>
1774	S1M10000012D07	<i>Staphylococcus aureus</i>
1775	S1M10000012D08	<i>Staphylococcus aureus</i>
1776	S1M10000012D09	<i>Staphylococcus aureus</i>
1777	S1M10000012D12	<i>Staphylococcus aureus</i>
1778	S1M10000012E01	<i>Staphylococcus aureus</i>
1779	S1M10000012E02	<i>Staphylococcus aureus</i>
1780	S1M10000012E04	<i>Staphylococcus aureus</i>
1781	S1M10000012E07	<i>Staphylococcus aureus</i>
1782	S1M10000012E08	<i>Staphylococcus aureus</i>
1783	S1M10000012E12	<i>Staphylococcus aureus</i>
1784	S1M10000012F04	<i>Staphylococcus aureus</i>
1785	S1M10000012F07	<i>Staphylococcus aureus</i>
1786	S1M10000012F08	<i>Staphylococcus aureus</i>
1787	S1M10000012F09	<i>Staphylococcus aureus</i>
1788	S1M10000012F10	<i>Staphylococcus aureus</i>
1789	S1M10000012F11	<i>Staphylococcus aureus</i>
1790	S1M10000012F12	<i>Staphylococcus aureus</i>
1791	S1M10000012G01	<i>Staphylococcus aureus</i>
1792	S1M10000012G02	<i>Staphylococcus aureus</i>
1793	S1M10000012G03	<i>Staphylococcus aureus</i>
1794	S1M10000012G06	<i>Staphylococcus aureus</i>
1795	S1M10000012G07	<i>Staphylococcus aureus</i>
1796	S1M10000012G08	<i>Staphylococcus aureus</i>
1797	S1M10000012G10	<i>Staphylococcus aureus</i>
1798	S1M10000012H05	<i>Staphylococcus aureus</i>
1799	S1M10000012H08	<i>Staphylococcus aureus</i>
1800	S1M10000012H09	<i>Staphylococcus aureus</i>
1801	S1M10000012H10	<i>Staphylococcus aureus</i>
1802	S1M10000012H11	<i>Staphylococcus aureus</i>
1803	S1M10000013A02	<i>Staphylococcus aureus</i>
1804	S1M10000013A03	<i>Staphylococcus aureus</i>
1805	S1M10000013A05	<i>Staphylococcus aureus</i>
1806	S1M10000013A07	<i>Staphylococcus aureus</i>
1807	S1M10000013A08	<i>Staphylococcus aureus</i>
1808	S1M10000013A09	<i>Staphylococcus aureus</i>
1809	S1M10000013A10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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1811	S1M10000013A12	<i>Staphylococcus aureus</i>
1812	S1M10000013B02	<i>Staphylococcus aureus</i>
1813	S1M10000013B03	<i>Staphylococcus aureus</i>
1814	S1M10000013B04	<i>Staphylococcus aureus</i>
1815	S1M10000013B05	<i>Staphylococcus aureus</i>
1816	S1M10000013B06	<i>Staphylococcus aureus</i>
1817	S1M10000013B07	<i>Staphylococcus aureus</i>
1818	S1M10000013B09	<i>Staphylococcus aureus</i>
1819	S1M10000013B11	<i>Staphylococcus aureus</i>
1820	S1M10000013C03	<i>Staphylococcus aureus</i>
1821	S1M10000013C05	<i>Staphylococcus aureus</i>
1822	S1M10000013C07	<i>Staphylococcus aureus</i>
1823	S1M10000013C08	<i>Staphylococcus aureus</i>
1824	S1M10000013C09	<i>Staphylococcus aureus</i>
1825	S1M10000013C10	<i>Staphylococcus aureus</i>
1826	S1M10000013C11	<i>Staphylococcus aureus</i>
1827	S1M10000013C12	<i>Staphylococcus aureus</i>
1828	S1M10000013D08	<i>Staphylococcus aureus</i>
1829	S1M10000013D09	<i>Staphylococcus aureus</i>
1830	S1M10000013D11	<i>Staphylococcus aureus</i>
1831	S1M10000013E01	<i>Staphylococcus aureus</i>
1832	S1M10000013E02	<i>Staphylococcus aureus</i>
1833	S1M10000013E04	<i>Staphylococcus aureus</i>
1834	S1M10000013E06	<i>Staphylococcus aureus</i>
1835	S1M10000013E08	<i>Staphylococcus aureus</i>
1836	S1M10000013E09	<i>Staphylococcus aureus</i>
1837	S1M10000013E10	<i>Staphylococcus aureus</i>
1838	S1M10000013F02	<i>Staphylococcus aureus</i>
1839	S1M10000013F03	<i>Staphylococcus aureus</i>
1840	S1M10000013F06	<i>Staphylococcus aureus</i>
1841	S1M10000013F07	<i>Staphylococcus aureus</i>
1842	S1M10000013F08	<i>Staphylococcus aureus</i>
1843	S1M10000013F09	<i>Staphylococcus aureus</i>
1844	S1M10000013F12	<i>Staphylococcus aureus</i>
1845	S1M10000013G01	<i>Staphylococcus aureus</i>
1846	S1M10000013G04	<i>Staphylococcus aureus</i>
1847	S1M10000013G05	<i>Staphylococcus aureus</i>
1848	S1M10000013G06	<i>Staphylococcus aureus</i>
1849	S1M10000013G07	<i>Staphylococcus aureus</i>
1850	S1M10000013G10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1851	S1M10000013G11	<i>Staphylococcus aureus</i>
1852	S1M10000013G12	<i>Staphylococcus aureus</i>
1853	S1M10000013H03	<i>Staphylococcus aureus</i>
1854	S1M10000013H04	<i>Staphylococcus aureus</i>
1855	S1M10000013H05	<i>Staphylococcus aureus</i>
1856	S1M10000013H07	<i>Staphylococcus aureus</i>
1857	S1M10000013H09	<i>Staphylococcus aureus</i>
1858	S1M10000013H10	<i>Staphylococcus aureus</i>
1859	S1M10000013H11	<i>Staphylococcus aureus</i>
1860	S1M10000014A02	<i>Staphylococcus aureus</i>
1861	S1M10000014A03	<i>Staphylococcus aureus</i>
1862	S1M10000014A05	<i>Staphylococcus aureus</i>
1863	S1M10000014A07	<i>Staphylococcus aureus</i>
1864	S1M10000014A08	<i>Staphylococcus aureus</i>
1865	S1M10000014A11	<i>Staphylococcus aureus</i>
1866	S1M10000014A12	<i>Staphylococcus aureus</i>
1867	S1M10000014B01	<i>Staphylococcus aureus</i>
1868	S1M10000014B02	<i>Staphylococcus aureus</i>
1869	S1M10000014B03	<i>Staphylococcus aureus</i>
1870	S1M10000014B04	<i>Staphylococcus aureus</i>
1871	S1M10000014B05	<i>Staphylococcus aureus</i>
1872	S1M10000014B06	<i>Staphylococcus aureus</i>
1873	S1M10000014B07	<i>Staphylococcus aureus</i>
1874	S1M10000014B08	<i>Staphylococcus aureus</i>
1875	S1M10000014B10	<i>Staphylococcus aureus</i>
1876	S1M10000014B11	<i>Staphylococcus aureus</i>
1877	S1M10000014B12	<i>Staphylococcus aureus</i>
1878	S1M10000014C01	<i>Staphylococcus aureus</i>
1879	S1M10000014C05	<i>Staphylococcus aureus</i>
1880	S1M10000014C06	<i>Staphylococcus aureus</i>
1881	S1M10000014C07	<i>Staphylococcus aureus</i>
1882	S1M10000014C09	<i>Staphylococcus aureus</i>
1883	S1M10000014C10	<i>Staphylococcus aureus</i>
1884	S1M10000014C11	<i>Staphylococcus aureus</i>
1885	S1M10000014C12	<i>Staphylococcus aureus</i>
1886	S1M10000014D03	<i>Staphylococcus aureus</i>
1887	S1M10000014D06	<i>Staphylococcus aureus</i>
1888	S1M10000014D08	<i>Staphylococcus aureus</i>
1889	S1M10000014D09	<i>Staphylococcus aureus</i>
1890	S1M10000014D10	<i>Staphylococcus aureus</i>
1891	S1M10000014E01	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1892	S1M10000014E04	<i>Staphylococcus aureus</i>
1893	S1M10000014E05	<i>Staphylococcus aureus</i>
1894	S1M10000014E07	<i>Staphylococcus aureus</i>
1895	S1M10000014E08	<i>Staphylococcus aureus</i>
1896	S1M10000014E09	<i>Staphylococcus aureus</i>
1897	S1M10000014E10	<i>Staphylococcus aureus</i>
1898	S1M10000014E12	<i>Staphylococcus aureus</i>
1899	S1M10000014F02	<i>Staphylococcus aureus</i>
1900	S1M10000014F03	<i>Staphylococcus aureus</i>
1901	S1M10000014F04	<i>Staphylococcus aureus</i>
1902	S1M10000014F05	<i>Staphylococcus aureus</i>
1903	S1M10000014F08	<i>Staphylococcus aureus</i>
1904	S1M10000014F09	<i>Staphylococcus aureus</i>
1905	S1M10000014F10	<i>Staphylococcus aureus</i>
1906	S1M10000014G02	<i>Staphylococcus aureus</i>
1907	S1M10000014G04	<i>Staphylococcus aureus</i>
1908	S1M10000014G06	<i>Staphylococcus aureus</i>
1909	S1M10000014G07	<i>Staphylococcus aureus</i>
1910	S1M10000014G08	<i>Staphylococcus aureus</i>
1911	S1M10000014G12	<i>Staphylococcus aureus</i>
1912	S1M10000014H02	<i>Staphylococcus aureus</i>
1913	S1M10000014H03	<i>Staphylococcus aureus</i>
1914	S1M10000014H04	<i>Staphylococcus aureus</i>
1915	S1M10000014H05	<i>Staphylococcus aureus</i>
1916	S1M10000014H06	<i>Staphylococcus aureus</i>
1917	S1M10000014H07	<i>Staphylococcus aureus</i>
1918	S1M10000014H08	<i>Staphylococcus aureus</i>
1919	S1M10000014H11	<i>Staphylococcus aureus</i>
1920	S1M10000015A02	<i>Staphylococcus aureus</i>
1921	S1M10000015A03	<i>Staphylococcus aureus</i>
1922	S1M10000015A05	<i>Staphylococcus aureus</i>
1923	S1M10000015A06	<i>Staphylococcus aureus</i>
1924	S1M10000015A09	<i>Staphylococcus aureus</i>
1925	S1M10000015A10	<i>Staphylococcus aureus</i>
1926	S1M10000015A11	<i>Staphylococcus aureus</i>
1927	S1M10000015A12	<i>Staphylococcus aureus</i>
1928	S1M10000015B02	<i>Staphylococcus aureus</i>
1929	S1M10000015B05	<i>Staphylococcus aureus</i>
1930	S1M10000015B08	<i>Staphylococcus aureus</i>
1931	S1M10000015B09	<i>Staphylococcus aureus</i>
1932	S1M10000015B10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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1934	S1M10000015C02	<i>Staphylococcus aureus</i>
1935	S1M10000015C03	<i>Staphylococcus aureus</i>
1936	S1M10000015C05	<i>Staphylococcus aureus</i>
1937	S1M10000015C06	<i>Staphylococcus aureus</i>
1938	S1M10000015C08	<i>Staphylococcus aureus</i>
1939	S1M10000015C10	<i>Staphylococcus aureus</i>
1940	S1M10000015C12	<i>Staphylococcus aureus</i>
1941	S1M10000015D02	<i>Staphylococcus aureus</i>
1942	S1M10000015D03	<i>Staphylococcus aureus</i>
1943	S1M10000015D04	<i>Staphylococcus aureus</i>
1944	S1M10000015D05	<i>Staphylococcus aureus</i>
1945	S1M10000015D06	<i>Staphylococcus aureus</i>
1946	S1M10000015D12	<i>Staphylococcus aureus</i>
1947	S1M10000015E02	<i>Staphylococcus aureus</i>
1948	S1M10000015E03	<i>Staphylococcus aureus</i>
1949	S1M10000015E06	<i>Staphylococcus aureus</i>
1950	S1M10000015E07	<i>Staphylococcus aureus</i>
1951	S1M10000015E09	<i>Staphylococcus aureus</i>
1952	S1M10000015E10	<i>Staphylococcus aureus</i>
1953	S1M10000015E11	<i>Staphylococcus aureus</i>
1954	S1M10000015E12	<i>Staphylococcus aureus</i>
1955	S1M10000015F01	<i>Staphylococcus aureus</i>
1956	S1M10000015F02	<i>Staphylococcus aureus</i>
1957	S1M10000015F03	<i>Staphylococcus aureus</i>
1958	S1M10000015F04	<i>Staphylococcus aureus</i>
1959	S1M10000015F06	<i>Staphylococcus aureus</i>
1960	S1M10000015F07	<i>Staphylococcus aureus</i>
1961	S1M10000015F08	<i>Staphylococcus aureus</i>
1962	S1M10000015F09	<i>Staphylococcus aureus</i>
1963	S1M10000015F10	<i>Staphylococcus aureus</i>
1964	S1M10000015G01	<i>Staphylococcus aureus</i>
1965	S1M10000015G02	<i>Staphylococcus aureus</i>
1966	S1M10000015G03	<i>Staphylococcus aureus</i>
1967	S1M10000015G04	<i>Staphylococcus aureus</i>
1968	S1M10000015G05	<i>Staphylococcus aureus</i>
1969	S1M10000015G06	<i>Staphylococcus aureus</i>
1970	S1M10000015G07	<i>Staphylococcus aureus</i>
1971	S1M10000015G08	<i>Staphylococcus aureus</i>
1972	S1M10000015G09	<i>Staphylococcus aureus</i>
1973	S1M10000015G10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
1974	S1M10000015G11	<i>Staphylococcus aureus</i>
1975	S1M10000015H04	<i>Staphylococcus aureus</i>
1976	S1M10000015H06	<i>Staphylococcus aureus</i>
1977	S1M10000016A03	<i>Staphylococcus aureus</i>
1978	S1M10000016A04	<i>Staphylococcus aureus</i>
1979	S1M10000016A06	<i>Staphylococcus aureus</i>
1980	S1M10000016A07	<i>Staphylococcus aureus</i>
1981	S1M10000016A09	<i>Staphylococcus aureus</i>
1982	S1M10000016A10	<i>Staphylococcus aureus</i>
1983	S1M10000016A12	<i>Staphylococcus aureus</i>
1984	S1M10000016B02	<i>Staphylococcus aureus</i>
1985	S1M10000016B05	<i>Staphylococcus aureus</i>
1986	S1M10000016B06	<i>Staphylococcus aureus</i>
1987	S1M10000016B07	<i>Staphylococcus aureus</i>
1988	S1M10000016B08	<i>Staphylococcus aureus</i>
1989	S1M10000016B09	<i>Staphylococcus aureus</i>
1990	S1M10000016B10	<i>Staphylococcus aureus</i>
1991	S1M10000016B11	<i>Staphylococcus aureus</i>
1992	S1M10000016B12	<i>Staphylococcus aureus</i>
1993	S1M10000016C01	<i>Staphylococcus aureus</i>
1994	S1M10000016C02	<i>Staphylococcus aureus</i>
1995	S1M10000016C04	<i>Staphylococcus aureus</i>
1996	S1M10000016C05	<i>Staphylococcus aureus</i>
1997	S1M10000016C06	<i>Staphylococcus aureus</i>
1998	S1M10000016C08	<i>Staphylococcus aureus</i>
1999	S1M10000016C09	<i>Staphylococcus aureus</i>
2000	S1M10000016C10	<i>Staphylococcus aureus</i>
2001	S1M10000016C11	<i>Staphylococcus aureus</i>
2002	S1M10000016C12	<i>Staphylococcus aureus</i>
2003	S1M10000016D01	<i>Staphylococcus aureus</i>
2004	S1M10000016D02	<i>Staphylococcus aureus</i>
2005	S1M10000016D04	<i>Staphylococcus aureus</i>
2006	S1M10000016D05	<i>Staphylococcus aureus</i>
2007	S1M10000016D06	<i>Staphylococcus aureus</i>
2008	S1M10000016D08	<i>Staphylococcus aureus</i>
2009	S1M10000016D09	<i>Staphylococcus aureus</i>
2010	S1M10000016D10	<i>Staphylococcus aureus</i>
2011	S1M10000016D11	<i>Staphylococcus aureus</i>
2012	S1M10000016E04	<i>Staphylococcus aureus</i>
2013	S1M10000016E05	<i>Staphylococcus aureus</i>
2014	S1M10000016E06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2015	S1M10000016E07	<i>Staphylococcus aureus</i>
2016	S1M10000016E08	<i>Staphylococcus aureus</i>
2017	S1M10000016E09	<i>Staphylococcus aureus</i>
2018	S1M10000016E10	<i>Staphylococcus aureus</i>
2019	S1M10000016E11	<i>Staphylococcus aureus</i>
2020	S1M10000016E12	<i>Staphylococcus aureus</i>
2021	S1M10000016F02	<i>Staphylococcus aureus</i>
2022	S1M10000016F03	<i>Staphylococcus aureus</i>
2023	S1M10000016F05	<i>Staphylococcus aureus</i>
2024	S1M10000016F06	<i>Staphylococcus aureus</i>
2025	S1M10000016F08	<i>Staphylococcus aureus</i>
2026	S1M10000016F09	<i>Staphylococcus aureus</i>
2027	S1M10000016F11	<i>Staphylococcus aureus</i>
2028	S1M10000016G01	<i>Staphylococcus aureus</i>
2029	S1M10000016G03	<i>Staphylococcus aureus</i>
2030	S1M10000016G04	<i>Staphylococcus aureus</i>
2031	S1M10000016G05	<i>Staphylococcus aureus</i>
2032	S1M10000016H03	<i>Staphylococcus aureus</i>
2033	S1M10000016H04	<i>Staphylococcus aureus</i>
2034	S1M10000016H08	<i>Staphylococcus aureus</i>
2035	S1M10000016H10	<i>Staphylococcus aureus</i>
2036	S1M10000017A02	<i>Staphylococcus aureus</i>
2037	S1M10000017A03	<i>Staphylococcus aureus</i>
2038	S1M10000017A04	<i>Staphylococcus aureus</i>
2039	S1M10000017A08	<i>Staphylococcus aureus</i>
2040	S1M10000017A11	<i>Staphylococcus aureus</i>
2041	S1M10000017A12	<i>Staphylococcus aureus</i>
2042	S1M10000017B02	<i>Staphylococcus aureus</i>
2043	S1M10000017B05	<i>Staphylococcus aureus</i>
2044	S1M10000017B07	<i>Staphylococcus aureus</i>
2045	S1M10000017B08	<i>Staphylococcus aureus</i>
2046	S1M10000017B09	<i>Staphylococcus aureus</i>
2047	S1M10000017B10	<i>Staphylococcus aureus</i>
2048	S1M10000017B11	<i>Staphylococcus aureus</i>
2049	S1M10000017B12	<i>Staphylococcus aureus</i>
2050	S1M10000017C01	<i>Staphylococcus aureus</i>
2051	S1M10000017C03	<i>Staphylococcus aureus</i>
2052	S1M10000017C05	<i>Staphylococcus aureus</i>
2053	S1M10000017C08	<i>Staphylococcus aureus</i>
2054	S1M10000017C09	<i>Staphylococcus aureus</i>
2055	S1M10000017C10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2056	S1M10000017C11	<i>Staphylococcus aureus</i>
2057	S1M10000017C12	<i>Staphylococcus aureus</i>
2058	S1M10000017D03	<i>Staphylococcus aureus</i>
2059	S1M10000017D09	<i>Staphylococcus aureus</i>
2060	S1M10000017D10	<i>Staphylococcus aureus</i>
2061	S1M10000017E04	<i>Staphylococcus aureus</i>
2062	S1M10000017E05	<i>Staphylococcus aureus</i>
2063	S1M10000017E08	<i>Staphylococcus aureus</i>
2064	S1M10000017E11	<i>Staphylococcus aureus</i>
2065	S1M10000017F01	<i>Staphylococcus aureus</i>
2066	S1M10000017F04	<i>Staphylococcus aureus</i>
2067	S1M10000017F05	<i>Staphylococcus aureus</i>
2068	S1M10000017F06	<i>Staphylococcus aureus</i>
2069	S1M10000017F11	<i>Staphylococcus aureus</i>
2070	S1M10000017G02	<i>Staphylococcus aureus</i>
2071	S1M10000017G05	<i>Staphylococcus aureus</i>
2072	S1M10000017G06	<i>Staphylococcus aureus</i>
2073	S1M10000018A03	<i>Staphylococcus aureus</i>
2074	S1M10000018A04	<i>Staphylococcus aureus</i>
2075	S1M10000018A05	<i>Staphylococcus aureus</i>
2076	S1M10000018A06	<i>Staphylococcus aureus</i>
2077	S1M10000018A08	<i>Staphylococcus aureus</i>
2078	S1M10000018A09	<i>Staphylococcus aureus</i>
2079	S1M10000018A10	<i>Staphylococcus aureus</i>
2080	S1M10000018A11	<i>Staphylococcus aureus</i>
2081	S1M10000018B02	<i>Staphylococcus aureus</i>
2082	S1M10000018B03	<i>Staphylococcus aureus</i>
2083	S1M10000018B05	<i>Staphylococcus aureus</i>
2084	S1M10000018B09	<i>Staphylococcus aureus</i>
2085	S1M10000018B10	<i>Staphylococcus aureus</i>
2086	S1M10000018B11	<i>Staphylococcus aureus</i>
2087	S1M10000018C01	<i>Staphylococcus aureus</i>
2088	S1M10000018C02	<i>Staphylococcus aureus</i>
2089	S1M10000018C03	<i>Staphylococcus aureus</i>
2090	S1M10000018C04	<i>Staphylococcus aureus</i>
2091	S1M10000018C05	<i>Staphylococcus aureus</i>
2092	S1M10000018C06	<i>Staphylococcus aureus</i>
2093	S1M10000018C08	<i>Staphylococcus aureus</i>
2094	S1M10000018C09	<i>Staphylococcus aureus</i>
2095	S1M10000018C10	<i>Staphylococcus aureus</i>
2096	S1M10000018C11	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2097	S1M10000018C12	<i>Staphylococcus aureus</i>
2098	S1M10000018D01	<i>Staphylococcus aureus</i>
2099	S1M10000018D02	<i>Staphylococcus aureus</i>
2100	S1M10000018D03	<i>Staphylococcus aureus</i>
2101	S1M10000018D04	<i>Staphylococcus aureus</i>
2102	S1M10000018D09	<i>Staphylococcus aureus</i>
2103	S1M10000018D10	<i>Staphylococcus aureus</i>
2104	S1M10000018D11	<i>Staphylococcus aureus</i>
2105	S1M10000018D12	<i>Staphylococcus aureus</i>
2106	S1M10000018E01	<i>Staphylococcus aureus</i>
2107	S1M10000018E02	<i>Staphylococcus aureus</i>
2108	S1M10000018E03	<i>Staphylococcus aureus</i>
2109	S1M10000018E04	<i>Staphylococcus aureus</i>
2110	S1M10000018E05	<i>Staphylococcus aureus</i>
2111	S1M10000018E08	<i>Staphylococcus aureus</i>
2112	S1M10000018E09	<i>Staphylococcus aureus</i>
2113	S1M10000018E11	<i>Staphylococcus aureus</i>
2114	S1M10000018E12	<i>Staphylococcus aureus</i>
2115	S1M10000018F03	<i>Staphylococcus aureus</i>
2116	S1M10000018F04	<i>Staphylococcus aureus</i>
2117	S1M10000018F07	<i>Staphylococcus aureus</i>
2118	S1M10000018F09	<i>Staphylococcus aureus</i>
2119	S1M10000018F10	<i>Staphylococcus aureus</i>
2120	S1M10000018F12	<i>Staphylococcus aureus</i>
2121	S1M10000018G03	<i>Staphylococcus aureus</i>
2122	S1M10000018G05	<i>Staphylococcus aureus</i>
2123	S1M10000018G07	<i>Staphylococcus aureus</i>
2124	S1M10000018G08	<i>Staphylococcus aureus</i>
2125	S1M10000018G09	<i>Staphylococcus aureus</i>
2126	S1M10000018G10	<i>Staphylococcus aureus</i>
2127	S1M10000018G12	<i>Staphylococcus aureus</i>
2128	S1M10000018H01	<i>Staphylococcus aureus</i>
2129	S1M10000018H02	<i>Staphylococcus aureus</i>
2130	S1M10000018H07	<i>Staphylococcus aureus</i>
2131	S1M10000018H09	<i>Staphylococcus aureus</i>
2132	S1M10000018H10	<i>Staphylococcus aureus</i>
2133	S1M10000019A02	<i>Staphylococcus aureus</i>
2134	S1M10000019A03	<i>Staphylococcus aureus</i>
2135	S1M10000019A05	<i>Staphylococcus aureus</i>
2136	S1M10000019A06	<i>Staphylococcus aureus</i>
2137	S1M10000019A07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2138	S1M10000019A09	<i>Staphylococcus aureus</i>
2139	S1M10000019A11	<i>Staphylococcus aureus</i>
2140	S1M10000019A12	<i>Staphylococcus aureus</i>
2141	S1M10000019B03	<i>Staphylococcus aureus</i>
2142	S1M10000019B04	<i>Staphylococcus aureus</i>
2143	S1M10000019B07	<i>Staphylococcus aureus</i>
2144	S1M10000019B08	<i>Staphylococcus aureus</i>
2145	S1M10000019B09	<i>Staphylococcus aureus</i>
2146	S1M10000019B10	<i>Staphylococcus aureus</i>
2147	S1M10000019B11	<i>Staphylococcus aureus</i>
2148	S1M10000019B12	<i>Staphylococcus aureus</i>
2149	S1M10000019C01	<i>Staphylococcus aureus</i>
2150	S1M10000019C04	<i>Staphylococcus aureus</i>
2151	S1M10000019C05	<i>Staphylococcus aureus</i>
2152	S1M10000019C06	<i>Staphylococcus aureus</i>
2153	S1M10000019C07	<i>Staphylococcus aureus</i>
2154	S1M10000019C08	<i>Staphylococcus aureus</i>
2155	S1M10000019C11	<i>Staphylococcus aureus</i>
2156	S1M10000019C12	<i>Staphylococcus aureus</i>
2157	S1M10000019D01	<i>Staphylococcus aureus</i>
2158	S1M10000019D02	<i>Staphylococcus aureus</i>
2159	S1M10000019D04	<i>Staphylococcus aureus</i>
2160	S1M10000019D05	<i>Staphylococcus aureus</i>
2161	S1M10000019D06	<i>Staphylococcus aureus</i>
2162	S1M10000019D07	<i>Staphylococcus aureus</i>
2163	S1M10000019D09	<i>Staphylococcus aureus</i>
2164	S1M10000019D12	<i>Staphylococcus aureus</i>
2165	S1M10000019E01	<i>Staphylococcus aureus</i>
2166	S1M10000019E02	<i>Staphylococcus aureus</i>
2167	S1M10000019E07	<i>Staphylococcus aureus</i>
2168	S1M10000019F01	<i>Staphylococcus aureus</i>
2169	S1M10000019F05	<i>Staphylococcus aureus</i>
2170	S1M10000019F06	<i>Staphylococcus aureus</i>
2171	S1M10000019F08	<i>Staphylococcus aureus</i>
2172	S1M10000019F09	<i>Staphylococcus aureus</i>
2173	S1M10000019F11	<i>Staphylococcus aureus</i>
2174	S1M10000019G04	<i>Staphylococcus aureus</i>
2175	S1M10000019G07	<i>Staphylococcus aureus</i>
2176	S1M10000019G09	<i>Staphylococcus aureus</i>
2177	S1M10000019G10	<i>Staphylococcus aureus</i>
2178	S1M10000019G11	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2179	S1M10000019H05	<i>Staphylococcus aureus</i>
2180	S1M10000019H08	<i>Staphylococcus aureus</i>
2181	S1M10000020A05	<i>Staphylococcus aureus</i>
2182	S1M10000020A06	<i>Staphylococcus aureus</i>
2183	S1M10000020A07	<i>Staphylococcus aureus</i>
2184	S1M10000020A11	<i>Staphylococcus aureus</i>
2185	S1M10000020A12	<i>Staphylococcus aureus</i>
2186	S1M10000020B02	<i>Staphylococcus aureus</i>
2187	S1M10000020B03	<i>Staphylococcus aureus</i>
2188	S1M10000020B05	<i>Staphylococcus aureus</i>
2189	S1M10000020B06	<i>Staphylococcus aureus</i>
2190	S1M10000020B07	<i>Staphylococcus aureus</i>
2191	S1M10000020B09	<i>Staphylococcus aureus</i>
2192	S1M10000020B12	<i>Staphylococcus aureus</i>
2193	S1M10000020C09	<i>Staphylococcus aureus</i>
2194	S1M10000020C10	<i>Staphylococcus aureus</i>
2195	S1M10000020C11	<i>Staphylococcus aureus</i>
2196	S1M10000020D03	<i>Staphylococcus aureus</i>
2197	S1M10000020D04	<i>Staphylococcus aureus</i>
2198	S1M10000020D06	<i>Staphylococcus aureus</i>
2199	S1M10000020D07	<i>Staphylococcus aureus</i>
2200	S1M10000020D08	<i>Staphylococcus aureus</i>
2201	S1M10000020D09	<i>Staphylococcus aureus</i>
2202	S1M10000020D12	<i>Staphylococcus aureus</i>
2203	S1M10000020E01	<i>Staphylococcus aureus</i>
2204	S1M10000020E03	<i>Staphylococcus aureus</i>
2205	S1M10000020E04	<i>Staphylococcus aureus</i>
2206	S1M10000020E06	<i>Staphylococcus aureus</i>
2207	S1M10000020E08	<i>Staphylococcus aureus</i>
2208	S1M10000020E11	<i>Staphylococcus aureus</i>
2209	S1M10000020E12	<i>Staphylococcus aureus</i>
2210	S1M10000020F01	<i>Staphylococcus aureus</i>
2211	S1M10000020F05	<i>Staphylococcus aureus</i>
2212	S1M10000020F06	<i>Staphylococcus aureus</i>
2213	S1M10000020F07	<i>Staphylococcus aureus</i>
2214	S1M10000020F09	<i>Staphylococcus aureus</i>
2215	S1M10000020F11	<i>Staphylococcus aureus</i>
2216	S1M10000020F12	<i>Staphylococcus aureus</i>
2217	S1M10000020G01	<i>Staphylococcus aureus</i>
2218	S1M10000020G05	<i>Staphylococcus aureus</i>
2219	S1M10000020G07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2220	S1M10000020G08	<i>Staphylococcus aureus</i>
2221	S1M10000020G09	<i>Staphylococcus aureus</i>
2222	S1M10000020G10	<i>Staphylococcus aureus</i>
2223	S1M10000020G11	<i>Staphylococcus aureus</i>
2224	S1M10000020G12	<i>Staphylococcus aureus</i>
2225	S1M10000020H01	<i>Staphylococcus aureus</i>
2226	S1M10000020H02	<i>Staphylococcus aureus</i>
2227	S1M10000020H04	<i>Staphylococcus aureus</i>
2228	S1M10000020H06	<i>Staphylococcus aureus</i>
2229	S1M10000020H08	<i>Staphylococcus aureus</i>
2230	S1M10000020H10	<i>Staphylococcus aureus</i>
2231	S1M10000020H11	<i>Staphylococcus aureus</i>
2232	S1M10000021A04	<i>Staphylococcus aureus</i>
2233	S1M10000021A05	<i>Staphylococcus aureus</i>
2234	S1M10000021A06	<i>Staphylococcus aureus</i>
2235	S1M10000021A07	<i>Staphylococcus aureus</i>
2236	S1M10000021A08	<i>Staphylococcus aureus</i>
2237	S1M10000021A09	<i>Staphylococcus aureus</i>
2238	S1M10000021A10	<i>Staphylococcus aureus</i>
2239	S1M10000021B05	<i>Staphylococcus aureus</i>
2240	S1M10000021B06	<i>Staphylococcus aureus</i>
2241	S1M10000021B07	<i>Staphylococcus aureus</i>
2242	S1M10000021B10	<i>Staphylococcus aureus</i>
2243	S1M10000021C04	<i>Staphylococcus aureus</i>
2244	S1M10000021C05	<i>Staphylococcus aureus</i>
2245	S1M10000021C07	<i>Staphylococcus aureus</i>
2246	S1M10000021C08	<i>Staphylococcus aureus</i>
2247	S1M10000021C10	<i>Staphylococcus aureus</i>
2248	S1M10000021C11	<i>Staphylococcus aureus</i>
2249	S1M10000021C12	<i>Staphylococcus aureus</i>
2250	S1M10000021D01	<i>Staphylococcus aureus</i>
2251	S1M10000021D03	<i>Staphylococcus aureus</i>
2252	S1M10000021D04	<i>Staphylococcus aureus</i>
2253	S1M10000021D06	<i>Staphylococcus aureus</i>
2254	S1M10000021D09	<i>Staphylococcus aureus</i>
2255	S1M10000021D10	<i>Staphylococcus aureus</i>
2256	S1M10000021E01	<i>Staphylococcus aureus</i>
2257	S1M10000021E02	<i>Staphylococcus aureus</i>
2258	S1M10000021E03	<i>Staphylococcus aureus</i>
2259	S1M10000021E05	<i>Staphylococcus aureus</i>
2260	S1M10000021E06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2261	S1M10000021E09	<i>Staphylococcus aureus</i>
2262	S1M10000021E12	<i>Staphylococcus aureus</i>
2263	S1M10000021F02	<i>Staphylococcus aureus</i>
2264	S1M10000021F04	<i>Staphylococcus aureus</i>
2265	S1M10000021F05	<i>Staphylococcus aureus</i>
2266	S1M10000021F06	<i>Staphylococcus aureus</i>
2267	S1M10000021F07	<i>Staphylococcus aureus</i>
2268	S1M10000021F09	<i>Staphylococcus aureus</i>
2269	S1M10000021F11	<i>Staphylococcus aureus</i>
2270	S1M10000021G01	<i>Staphylococcus aureus</i>
2271	S1M10000021G03	<i>Staphylococcus aureus</i>
2272	S1M10000021G08	<i>Staphylococcus aureus</i>
2273	S1M10000021H04	<i>Staphylococcus aureus</i>
2274	S1M10000021H05	<i>Staphylococcus aureus</i>
2275	S1M10000021H07	<i>Staphylococcus aureus</i>
2276	S1M10000021H08	<i>Staphylococcus aureus</i>
2277	S1M10000021H11	<i>Staphylococcus aureus</i>
2278	S1M10000022A02	<i>Staphylococcus aureus</i>
2279	S1M10000022A03	<i>Staphylococcus aureus</i>
2280	S1M10000022A05	<i>Staphylococcus aureus</i>
2281	S1M10000022A08	<i>Staphylococcus aureus</i>
2282	S1M10000022A09	<i>Staphylococcus aureus</i>
2283	S1M10000022A12	<i>Staphylococcus aureus</i>
2284	S1M10000022B02	<i>Staphylococcus aureus</i>
2285	S1M10000022B03	<i>Staphylococcus aureus</i>
2286	S1M10000022B05	<i>Staphylococcus aureus</i>
2287	S1M10000022B06	<i>Staphylococcus aureus</i>
2288	S1M10000022B08	<i>Staphylococcus aureus</i>
2289	S1M10000022B09	<i>Staphylococcus aureus</i>
2290	S1M10000022B10	<i>Staphylococcus aureus</i>
2291	S1M10000022B11	<i>Staphylococcus aureus</i>
2292	S1M10000022B12	<i>Staphylococcus aureus</i>
2293	S1M10000022C02	<i>Staphylococcus aureus</i>
2294	S1M10000022C03	<i>Staphylococcus aureus</i>
2295	S1M10000022C04	<i>Staphylococcus aureus</i>
2296	S1M10000022C06	<i>Staphylococcus aureus</i>
2297	S1M10000022C07	<i>Staphylococcus aureus</i>
2298	S1M10000022C08	<i>Staphylococcus aureus</i>
2299	S1M10000022C11	<i>Staphylococcus aureus</i>
2300	S1M10000022D03	<i>Staphylococcus aureus</i>
2301	S1M10000022D05	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2302	S1M10000022D06	<i>Staphylococcus aureus</i>
2303	S1M10000022D07	<i>Staphylococcus aureus</i>
2304	S1M10000022D08	<i>Staphylococcus aureus</i>
2305	S1M10000022D09	<i>Staphylococcus aureus</i>
2306	S1M10000022D11	<i>Staphylococcus aureus</i>
2307	S1M10000022E01	<i>Staphylococcus aureus</i>
2308	S1M10000022E03	<i>Staphylococcus aureus</i>
2309	S1M10000022E05	<i>Staphylococcus aureus</i>
2310	S1M10000022E09	<i>Staphylococcus aureus</i>
2311	S1M10000022F04	<i>Staphylococcus aureus</i>
2312	S1M10000022F06	<i>Staphylococcus aureus</i>
2313	S1M10000022F07	<i>Staphylococcus aureus</i>
2314	S1M10000022F08	<i>Staphylococcus aureus</i>
2315	S1M10000022F11	<i>Staphylococcus aureus</i>
2316	S1M10000022G03	<i>Staphylococcus aureus</i>
2317	S1M10000022G04	<i>Staphylococcus aureus</i>
2318	S1M10000022G07	<i>Staphylococcus aureus</i>
2319	S1M10000022G08	<i>Staphylococcus aureus</i>
2320	S1M10000022G12	<i>Staphylococcus aureus</i>
2321	S1M10000022H03	<i>Staphylococcus aureus</i>
2322	S1M10000022H05	<i>Staphylococcus aureus</i>
2323	S1M10000022H06	<i>Staphylococcus aureus</i>
2324	S1M10000022H07	<i>Staphylococcus aureus</i>
2325	S1M10000022H08	<i>Staphylococcus aureus</i>
2326	S1M10000022H11	<i>Staphylococcus aureus</i>
2327	S1M10000023A05	<i>Staphylococcus aureus</i>
2328	S1M10000023A09	<i>Staphylococcus aureus</i>
2329	S1M10000023A11	<i>Staphylococcus aureus</i>
2330	S1M10000023A12	<i>Staphylococcus aureus</i>
2331	S1M10000023B01	<i>Staphylococcus aureus</i>
2332	S1M10000023B03	<i>Staphylococcus aureus</i>
2333	S1M10000023B07	<i>Staphylococcus aureus</i>
2334	S1M10000023B08	<i>Staphylococcus aureus</i>
2335	S1M10000023B09	<i>Staphylococcus aureus</i>
2336	S1M10000023B10	<i>Staphylococcus aureus</i>
2337	S1M10000023B11	<i>Staphylococcus aureus</i>
2338	S1M10000023B12	<i>Staphylococcus aureus</i>
2339	S1M10000023C02	<i>Staphylococcus aureus</i>
2340	S1M10000023C10	<i>Staphylococcus aureus</i>
2341	S1M10000023C11	<i>Staphylococcus aureus</i>
2342	S1M10000023C12	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2344	S1M10000023D03	<i>Staphylococcus aureus</i>
2345	S1M10000023D04	<i>Staphylococcus aureus</i>
2346	S1M10000023D07	<i>Staphylococcus aureus</i>
2347	S1M10000023D08	<i>Staphylococcus aureus</i>
2348	S1M10000023D09	<i>Staphylococcus aureus</i>
2349	S1M10000023D10	<i>Staphylococcus aureus</i>
2350	S1M10000023D12	<i>Staphylococcus aureus</i>
2351	S1M10000023E01	<i>Staphylococcus aureus</i>
2352	S1M10000023E04	<i>Staphylococcus aureus</i>
2353	S1M10000023E07	<i>Staphylococcus aureus</i>
2354	S1M10000023E10	<i>Staphylococcus aureus</i>
2355	S1M10000023E11	<i>Staphylococcus aureus</i>
2356	S1M10000023F04	<i>Staphylococcus aureus</i>
2357	S1M10000023F07	<i>Staphylococcus aureus</i>
2358	S1M10000023F08	<i>Staphylococcus aureus</i>
2359	S1M10000023F10	<i>Staphylococcus aureus</i>
2360	S1M10000023F11	<i>Staphylococcus aureus</i>
2361	S1M10000023F12	<i>Staphylococcus aureus</i>
2362	S1M10000023G02	<i>Staphylococcus aureus</i>
2363	S1M10000023G03	<i>Staphylococcus aureus</i>
2364	S1M10000023G06	<i>Staphylococcus aureus</i>
2365	S1M10000023G07	<i>Staphylococcus aureus</i>
2366	S1M10000023G08	<i>Staphylococcus aureus</i>
2367	S1M10000023G09	<i>Staphylococcus aureus</i>
2368	S1M10000023G11	<i>Staphylococcus aureus</i>
2369	S1M10000023H02	<i>Staphylococcus aureus</i>
2370	S1M10000023H06	<i>Staphylococcus aureus</i>
2371	S1M10000023H07	<i>Staphylococcus aureus</i>
2372	S1M10000023H09	<i>Staphylococcus aureus</i>
2373	S1M10000023H10	<i>Staphylococcus aureus</i>
2374	S1M10000024A02	<i>Staphylococcus aureus</i>
2375	S1M10000024A04	<i>Staphylococcus aureus</i>
2376	S1M10000024A07	<i>Staphylococcus aureus</i>
2377	S1M10000024A08	<i>Staphylococcus aureus</i>
2378	S1M10000024A11	<i>Staphylococcus aureus</i>
2379	S1M10000024B05	<i>Staphylococcus aureus</i>
2380	S1M10000024B06	<i>Staphylococcus aureus</i>
2381	S1M10000024B08	<i>Staphylococcus aureus</i>
2382	S1M10000024B09	<i>Staphylococcus aureus</i>
2383	S1M10000024B10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2385	S1M10000024C04	<i>Staphylococcus aureus</i>
2386	S1M10000024C07	<i>Staphylococcus aureus</i>
2387	S1M10000024D02	<i>Staphylococcus aureus</i>
2388	S1M10000024D03	<i>Staphylococcus aureus</i>
2389	S1M10000024D10	<i>Staphylococcus aureus</i>
2390	S1M10000024D11	<i>Staphylococcus aureus</i>
2391	S1M10000024E03	<i>Staphylococcus aureus</i>
2392	S1M10000024E05	<i>Staphylococcus aureus</i>
2393	S1M10000024E06	<i>Staphylococcus aureus</i>
2394	S1M10000024E07	<i>Staphylococcus aureus</i>
2395	S1M10000024E08	<i>Staphylococcus aureus</i>
2396	S1M10000024F02	<i>Staphylococcus aureus</i>
2397	S1M10000024F03	<i>Staphylococcus aureus</i>
2398	S1M10000024F05	<i>Staphylococcus aureus</i>
2399	S1M10000024F08	<i>Staphylococcus aureus</i>
2400	S1M10000024F10	<i>Staphylococcus aureus</i>
2401	S1M10000024G05	<i>Staphylococcus aureus</i>
2402	S1M10000024G06	<i>Staphylococcus aureus</i>
2403	S1M10000024G07	<i>Staphylococcus aureus</i>
2404	S1M10000024G08	<i>Staphylococcus aureus</i>
2405	S1M10000024G10	<i>Staphylococcus aureus</i>
2406	S1M10000024G12	<i>Staphylococcus aureus</i>
2407	S1M10000024H02	<i>Staphylococcus aureus</i>
2408	S1M10000024H04	<i>Staphylococcus aureus</i>
2409	S1M10000024H07	<i>Staphylococcus aureus</i>
2410	S1M10000024H08	<i>Staphylococcus aureus</i>
2411	S1M10000025A03	<i>Staphylococcus aureus</i>
2412	S1M10000025A08	<i>Staphylococcus aureus</i>
2413	S1M10000025A09	<i>Staphylococcus aureus</i>
2414	S1M10000025A10	<i>Staphylococcus aureus</i>
2415	S1M10000025B01	<i>Staphylococcus aureus</i>
2416	S1M10000025B02	<i>Staphylococcus aureus</i>
2417	S1M10000025B03	<i>Staphylococcus aureus</i>
2418	S1M10000025B05	<i>Staphylococcus aureus</i>
2419	S1M10000025B06	<i>Staphylococcus aureus</i>
2420	S1M10000025B09	<i>Staphylococcus aureus</i>
2421	S1M10000025B12	<i>Staphylococcus aureus</i>
2422	S1M10000025C01	<i>Staphylococcus aureus</i>
2423	S1M10000025C03	<i>Staphylococcus aureus</i>
2424	S1M10000025C05	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2426	S1M10000025C10	<i>Staphylococcus aureus</i>
2427	S1M10000025C11	<i>Staphylococcus aureus</i>
2428	S1M10000025D01	<i>Staphylococcus aureus</i>
2429	S1M10000025D03	<i>Staphylococcus aureus</i>
2430	S1M10000025D04	<i>Staphylococcus aureus</i>
2431	S1M10000025D06	<i>Staphylococcus aureus</i>
2432	S1M10000025D08	<i>Staphylococcus aureus</i>
2433	S1M10000025D09	<i>Staphylococcus aureus</i>
2434	S1M10000025D10	<i>Staphylococcus aureus</i>
2435	S1M10000025E01	<i>Staphylococcus aureus</i>
2436	S1M10000025E04	<i>Staphylococcus aureus</i>
2437	S1M10000025E09	<i>Staphylococcus aureus</i>
2438	S1M10000025E11	<i>Staphylococcus aureus</i>
2439	S1M10000025F03	<i>Staphylococcus aureus</i>
2440	S1M10000025F05	<i>Staphylococcus aureus</i>
2441	S1M10000025F08	<i>Staphylococcus aureus</i>
2442	S1M10000025F09	<i>Staphylococcus aureus</i>
2443	S1M10000025F10	<i>Staphylococcus aureus</i>
2444	S1M10000025F12	<i>Staphylococcus aureus</i>
2445	S1M10000025G04	<i>Staphylococcus aureus</i>
2446	S1M10000025G06	<i>Staphylococcus aureus</i>
2447	S1M10000025G10	<i>Staphylococcus aureus</i>
2448	S1M10000025H05	<i>Staphylococcus aureus</i>
2449	S1M10000025H06	<i>Staphylococcus aureus</i>
2450	S1M10000025H07	<i>Staphylococcus aureus</i>
2451	S1M10000025H10	<i>Staphylococcus aureus</i>
2452	S1M10000026A02	<i>Staphylococcus aureus</i>
2453	S1M10000026A04	<i>Staphylococcus aureus</i>
2454	S1M10000026A05	<i>Staphylococcus aureus</i>
2455	S1M10000026A06	<i>Staphylococcus aureus</i>
2456	S1M10000026A07	<i>Staphylococcus aureus</i>
2457	S1M10000026A08	<i>Staphylococcus aureus</i>
2458	S1M10000026A09	<i>Staphylococcus aureus</i>
2459	S1M10000026A10	<i>Staphylococcus aureus</i>
2460	S1M10000026A11	<i>Staphylococcus aureus</i>
2461	S1M10000026B02	<i>Staphylococcus aureus</i>
2462	S1M10000026B03	<i>Staphylococcus aureus</i>
2463	S1M10000026B05	<i>Staphylococcus aureus</i>
2464	S1M10000026B06	<i>Staphylococcus aureus</i>
2465	S1M10000026B07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2467	S1M10000026B11	<i>Staphylococcus aureus</i>
2468	S1M10000026B12	<i>Staphylococcus aureus</i>
2469	S1M10000026C01	<i>Staphylococcus aureus</i>
2470	S1M10000026C06	<i>Staphylococcus aureus</i>
2471	S1M10000026C07	<i>Staphylococcus aureus</i>
2472	S1M10000026C08	<i>Staphylococcus aureus</i>
2473	S1M10000026C11	<i>Staphylococcus aureus</i>
2474	S1M10000026C12	<i>Staphylococcus aureus</i>
2475	S1M10000026D04	<i>Staphylococcus aureus</i>
2476	S1M10000026D05	<i>Staphylococcus aureus</i>
2477	S1M10000026D06	<i>Staphylococcus aureus</i>
2478	S1M10000026D07	<i>Staphylococcus aureus</i>
2479	S1M10000026D08	<i>Staphylococcus aureus</i>
2480	S1M10000026D10	<i>Staphylococcus aureus</i>
2481	S1M10000026D12	<i>Staphylococcus aureus</i>
2482	S1M10000026E01	<i>Staphylococcus aureus</i>
2483	S1M10000026E07	<i>Staphylococcus aureus</i>
2484	S1M10000026E09	<i>Staphylococcus aureus</i>
2485	S1M10000026E10	<i>Staphylococcus aureus</i>
2486	S1M10000026E11	<i>Staphylococcus aureus</i>
2487	S1M10000026E12	<i>Staphylococcus aureus</i>
2488	S1M10000026F01	<i>Staphylococcus aureus</i>
2489	S1M10000026F03	<i>Staphylococcus aureus</i>
2490	S1M10000026F04	<i>Staphylococcus aureus</i>
2491	S1M10000026F05	<i>Staphylococcus aureus</i>
2492	S1M10000026F06	<i>Staphylococcus aureus</i>
2493	S1M10000026F07	<i>Staphylococcus aureus</i>
2494	S1M10000026F08	<i>Staphylococcus aureus</i>
2495	S1M10000026F09	<i>Staphylococcus aureus</i>
2496	S1M10000026F10	<i>Staphylococcus aureus</i>
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2498	S1M10000026F12	<i>Staphylococcus aureus</i>
2499	S1M10000026G01	<i>Staphylococcus aureus</i>
2500	S1M10000026G03	<i>Staphylococcus aureus</i>
2501	S1M10000026G04	<i>Staphylococcus aureus</i>
2502	S1M10000026G05	<i>Staphylococcus aureus</i>
2503	S1M10000026G06	<i>Staphylococcus aureus</i>
2504	S1M10000026G07	<i>Staphylococcus aureus</i>
2505	S1M10000026G09	<i>Staphylococcus aureus</i>
2506	S1M10000026G10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2507	S1M10000026G12	<i>Staphylococcus aureus</i>
2508	S1M10000026H01	<i>Staphylococcus aureus</i>
2509	S1M10000026H02	<i>Staphylococcus aureus</i>
2510	S1M10000026H03	<i>Staphylococcus aureus</i>
2511	S1M10000026H04	<i>Staphylococcus aureus</i>
2512	S1M10000026H05	<i>Staphylococcus aureus</i>
2513	S1M10000026H07	<i>Staphylococcus aureus</i>
2514	S1M10000026H09	<i>Staphylococcus aureus</i>
2515	S1M10000026H10	<i>Staphylococcus aureus</i>
2516	S1M10000027A04	<i>Staphylococcus aureus</i>
2517	S1M10000027A05	<i>Staphylococcus aureus</i>
2518	S1M10000027A08	<i>Staphylococcus aureus</i>
2519	S1M10000027A11	<i>Staphylococcus aureus</i>
2520	S1M10000027B04	<i>Staphylococcus aureus</i>
2521	S1M10000027B06	<i>Staphylococcus aureus</i>
2522	S1M10000027B07	<i>Staphylococcus aureus</i>
2523	S1M10000027B08	<i>Staphylococcus aureus</i>
2524	S1M10000027B09	<i>Staphylococcus aureus</i>
2525	S1M10000027B11	<i>Staphylococcus aureus</i>
2526	S1M10000027C02	<i>Staphylococcus aureus</i>
2527	S1M10000027C04	<i>Staphylococcus aureus</i>
2528	S1M10000027C05	<i>Staphylococcus aureus</i>
2529	S1M10000027C06	<i>Staphylococcus aureus</i>
2530	S1M10000027C08	<i>Staphylococcus aureus</i>
2531	S1M10000027C09	<i>Staphylococcus aureus</i>
2532	S1M10000027D02	<i>Staphylococcus aureus</i>
2533	S1M10000027D03	<i>Staphylococcus aureus</i>
2534	S1M10000027D05	<i>Staphylococcus aureus</i>
2535	S1M10000027D06	<i>Staphylococcus aureus</i>
2536	S1M10000027D08	<i>Staphylococcus aureus</i>
2537	S1M10000027D09	<i>Staphylococcus aureus</i>
2538	S1M10000027D10	<i>Staphylococcus aureus</i>
2539	S1M10000027D11	<i>Staphylococcus aureus</i>
2540	S1M10000027E05	<i>Staphylococcus aureus</i>
2541	S1M10000027E06	<i>Staphylococcus aureus</i>
2542	S1M10000027E07	<i>Staphylococcus aureus</i>
2543	S1M10000027E08	<i>Staphylococcus aureus</i>
2544	S1M10000027E09	<i>Staphylococcus aureus</i>
2545	S1M10000027E11	<i>Staphylococcus aureus</i>
2546	S1M10000027F01	<i>Staphylococcus aureus</i>
2547	S1M10000027F02	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2549	S1M10000027F06	<i>Staphylococcus aureus</i>
2550	S1M10000027F08	<i>Staphylococcus aureus</i>
2551	S1M10000027F09	<i>Staphylococcus aureus</i>
2552	S1M10000027G03	<i>Staphylococcus aureus</i>
2553	S1M10000027G04	<i>Staphylococcus aureus</i>
2554	S1M10000027G05	<i>Staphylococcus aureus</i>
2555	S1M10000027G06	<i>Staphylococcus aureus</i>
2556	S1M10000027G07	<i>Staphylococcus aureus</i>
2557	S1M10000027G09	<i>Staphylococcus aureus</i>
2558	S1M10000027G11	<i>Staphylococcus aureus</i>
2559	S1M10000027H02	<i>Staphylococcus aureus</i>
2560	S1M10000027H04	<i>Staphylococcus aureus</i>
2561	S1M10000027H05	<i>Staphylococcus aureus</i>
2562	S1M10000027H06	<i>Staphylococcus aureus</i>
2563	S1M10000027H07	<i>Staphylococcus aureus</i>
2564	S1M10000027H08	<i>Staphylococcus aureus</i>
2565	S1M10000027H09	<i>Staphylococcus aureus</i>
2566	S1M10000027H10	<i>Staphylococcus aureus</i>
2567	S1M10000027H11	<i>Staphylococcus aureus</i>
2568	S1M10000028A02	<i>Staphylococcus aureus</i>
2569	S1M10000028A04	<i>Staphylococcus aureus</i>
2570	S1M10000028A06	<i>Staphylococcus aureus</i>
2571	S1M10000028A08	<i>Staphylococcus aureus</i>
2572	S1M10000028B01	<i>Staphylococcus aureus</i>
2573	S1M10000028B02	<i>Staphylococcus aureus</i>
2574	S1M10000028B03	<i>Staphylococcus aureus</i>
2575	S1M10000028B04	<i>Staphylococcus aureus</i>
2576	S1M10000028B05	<i>Staphylococcus aureus</i>
2577	S1M10000028B06	<i>Staphylococcus aureus</i>
2578	S1M10000028B08	<i>Staphylococcus aureus</i>
2579	S1M10000028B09	<i>Staphylococcus aureus</i>
2580	S1M10000028C02	<i>Staphylococcus aureus</i>
2581	S1M10000028C04	<i>Staphylococcus aureus</i>
2582	S1M10000028C05	<i>Staphylococcus aureus</i>
2583	S1M10000028C06	<i>Staphylococcus aureus</i>
2584	S1M10000028C08	<i>Staphylococcus aureus</i>
2585	S1M10000028D03	<i>Staphylococcus aureus</i>
2586	S1M10000028D04	<i>Staphylococcus aureus</i>
2587	S1M10000028D06	<i>Staphylococcus aureus</i>
2588	S1M10000028D07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2589	S1M10000028D08	<i>Staphylococcus aureus</i>
2590	S1M10000028D09	<i>Staphylococcus aureus</i>
2591	S1M10000028E01	<i>Staphylococcus aureus</i>
2592	S1M10000028E03	<i>Staphylococcus aureus</i>
2593	S1M10000028E08	<i>Staphylococcus aureus</i>
2594	S1M10000028F01	<i>Staphylococcus aureus</i>
2595	S1M10000028F03	<i>Staphylococcus aureus</i>
2596	S1M10000028F04	<i>Staphylococcus aureus</i>
2597	S1M10000028F05	<i>Staphylococcus aureus</i>
2598	S1M10000028F06	<i>Staphylococcus aureus</i>
2599	S1M10000028F07	<i>Staphylococcus aureus</i>
2600	S1M10000028G01	<i>Staphylococcus aureus</i>
2601	S1M10000028G02	<i>Staphylococcus aureus</i>
2602	S1M10000028G03	<i>Staphylococcus aureus</i>
2603	S1M10000028G04	<i>Staphylococcus aureus</i>
2604	S1M10000028G05	<i>Staphylococcus aureus</i>
2605	S1M10000028G06	<i>Staphylococcus aureus</i>
2606	S1M10000028G08	<i>Staphylococcus aureus</i>
2607	S1M10000028H03	<i>Staphylococcus aureus</i>
2608	S1M10000028H04	<i>Staphylococcus aureus</i>
2609	S1M10000028H05	<i>Staphylococcus aureus</i>
2610	S1M10000029A02	<i>Staphylococcus aureus</i>
2611	S1M10000029A04	<i>Staphylococcus aureus</i>
2612	S1M10000029A09	<i>Staphylococcus aureus</i>
2613	S1M10000029A10	<i>Staphylococcus aureus</i>
2614	S1M10000029A11	<i>Staphylococcus aureus</i>
2615	S1M10000029A12	<i>Staphylococcus aureus</i>
2616	S1M10000029B02	<i>Staphylococcus aureus</i>
2617	S1M10000029B03	<i>Staphylococcus aureus</i>
2618	S1M10000029B04	<i>Staphylococcus aureus</i>
2619	S1M10000029B05	<i>Staphylococcus aureus</i>
2620	S1M10000029B06	<i>Staphylococcus aureus</i>
2621	S1M10000029B08	<i>Staphylococcus aureus</i>
2622	S1M10000029B10	<i>Staphylococcus aureus</i>
2623	S1M10000029C02	<i>Staphylococcus aureus</i>
2624	S1M10000029C03	<i>Staphylococcus aureus</i>
2625	S1M10000029C05	<i>Staphylococcus aureus</i>
2626	S1M10000029C07	<i>Staphylococcus aureus</i>
2627	S1M10000029C09	<i>Staphylococcus aureus</i>
2628	S1M10000029C10	<i>Staphylococcus aureus</i>
2629	S1M10000029C12	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2631	S1M10000029D05	<i>Staphylococcus aureus</i>
2632	S1M10000029D09	<i>Staphylococcus aureus</i>
2633	S1M10000029D10	<i>Staphylococcus aureus</i>
2634	S1M10000029D12	<i>Staphylococcus aureus</i>
2635	S1M10000029E02	<i>Staphylococcus aureus</i>
2636	S1M10000029E05	<i>Staphylococcus aureus</i>
2637	S1M10000029E10	<i>Staphylococcus aureus</i>
2638	S1M10000029E11	<i>Staphylococcus aureus</i>
2639	S1M10000029F01	<i>Staphylococcus aureus</i>
2640	S1M10000029F02	<i>Staphylococcus aureus</i>
2641	S1M10000029F04	<i>Staphylococcus aureus</i>
2642	S1M10000029F09	<i>Staphylococcus aureus</i>
2643	S1M10000029F10	<i>Staphylococcus aureus</i>
2644	S1M10000029F11	<i>Staphylococcus aureus</i>
2645	S1M10000029F12	<i>Staphylococcus aureus</i>
2646	S1M10000029G01	<i>Staphylococcus aureus</i>
2647	S1M10000029G02	<i>Staphylococcus aureus</i>
2648	S1M10000029G03	<i>Staphylococcus aureus</i>
2649	S1M10000029G05	<i>Staphylococcus aureus</i>
2650	S1M10000029G07	<i>Staphylococcus aureus</i>
2651	S1M10000029G08	<i>Staphylococcus aureus</i>
2652	S1M10000029G12	<i>Staphylococcus aureus</i>
2653	S1M10000029H01	<i>Staphylococcus aureus</i>
2654	S1M10000029H05	<i>Staphylococcus aureus</i>
2655	S1M10000029H06	<i>Staphylococcus aureus</i>
2656	S1M10000029H08	<i>Staphylococcus aureus</i>
2657	S1M10000029H09	<i>Staphylococcus aureus</i>
2658	S1M10000029H10	<i>Staphylococcus aureus</i>
2659	S1M10000030A02	<i>Staphylococcus aureus</i>
2660	S1M10000030A05	<i>Staphylococcus aureus</i>
2661	S1M10000030A09	<i>Staphylococcus aureus</i>
2662	S1M10000030A10	<i>Staphylococcus aureus</i>
2663	S1M10000030A11	<i>Staphylococcus aureus</i>
2664	S1M10000030B02	<i>Staphylococcus aureus</i>
2665	S1M10000030B05	<i>Staphylococcus aureus</i>
2666	S1M10000030B07	<i>Staphylococcus aureus</i>
2667	S1M10000030B09	<i>Staphylococcus aureus</i>
2668	S1M10000030C02	<i>Staphylococcus aureus</i>
2669	S1M10000030C03	<i>Staphylococcus aureus</i>
2670	S1M10000030C04	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2671	S1M10000030C05	<i>Staphylococcus aureus</i>
2672	S1M10000030C08	<i>Staphylococcus aureus</i>
2673	S1M10000030C09	<i>Staphylococcus aureus</i>
2674	S1M10000030C10	<i>Staphylococcus aureus</i>
2675	S1M10000030C12	<i>Staphylococcus aureus</i>
2676	S1M10000030D01	<i>Staphylococcus aureus</i>
2677	S1M10000030D02	<i>Staphylococcus aureus</i>
2678	S1M10000030D03	<i>Staphylococcus aureus</i>
2679	S1M10000030D05	<i>Staphylococcus aureus</i>
2680	S1M10000030D06	<i>Staphylococcus aureus</i>
2681	S1M10000030D07	<i>Staphylococcus aureus</i>
2682	S1M10000030D09	<i>Staphylococcus aureus</i>
2683	S1M10000030D10	<i>Staphylococcus aureus</i>
2684	S1M10000030D11	<i>Staphylococcus aureus</i>
2685	S1M10000030E02	<i>Staphylococcus aureus</i>
2686	S1M10000030E06	<i>Staphylococcus aureus</i>
2687	S1M10000030E07	<i>Staphylococcus aureus</i>
2688	S1M10000030E11	<i>Staphylococcus aureus</i>
2689	S1M10000030E12	<i>Staphylococcus aureus</i>
2690	S1M10000030F01	<i>Staphylococcus aureus</i>
2691	S1M10000030F07	<i>Staphylococcus aureus</i>
2692	S1M10000030F08	<i>Staphylococcus aureus</i>
2693	S1M10000030F09	<i>Staphylococcus aureus</i>
2694	S1M10000030F10	<i>Staphylococcus aureus</i>
2695	S1M10000030G03	<i>Staphylococcus aureus</i>
2696	S1M10000030G05	<i>Staphylococcus aureus</i>
2697	S1M10000030G07	<i>Staphylococcus aureus</i>
2698	S1M10000030G08	<i>Staphylococcus aureus</i>
2699	S1M10000030G09	<i>Staphylococcus aureus</i>
2700	S1M10000030G10	<i>Staphylococcus aureus</i>
2701	S1M10000030G11	<i>Staphylococcus aureus</i>
2702	S1M10000030G12	<i>Staphylococcus aureus</i>
2703	S1M10000030H01	<i>Staphylococcus aureus</i>
2704	S1M10000030H02	<i>Staphylococcus aureus</i>
2705	S1M10000030H03	<i>Staphylococcus aureus</i>
2706	S1M10000030H05	<i>Staphylococcus aureus</i>
2707	S1M10000030H07	<i>Staphylococcus aureus</i>
2708	S1M10000030H09	<i>Staphylococcus aureus</i>
2709	S1M10000031A03	<i>Staphylococcus aureus</i>
2710	S1M10000031A08	<i>Staphylococcus aureus</i>
2711	S1M10000031A10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2712	S1M10000031B01	<i>Staphylococcus aureus</i>
2713	S1M10000031B02	<i>Staphylococcus aureus</i>
2714	S1M10000031B04	<i>Staphylococcus aureus</i>
2715	S1M10000031B11	<i>Staphylococcus aureus</i>
2716	S1M10000031B12	<i>Staphylococcus aureus</i>
2717	S1M10000031C04	<i>Staphylococcus aureus</i>
2718	S1M10000031C07	<i>Staphylococcus aureus</i>
2719	S1M10000031C09	<i>Staphylococcus aureus</i>
2720	S1M10000031C11	<i>Staphylococcus aureus</i>
2721	S1M10000031D06	<i>Staphylococcus aureus</i>
2722	S1M10000031D07	<i>Staphylococcus aureus</i>
2723	S1M10000031D08	<i>Staphylococcus aureus</i>
2724	S1M10000031D09	<i>Staphylococcus aureus</i>
2725	S1M10000031E02	<i>Staphylococcus aureus</i>
2726	S1M10000031E03	<i>Staphylococcus aureus</i>
2727	S1M10000031E04	<i>Staphylococcus aureus</i>
2728	S1M10000031E07	<i>Staphylococcus aureus</i>
2729	S1M10000031E08	<i>Staphylococcus aureus</i>
2730	S1M10000031E10	<i>Staphylococcus aureus</i>
2731	S1M10000031E12	<i>Staphylococcus aureus</i>
2732	S1M10000031F02	<i>Staphylococcus aureus</i>
2733	S1M10000031F03	<i>Staphylococcus aureus</i>
2734	S1M10000031F04	<i>Staphylococcus aureus</i>
2735	S1M10000031F05	<i>Staphylococcus aureus</i>
2736	S1M10000031F08	<i>Staphylococcus aureus</i>
2737	S1M10000031F10	<i>Staphylococcus aureus</i>
2738	S1M10000031F11	<i>Staphylococcus aureus</i>
2739	S1M10000031F12	<i>Staphylococcus aureus</i>
2740	S1M10000031G02	<i>Staphylococcus aureus</i>
2741	S1M10000031G03	<i>Staphylococcus aureus</i>
2742	S1M10000031G04	<i>Staphylococcus aureus</i>
2743	S1M10000031G06	<i>Staphylococcus aureus</i>
2744	S1M10000031G09	<i>Staphylococcus aureus</i>
2745	S1M10000031G10	<i>Staphylococcus aureus</i>
2746	S1M10000031G11	<i>Staphylococcus aureus</i>
2747	S1M10000031H01	<i>Staphylococcus aureus</i>
2748	S1M10000031H02	<i>Staphylococcus aureus</i>
2749	S1M10000031H06	<i>Staphylococcus aureus</i>
2750	S1M10000031H09	<i>Staphylococcus aureus</i>
2751	S1M10000031H11	<i>Staphylococcus aureus</i>
2752	S1M10000032A03	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2754	S1M10000032A06	<i>Staphylococcus aureus</i>
2755	S1M10000032A07	<i>Staphylococcus aureus</i>
2756	S1M10000032A08	<i>Staphylococcus aureus</i>
2757	S1M10000032A10	<i>Staphylococcus aureus</i>
2758	S1M10000032B01	<i>Staphylococcus aureus</i>
2759	S1M10000032B05	<i>Staphylococcus aureus</i>
2760	S1M10000032B07	<i>Staphylococcus aureus</i>
2761	S1M10000032B08	<i>Staphylococcus aureus</i>
2762	S1M10000032B11	<i>Staphylococcus aureus</i>
2763	S1M10000032B12	<i>Staphylococcus aureus</i>
2764	S1M10000032C01	<i>Staphylococcus aureus</i>
2765	S1M10000032C03	<i>Staphylococcus aureus</i>
2766	S1M10000032C04	<i>Staphylococcus aureus</i>
2767	S1M10000032C05	<i>Staphylococcus aureus</i>
2768	S1M10000032C09	<i>Staphylococcus aureus</i>
2769	S1M10000032C10	<i>Staphylococcus aureus</i>
2770	S1M10000032C11	<i>Staphylococcus aureus</i>
2771	S1M10000032C12	<i>Staphylococcus aureus</i>
2772	S1M10000032D03	<i>Staphylococcus aureus</i>
2773	S1M10000032D06	<i>Staphylococcus aureus</i>
2774	S1M10000032D07	<i>Staphylococcus aureus</i>
2775	S1M10000032D09	<i>Staphylococcus aureus</i>
2776	S1M10000032D11	<i>Staphylococcus aureus</i>
2777	S1M10000032E02	<i>Staphylococcus aureus</i>
2778	S1M10000032E03	<i>Staphylococcus aureus</i>
2779	S1M10000032E04	<i>Staphylococcus aureus</i>
2780	S1M10000032E06	<i>Staphylococcus aureus</i>
2781	S1M10000032E08	<i>Staphylococcus aureus</i>
2782	S1M10000032E09	<i>Staphylococcus aureus</i>
2783	S1M10000032E10	<i>Staphylococcus aureus</i>
2784	S1M10000032E11	<i>Staphylococcus aureus</i>
2785	S1M10000032E12	<i>Staphylococcus aureus</i>
2786	S1M10000032F01	<i>Staphylococcus aureus</i>
2787	S1M10000032F04	<i>Staphylococcus aureus</i>
2788	S1M10000032F05	<i>Staphylococcus aureus</i>
2789	S1M10000032F10	<i>Staphylococcus aureus</i>
2790	S1M10000032F11	<i>Staphylococcus aureus</i>
2791	S1M10000032F12	<i>Staphylococcus aureus</i>
2792	S1M10000032G02	<i>Staphylococcus aureus</i>
2793	S1M10000032G03	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2795	S1M10000032G06	<i>Staphylococcus aureus</i>
2796	S1M10000032G08	<i>Staphylococcus aureus</i>
2797	S1M10000032G10	<i>Staphylococcus aureus</i>
2798	S1M10000032G12	<i>Staphylococcus aureus</i>
2799	S1M10000032H01	<i>Staphylococcus aureus</i>
2800	S1M10000032H04	<i>Staphylococcus aureus</i>
2801	S1M10000032H07	<i>Staphylococcus aureus</i>
2802	S1M10000032H09	<i>Staphylococcus aureus</i>
2803	S1M10000032H11	<i>Staphylococcus aureus</i>
2804	S1M10000033A02	<i>Staphylococcus aureus</i>
2805	S1M10000033A07	<i>Staphylococcus aureus</i>
2806	S1M10000033A08	<i>Staphylococcus aureus</i>
2807	S1M10000033A10	<i>Staphylococcus aureus</i>
2808	S1M10000033B02	<i>Staphylococcus aureus</i>
2809	S1M10000033B07	<i>Staphylococcus aureus</i>
2810	S1M10000033B08	<i>Staphylococcus aureus</i>
2811	S1M10000033B11	<i>Staphylococcus aureus</i>
2812	S1M10000033B12	<i>Staphylococcus aureus</i>
2813	S1M10000033C04	<i>Staphylococcus aureus</i>
2814	S1M10000033D02	<i>Staphylococcus aureus</i>
2815	S1M10000033D03	<i>Staphylococcus aureus</i>
2816	S1M10000033D04	<i>Staphylococcus aureus</i>
2817	S1M10000033D05	<i>Staphylococcus aureus</i>
2818	S1M10000033D06	<i>Staphylococcus aureus</i>
2819	S1M10000033D10	<i>Staphylococcus aureus</i>
2820	S1M10000033D12	<i>Staphylococcus aureus</i>
2821	S1M10000033E04	<i>Staphylococcus aureus</i>
2822	S1M10000033E10	<i>Staphylococcus aureus</i>
2823	S1M10000033E12	<i>Staphylococcus aureus</i>
2824	S1M10000033F02	<i>Staphylococcus aureus</i>
2825	S1M10000033F03	<i>Staphylococcus aureus</i>
2826	S1M10000033F06	<i>Staphylococcus aureus</i>
2827	S1M10000033F07	<i>Staphylococcus aureus</i>
2828	S1M10000033F09	<i>Staphylococcus aureus</i>
2829	S1M10000033F11	<i>Staphylococcus aureus</i>
2830	S1M10000033G05	<i>Staphylococcus aureus</i>
2831	S1M10000033G07	<i>Staphylococcus aureus</i>
2832	S1M10000033G09	<i>Staphylococcus aureus</i>
2833	S1M10000033G10	<i>Staphylococcus aureus</i>
2834	S1M10000033G11	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2836	S1M10000033H01	<i>Staphylococcus aureus</i>
2837	S1M10000033H02	<i>Staphylococcus aureus</i>
2838	S1M10000033H03	<i>Staphylococcus aureus</i>
2839	S1M10000033H07	<i>Staphylococcus aureus</i>
2840	S1M10000033H08	<i>Staphylococcus aureus</i>
2841	S1M10000033H09	<i>Staphylococcus aureus</i>
2842	S1M10000033H10	<i>Staphylococcus aureus</i>
2843	S1M10000033H11	<i>Staphylococcus aureus</i>
2844	S1M10000034A02	<i>Staphylococcus aureus</i>
2845	S1M10000034A03	<i>Staphylococcus aureus</i>
2846	S1M10000034A04	<i>Staphylococcus aureus</i>
2847	S1M10000034A05	<i>Staphylococcus aureus</i>
2848	S1M10000034A08	<i>Staphylococcus aureus</i>
2849	S1M10000034A09	<i>Staphylococcus aureus</i>
2850	S1M10000034A11	<i>Staphylococcus aureus</i>
2851	S1M10000034A12	<i>Staphylococcus aureus</i>
2852	S1M10000034B03	<i>Staphylococcus aureus</i>
2853	S1M10000034B05	<i>Staphylococcus aureus</i>
2854	S1M10000034B06	<i>Staphylococcus aureus</i>
2855	S1M10000034B07	<i>Staphylococcus aureus</i>
2856	S1M10000034B08	<i>Staphylococcus aureus</i>
2857	S1M10000034B09	<i>Staphylococcus aureus</i>
2858	S1M10000034B10	<i>Staphylococcus aureus</i>
2859	S1M10000034B12	<i>Staphylococcus aureus</i>
2860	S1M10000034C02	<i>Staphylococcus aureus</i>
2861	S1M10000034C06	<i>Staphylococcus aureus</i>
2862	S1M10000034C07	<i>Staphylococcus aureus</i>
2863	S1M10000034C09	<i>Staphylococcus aureus</i>
2864	S1M10000034C12	<i>Staphylococcus aureus</i>
2865	S1M10000034D01	<i>Staphylococcus aureus</i>
2866	S1M10000034D05	<i>Staphylococcus aureus</i>
2867	S1M10000034D06	<i>Staphylococcus aureus</i>
2868	S1M10000034D07	<i>Staphylococcus aureus</i>
2869	S1M10000034D08	<i>Staphylococcus aureus</i>
2870	S1M10000034D10	<i>Staphylococcus aureus</i>
2871	S1M10000034D11	<i>Staphylococcus aureus</i>
2872	S1M10000034D12	<i>Staphylococcus aureus</i>
2873	S1M10000034E01	<i>Staphylococcus aureus</i>
2874	S1M10000034E02	<i>Staphylococcus aureus</i>
2875	S1M10000034E04	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2877	S1M10000034E06	<i>Staphylococcus aureus</i>
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2879	S1M10000034E10	<i>Staphylococcus aureus</i>
2880	S1M10000034E11	<i>Staphylococcus aureus</i>
2881	S1M10000034E12	<i>Staphylococcus aureus</i>
2882	S1M10000034F01	<i>Staphylococcus aureus</i>
2883	S1M10000034F02	<i>Staphylococcus aureus</i>
2884	S1M10000034F03	<i>Staphylococcus aureus</i>
2885	S1M10000034F04	<i>Staphylococcus aureus</i>
2886	S1M10000034F05	<i>Staphylococcus aureus</i>
2887	S1M10000034F07	<i>Staphylococcus aureus</i>
2888	S1M10000034F08	<i>Staphylococcus aureus</i>
2889	S1M10000034F09	<i>Staphylococcus aureus</i>
2890	S1M10000034F10	<i>Staphylococcus aureus</i>
2891	S1M10000034F12	<i>Staphylococcus aureus</i>
2892	S1M10000034G02	<i>Staphylococcus aureus</i>
2893	S1M10000034G03	<i>Staphylococcus aureus</i>
2894	S1M10000034G06	<i>Staphylococcus aureus</i>
2895	S1M10000034G07	<i>Staphylococcus aureus</i>
2896	S1M10000034G08	<i>Staphylococcus aureus</i>
2897	S1M10000034G09	<i>Staphylococcus aureus</i>
2898	S1M10000034G11	<i>Staphylococcus aureus</i>
2899	S1M10000034G12	<i>Staphylococcus aureus</i>
2900	S1M10000034H01	<i>Staphylococcus aureus</i>
2901	S1M10000034H02	<i>Staphylococcus aureus</i>
2902	S1M10000034H03	<i>Staphylococcus aureus</i>
2903	S1M10000034H06	<i>Staphylococcus aureus</i>
2904	S1M10000034H07	<i>Staphylococcus aureus</i>
2905	S1M10000034H08	<i>Staphylococcus aureus</i>
2906	S1M10000034H09	<i>Staphylococcus aureus</i>
2907	S1M10000034H10	<i>Staphylococcus aureus</i>
2908	S1M10000035A03	<i>Staphylococcus aureus</i>
2909	S1M10000035A08	<i>Staphylococcus aureus</i>
2910	S1M10000035A09	<i>Staphylococcus aureus</i>
2911	S1M10000035A10	<i>Staphylococcus aureus</i>
2912	S1M10000035A11	<i>Staphylococcus aureus</i>
2913	S1M10000035A12	<i>Staphylococcus aureus</i>
2914	S1M10000035B01	<i>Staphylococcus aureus</i>
2915	S1M10000035B03	<i>Staphylococcus aureus</i>
2916	S1M10000035B04	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2918	S1M10000035B11	<i>Staphylococcus aureus</i>
2919	S1M10000035C01	<i>Staphylococcus aureus</i>
2920	S1M10000035C02	<i>Staphylococcus aureus</i>
2921	S1M10000035C04	<i>Staphylococcus aureus</i>
2922	S1M10000035C06	<i>Staphylococcus aureus</i>
2923	S1M10000035C11	<i>Staphylococcus aureus</i>
2924	S1M10000035D01	<i>Staphylococcus aureus</i>
2925	S1M10000035D04	<i>Staphylococcus aureus</i>
2926	S1M10000035D06	<i>Staphylococcus aureus</i>
2927	S1M10000035D09	<i>Staphylococcus aureus</i>
2928	S1M10000035D12	<i>Staphylococcus aureus</i>
2929	S1M10000035E02	<i>Staphylococcus aureus</i>
2930	S1M10000035E03	<i>Staphylococcus aureus</i>
2931	S1M10000035E04	<i>Staphylococcus aureus</i>
2932	S1M10000035E08	<i>Staphylococcus aureus</i>
2933	S1M10000035E09	<i>Staphylococcus aureus</i>
2934	S1M10000035E12	<i>Staphylococcus aureus</i>
2935	S1M10000035F03	<i>Staphylococcus aureus</i>
2936	S1M10000035F04	<i>Staphylococcus aureus</i>
2937	S1M10000035F09	<i>Staphylococcus aureus</i>
2938	S1M10000035F12	<i>Staphylococcus aureus</i>
2939	S1M10000035G02	<i>Staphylococcus aureus</i>
2940	S1M10000035G09	<i>Staphylococcus aureus</i>
2941	S1M10000035G11	<i>Staphylococcus aureus</i>
2942	S1M10000035G12	<i>Staphylococcus aureus</i>
2943	S1M10000035H01	<i>Staphylococcus aureus</i>
2944	S1M10000035H07	<i>Staphylococcus aureus</i>
2945	S1M10000035H08	<i>Staphylococcus aureus</i>
2946	S1M10000035H09	<i>Staphylococcus aureus</i>
2947	S1M10000035H10	<i>Staphylococcus aureus</i>
2948	S1M10000035H11	<i>Staphylococcus aureus</i>
2949	S1M10000036A02	<i>Staphylococcus aureus</i>
2950	S1M10000036A03	<i>Staphylococcus aureus</i>
2951	S1M10000036A04	<i>Staphylococcus aureus</i>
2952	S1M10000036A05	<i>Staphylococcus aureus</i>
2953	S1M10000036A08	<i>Staphylococcus aureus</i>
2954	S1M10000036A11	<i>Staphylococcus aureus</i>
2955	S1M10000036A12	<i>Staphylococcus aureus</i>
2956	S1M10000036B04	<i>Staphylococcus aureus</i>
2957	S1M10000036B06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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2959	S1M10000036B08	<i>Staphylococcus aureus</i>
2960	S1M10000036B11	<i>Staphylococcus aureus</i>
2961	S1M10000036B12	<i>Staphylococcus aureus</i>
2962	S1M10000036C01	<i>Staphylococcus aureus</i>
2963	S1M10000036C03	<i>Staphylococcus aureus</i>
2964	S1M10000036C04	<i>Staphylococcus aureus</i>
2965	S1M10000036C05	<i>Staphylococcus aureus</i>
2966	S1M10000036C06	<i>Staphylococcus aureus</i>
2967	S1M10000036C07	<i>Staphylococcus aureus</i>
2968	S1M10000036C09	<i>Staphylococcus aureus</i>
2969	S1M10000036C10	<i>Staphylococcus aureus</i>
2970	S1M10000036D02	<i>Staphylococcus aureus</i>
2971	S1M10000036D03	<i>Staphylococcus aureus</i>
2972	S1M10000036D06	<i>Staphylococcus aureus</i>
2973	S1M10000036D08	<i>Staphylococcus aureus</i>
2974	S1M10000036D10	<i>Staphylococcus aureus</i>
2975	S1M10000036D11	<i>Staphylococcus aureus</i>
2976	S1M10000036D12	<i>Staphylococcus aureus</i>
2977	S1M10000036E06	<i>Staphylococcus aureus</i>
2978	S1M10000036E08	<i>Staphylococcus aureus</i>
2979	S1M10000036E11	<i>Staphylococcus aureus</i>
2980	S1M10000036F06	<i>Staphylococcus aureus</i>
2981	S1M10000036F07	<i>Staphylococcus aureus</i>
2982	S1M10000036F08	<i>Staphylococcus aureus</i>
2983	S1M10000036F09	<i>Staphylococcus aureus</i>
2984	S1M10000036F10	<i>Staphylococcus aureus</i>
2985	S1M10000036F11	<i>Staphylococcus aureus</i>
2986	S1M10000036G03	<i>Staphylococcus aureus</i>
2987	S1M10000036G07	<i>Staphylococcus aureus</i>
2988	S1M10000036G08	<i>Staphylococcus aureus</i>
2989	S1M10000036G11	<i>Staphylococcus aureus</i>
2990	S1M10000036H01	<i>Staphylococcus aureus</i>
2991	S1M10000036H02	<i>Staphylococcus aureus</i>
2992	S1M10000036H03	<i>Staphylococcus aureus</i>
2993	S1M10000036H04	<i>Staphylococcus aureus</i>
2994	S1M10000036H05	<i>Staphylococcus aureus</i>
2995	S1M10000036H06	<i>Staphylococcus aureus</i>
2996	S1M10000036H08	<i>Staphylococcus aureus</i>
2997	S1M10000036H11	<i>Staphylococcus aureus</i>
2998	S1M10000037A02	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
2999	S1M10000037A03	<i>Staphylococcus aureus</i>
3000	S1M10000037A06	<i>Staphylococcus aureus</i>
3001	S1M10000037A08	<i>Staphylococcus aureus</i>
3002	S1M10000037A09	<i>Staphylococcus aureus</i>
3003	S1M10000037A11	<i>Staphylococcus aureus</i>
3004	S1M10000037A12	<i>Staphylococcus aureus</i>
3005	S1M10000037B03	<i>Staphylococcus aureus</i>
3006	S1M10000037B04	<i>Staphylococcus aureus</i>
3007	S1M10000037B05	<i>Staphylococcus aureus</i>
3008	S1M10000037B06	<i>Staphylococcus aureus</i>
3009	S1M10000037B07	<i>Staphylococcus aureus</i>
3010	S1M10000037B08	<i>Staphylococcus aureus</i>
3011	S1M10000037B10	<i>Staphylococcus aureus</i>
3012	S1M10000037B11	<i>Staphylococcus aureus</i>
3013	S1M10000037B12	<i>Staphylococcus aureus</i>
3014	S1M10000037C05	<i>Staphylococcus aureus</i>
3015	S1M10000037C06	<i>Staphylococcus aureus</i>
3016	S1M10000037C07	<i>Staphylococcus aureus</i>
3017	S1M10000037C08	<i>Staphylococcus aureus</i>
3018	S1M10000037C09	<i>Staphylococcus aureus</i>
3019	S1M10000037C10	<i>Staphylococcus aureus</i>
3020	S1M10000037D04	<i>Staphylococcus aureus</i>
3021	S1M10000037D05	<i>Staphylococcus aureus</i>
3022	S1M10000037D06	<i>Staphylococcus aureus</i>
3023	S1M10000037D09	<i>Staphylococcus aureus</i>
3024	S1M10000037D12	<i>Staphylococcus aureus</i>
3025	S1M10000037E02	<i>Staphylococcus aureus</i>
3026	S1M10000037E03	<i>Staphylococcus aureus</i>
3027	S1M10000037E06	<i>Staphylococcus aureus</i>
3028	S1M10000037E08	<i>Staphylococcus aureus</i>
3029	S1M10000037E09	<i>Staphylococcus aureus</i>
3030	S1M10000037E10	<i>Staphylococcus aureus</i>
3031	S1M10000037E11	<i>Staphylococcus aureus</i>
3032	S1M10000037E12	<i>Staphylococcus aureus</i>
3033	S1M10000037F02	<i>Staphylococcus aureus</i>
3034	S1M10000037F03	<i>Staphylococcus aureus</i>
3035	S1M10000037F04	<i>Staphylococcus aureus</i>
3036	S1M10000037F05	<i>Staphylococcus aureus</i>
3037	S1M10000037F06	<i>Staphylococcus aureus</i>
3038	S1M10000037F07	<i>Staphylococcus aureus</i>
3039	S1M10000037F08	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3041	S1M10000037F10	<i>Staphylococcus aureus</i>
3042	S1M10000037G01	<i>Staphylococcus aureus</i>
3043	S1M10000037G02	<i>Staphylococcus aureus</i>
3044	S1M10000037G03	<i>Staphylococcus aureus</i>
3045	S1M10000037G06	<i>Staphylococcus aureus</i>
3046	S1M10000037G07	<i>Staphylococcus aureus</i>
3047	S1M10000037G08	<i>Staphylococcus aureus</i>
3048	S1M10000037G10	<i>Staphylococcus aureus</i>
3049	S1M10000037H02	<i>Staphylococcus aureus</i>
3050	S1M10000037H03	<i>Staphylococcus aureus</i>
3051	S1M10000037H05	<i>Staphylococcus aureus</i>
3052	S1M10000037H07	<i>Staphylococcus aureus</i>
3053	S1M10000037H08	<i>Staphylococcus aureus</i>
3054	S1M10000037H09	<i>Staphylococcus aureus</i>
3055	S1M10000037H11	<i>Staphylococcus aureus</i>
3056	S1M10000038A04	<i>Staphylococcus aureus</i>
3057	S1M10000038A07	<i>Staphylococcus aureus</i>
3058	S1M10000038A08	<i>Staphylococcus aureus</i>
3059	S1M10000038A09	<i>Staphylococcus aureus</i>
3060	S1M10000038A11	<i>Staphylococcus aureus</i>
3061	S1M10000038A12	<i>Staphylococcus aureus</i>
3062	S1M10000038B01	<i>Staphylococcus aureus</i>
3063	S1M10000038B03	<i>Staphylococcus aureus</i>
3064	S1M10000038B07	<i>Staphylococcus aureus</i>
3065	S1M10000038B08	<i>Staphylococcus aureus</i>
3066	S1M10000038B09	<i>Staphylococcus aureus</i>
3067	S1M10000038B12	<i>Staphylococcus aureus</i>
3068	S1M10000038C01	<i>Staphylococcus aureus</i>
3069	S1M10000038C02	<i>Staphylococcus aureus</i>
3070	S1M10000038C06	<i>Staphylococcus aureus</i>
3071	S1M10000038C08	<i>Staphylococcus aureus</i>
3072	S1M10000038C10	<i>Staphylococcus aureus</i>
3073	S1M10000038C11	<i>Staphylococcus aureus</i>
3074	S1M10000038C12	<i>Staphylococcus aureus</i>
3075	S1M10000038D02	<i>Staphylococcus aureus</i>
3076	S1M10000038D05	<i>Staphylococcus aureus</i>
3077	S1M10000038D07	<i>Staphylococcus aureus</i>
3078	S1M10000038D08	<i>Staphylococcus aureus</i>
3079	S1M10000038D09	<i>Staphylococcus aureus</i>
3080	S1M10000038D10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3082	S1M10000038D12	<i>Staphylococcus aureus</i>
3083	S1M10000038E01	<i>Staphylococcus aureus</i>
3084	S1M10000038E02	<i>Staphylococcus aureus</i>
3085	S1M10000038E03	<i>Staphylococcus aureus</i>
3086	S1M10000038E04	<i>Staphylococcus aureus</i>
3087	S1M10000038E05	<i>Staphylococcus aureus</i>
3088	S1M10000038E06	<i>Staphylococcus aureus</i>
3089	S1M10000038E07	<i>Staphylococcus aureus</i>
3090	S1M10000038E10	<i>Staphylococcus aureus</i>
3091	S1M10000038E12	<i>Staphylococcus aureus</i>
3092	S1M10000038F03	<i>Staphylococcus aureus</i>
3093	S1M10000038F04	<i>Staphylococcus aureus</i>
3094	S1M10000038F05	<i>Staphylococcus aureus</i>
3095	S1M10000038F06	<i>Staphylococcus aureus</i>
3096	S1M10000038F08	<i>Staphylococcus aureus</i>
3097	S1M10000038F09	<i>Staphylococcus aureus</i>
3098	S1M10000038F10	<i>Staphylococcus aureus</i>
3099	S1M10000038F11	<i>Staphylococcus aureus</i>
3100	S1M10000038F12	<i>Staphylococcus aureus</i>
3101	S1M10000038G01	<i>Staphylococcus aureus</i>
3102	S1M10000038G03	<i>Staphylococcus aureus</i>
3103	S1M10000038G04	<i>Staphylococcus aureus</i>
3104	S1M10000038G06	<i>Staphylococcus aureus</i>
3105	S1M10000038G08	<i>Staphylococcus aureus</i>
3106	S1M10000038G10	<i>Staphylococcus aureus</i>
3107	S1M10000038G11	<i>Staphylococcus aureus</i>
3108	S1M10000038G12	<i>Staphylococcus aureus</i>
3109	S1M10000038H03	<i>Staphylococcus aureus</i>
3110	S1M10000038H07	<i>Staphylococcus aureus</i>
3111	S1M10000038H09	<i>Staphylococcus aureus</i>
3112	S1M10000038H11	<i>Staphylococcus aureus</i>
3113	S1M10000039A02	<i>Staphylococcus aureus</i>
3114	S1M10000039A05	<i>Staphylococcus aureus</i>
3115	S1M10000039A07	<i>Staphylococcus aureus</i>
3116	S1M10000039A08	<i>Staphylococcus aureus</i>
3117	S1M10000039A11	<i>Staphylococcus aureus</i>
3118	S1M10000039A12	<i>Staphylococcus aureus</i>
3119	S1M10000039B02	<i>Staphylococcus aureus</i>
3120	S1M10000039B06	<i>Staphylococcus aureus</i>
3121	S1M10000039B07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3123	S1M10000039B12	<i>Staphylococcus aureus</i>
3124	S1M10000039C04	<i>Staphylococcus aureus</i>
3125	S1M10000039C06	<i>Staphylococcus aureus</i>
3126	S1M10000039C07	<i>Staphylococcus aureus</i>
3127	S1M10000039C08	<i>Staphylococcus aureus</i>
3128	S1M10000039C09	<i>Staphylococcus aureus</i>
3129	S1M10000039C10	<i>Staphylococcus aureus</i>
3130	S1M10000039C11	<i>Staphylococcus aureus</i>
3131	S1M10000039D02	<i>Staphylococcus aureus</i>
3132	S1M10000039D09	<i>Staphylococcus aureus</i>
3133	S1M10000039D10	<i>Staphylococcus aureus</i>
3134	S1M10000039E01	<i>Staphylococcus aureus</i>
3135	S1M10000039E08	<i>Staphylococcus aureus</i>
3136	S1M10000039E09	<i>Staphylococcus aureus</i>
3137	S1M10000039E10	<i>Staphylococcus aureus</i>
3138	S1M10000039E11	<i>Staphylococcus aureus</i>
3139	S1M10000039F02	<i>Staphylococcus aureus</i>
3140	S1M10000039F03	<i>Staphylococcus aureus</i>
3141	S1M10000039F05	<i>Staphylococcus aureus</i>
3142	S1M10000039F07	<i>Staphylococcus aureus</i>
3143	S1M10000039F08	<i>Staphylococcus aureus</i>
3144	S1M10000039F09	<i>Staphylococcus aureus</i>
3145	S1M10000039F10	<i>Staphylococcus aureus</i>
3146	S1M10000039F12	<i>Staphylococcus aureus</i>
3147	S1M10000039G03	<i>Staphylococcus aureus</i>
3148	S1M10000039G04	<i>Staphylococcus aureus</i>
3149	S1M10000039G07	<i>Staphylococcus aureus</i>
3150	S1M10000039G10	<i>Staphylococcus aureus</i>
3151	S1M10000039H02	<i>Staphylococcus aureus</i>
3152	S1M10000039H03	<i>Staphylococcus aureus</i>
3153	S1M10000039H04	<i>Staphylococcus aureus</i>
3154	S1M10000039H06	<i>Staphylococcus aureus</i>
3155	S1M10000039H07	<i>Staphylococcus aureus</i>
3156	S1M10000039H08	<i>Staphylococcus aureus</i>
3157	S1M10000040A04	<i>Staphylococcus aureus</i>
3158	S1M10000040A05	<i>Staphylococcus aureus</i>
3159	S1M10000040A07	<i>Staphylococcus aureus</i>
3160	S1M10000040A08	<i>Staphylococcus aureus</i>
3161	S1M10000040A10	<i>Staphylococcus aureus</i>
3162	S1M10000040A11	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3164	S1M10000040B03	<i>Staphylococcus aureus</i>
3165	S1M10000040B07	<i>Staphylococcus aureus</i>
3166	S1M10000040B11	<i>Staphylococcus aureus</i>
3167	S1M10000040C03	<i>Staphylococcus aureus</i>
3168	S1M10000040C04	<i>Staphylococcus aureus</i>
3169	S1M10000040C05	<i>Staphylococcus aureus</i>
3170	S1M10000040C06	<i>Staphylococcus aureus</i>
3171	S1M10000040C07	<i>Staphylococcus aureus</i>
3172	S1M10000040C08	<i>Staphylococcus aureus</i>
3173	S1M10000040C10	<i>Staphylococcus aureus</i>
3174	S1M10000040C11	<i>Staphylococcus aureus</i>
3175	S1M10000040D01	<i>Staphylococcus aureus</i>
3176	S1M10000040D03	<i>Staphylococcus aureus</i>
3177	S1M10000040D08	<i>Staphylococcus aureus</i>
3178	S1M10000040D09	<i>Staphylococcus aureus</i>
3179	S1M10000040D11	<i>Staphylococcus aureus</i>
3180	S1M10000040E01	<i>Staphylococcus aureus</i>
3181	S1M10000040E02	<i>Staphylococcus aureus</i>
3182	S1M10000040E04	<i>Staphylococcus aureus</i>
3183	S1M10000040E05	<i>Staphylococcus aureus</i>
3184	S1M10000040E06	<i>Staphylococcus aureus</i>
3185	S1M10000040E07	<i>Staphylococcus aureus</i>
3186	S1M10000040E09	<i>Staphylococcus aureus</i>
3187	S1M10000040E10	<i>Staphylococcus aureus</i>
3188	S1M10000040E11	<i>Staphylococcus aureus</i>
3189	S1M10000040E12	<i>Staphylococcus aureus</i>
3190	S1M10000040F01	<i>Staphylococcus aureus</i>
3191	S1M10000040F02	<i>Staphylococcus aureus</i>
3192	S1M10000040F03	<i>Staphylococcus aureus</i>
3193	S1M10000040F04	<i>Staphylococcus aureus</i>
3194	S1M10000040F05	<i>Staphylococcus aureus</i>
3195	S1M10000040F06	<i>Staphylococcus aureus</i>
3196	S1M10000040F08	<i>Staphylococcus aureus</i>
3197	S1M10000040F09	<i>Staphylococcus aureus</i>
3198	S1M10000040F12	<i>Staphylococcus aureus</i>
3199	S1M10000040G01	<i>Staphylococcus aureus</i>
3200	S1M10000040G02	<i>Staphylococcus aureus</i>
3201	S1M10000040G04	<i>Staphylococcus aureus</i>
3202	S1M10000040G07	<i>Staphylococcus aureus</i>
3203	S1M10000040G08	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3205	S1M10000040H02	<i>Staphylococcus aureus</i>
3206	S1M10000040H03	<i>Staphylococcus aureus</i>
3207	S1M10000040H04	<i>Staphylococcus aureus</i>
3208	S1M10000040H05	<i>Staphylococcus aureus</i>
3209	S1M10000040H07	<i>Staphylococcus aureus</i>
3210	S1M10000040H10	<i>Staphylococcus aureus</i>
3211	S1M10000041A03	<i>Staphylococcus aureus</i>
3212	S1M10000041B02	<i>Staphylococcus aureus</i>
3213	S1M10000041B03	<i>Staphylococcus aureus</i>
3214	S1M10000041B05	<i>Staphylococcus aureus</i>
3215	S1M10000041B06	<i>Staphylococcus aureus</i>
3216	S1M10000041B07	<i>Staphylococcus aureus</i>
3217	S1M10000041B12	<i>Staphylococcus aureus</i>
3218	S1M10000041C08	<i>Staphylococcus aureus</i>
3219	S1M10000041C10	<i>Staphylococcus aureus</i>
3220	S1M10000041C11	<i>Staphylococcus aureus</i>
3221	S1M10000041D06	<i>Staphylococcus aureus</i>
3222	S1M10000041D07	<i>Staphylococcus aureus</i>
3223	S1M10000041D08	<i>Staphylococcus aureus</i>
3224	S1M10000041D10	<i>Staphylococcus aureus</i>
3225	S1M10000041D12	<i>Staphylococcus aureus</i>
3226	S1M10000041E03	<i>Staphylococcus aureus</i>
3227	S1M10000041E06	<i>Staphylococcus aureus</i>
3228	S1M10000041E09	<i>Staphylococcus aureus</i>
3229	S1M10000041E12	<i>Staphylococcus aureus</i>
3230	S1M10000041F03	<i>Staphylococcus aureus</i>
3231	S1M10000041F11	<i>Staphylococcus aureus</i>
3232	S1M10000041F12	<i>Staphylococcus aureus</i>
3233	S1M10000041G01	<i>Staphylococcus aureus</i>
3234	S1M10000041G06	<i>Staphylococcus aureus</i>
3235	S1M10000041G08	<i>Staphylococcus aureus</i>
3236	S1M10000041G10	<i>Staphylococcus aureus</i>
3237	S1M10000041G11	<i>Staphylococcus aureus</i>
3238	S1M10000041H01	<i>Staphylococcus aureus</i>
3239	S1M10000041H04	<i>Staphylococcus aureus</i>
3240	S1M10000041H05	<i>Staphylococcus aureus</i>
3241	S1M10000041H07	<i>Staphylococcus aureus</i>
3242	S1M10000041H08	<i>Staphylococcus aureus</i>
3243	S1M10000041H09	<i>Staphylococcus aureus</i>
3244	S1M10000042A04	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3246	S1M10000042A06	<i>Staphylococcus aureus</i>
3247	S1M10000042A07	<i>Staphylococcus aureus</i>
3248	S1M10000042A09	<i>Staphylococcus aureus</i>
3249	S1M10000042A11	<i>Staphylococcus aureus</i>
3250	S1M10000042A12	<i>Staphylococcus aureus</i>
3251	S1M10000042B02	<i>Staphylococcus aureus</i>
3252	S1M10000042B03	<i>Staphylococcus aureus</i>
3253	S1M10000042B06	<i>Staphylococcus aureus</i>
3254	S1M10000042B07	<i>Staphylococcus aureus</i>
3255	S1M10000042B08	<i>Staphylococcus aureus</i>
3256	S1M10000042B09	<i>Staphylococcus aureus</i>
3257	S1M10000042B10	<i>Staphylococcus aureus</i>
3258	S1M10000042B11	<i>Staphylococcus aureus</i>
3259	S1M10000042B12	<i>Staphylococcus aureus</i>
3260	S1M10000042C02	<i>Staphylococcus aureus</i>
3261	S1M10000042C06	<i>Staphylococcus aureus</i>
3262	S1M10000042C10	<i>Staphylococcus aureus</i>
3263	S1M10000042C11	<i>Staphylococcus aureus</i>
3264	S1M10000042D04	<i>Staphylococcus aureus</i>
3265	S1M10000042D07	<i>Staphylococcus aureus</i>
3266	S1M10000042D10	<i>Staphylococcus aureus</i>
3267	S1M10000042D11	<i>Staphylococcus aureus</i>
3268	S1M10000042E03	<i>Staphylococcus aureus</i>
3269	S1M10000042E06	<i>Staphylococcus aureus</i>
3270	S1M10000042E08	<i>Staphylococcus aureus</i>
3271	S1M10000042F01	<i>Staphylococcus aureus</i>
3272	S1M10000042F02	<i>Staphylococcus aureus</i>
3273	S1M10000042F05	<i>Staphylococcus aureus</i>
3274	S1M10000042F06	<i>Staphylococcus aureus</i>
3275	S1M10000042F08	<i>Staphylococcus aureus</i>
3276	S1M10000042F09	<i>Staphylococcus aureus</i>
3277	S1M10000042F10	<i>Staphylococcus aureus</i>
3278	S1M10000042F11	<i>Staphylococcus aureus</i>
3279	S1M10000042G01	<i>Staphylococcus aureus</i>
3280	S1M10000042G03	<i>Staphylococcus aureus</i>
3281	S1M10000042G08	<i>Staphylococcus aureus</i>
3282	S1M10000042G09	<i>Staphylococcus aureus</i>
3283	S1M10000042G12	<i>Staphylococcus aureus</i>
3284	S1M10000042H05	<i>Staphylococcus aureus</i>
3285	S1M10000042H07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3287	S1M10000043A02	<i>Staphylococcus aureus</i>
3288	S1M10000043A03	<i>Staphylococcus aureus</i>
3289	S1M10000043A04	<i>Staphylococcus aureus</i>
3290	S1M10000043A06	<i>Staphylococcus aureus</i>
3291	S1M10000043A07	<i>Staphylococcus aureus</i>
3292	S1M10000043A08	<i>Staphylococcus aureus</i>
3293	S1M10000043A10	<i>Staphylococcus aureus</i>
3294	S1M10000043A11	<i>Staphylococcus aureus</i>
3295	S1M10000043A12	<i>Staphylococcus aureus</i>
3296	S1M10000043B01	<i>Staphylococcus aureus</i>
3297	S1M10000043B02	<i>Staphylococcus aureus</i>
3298	S1M10000043B07	<i>Staphylococcus aureus</i>
3299	S1M10000043B08	<i>Staphylococcus aureus</i>
3300	S1M10000043B09	<i>Staphylococcus aureus</i>
3301	S1M10000043B10	<i>Staphylococcus aureus</i>
3302	S1M10000043B12	<i>Staphylococcus aureus</i>
3303	S1M10000043C02	<i>Staphylococcus aureus</i>
3304	S1M10000043C07	<i>Staphylococcus aureus</i>
3305	S1M10000043C11	<i>Staphylococcus aureus</i>
3306	S1M10000043C12	<i>Staphylococcus aureus</i>
3307	S1M10000043D01	<i>Staphylococcus aureus</i>
3308	S1M10000043D02	<i>Staphylococcus aureus</i>
3309	S1M10000043D04	<i>Staphylococcus aureus</i>
3310	S1M10000043D10	<i>Staphylococcus aureus</i>
3311	S1M10000043D12	<i>Staphylococcus aureus</i>
3312	S1M10000043E02	<i>Staphylococcus aureus</i>
3313	S1M10000043E03	<i>Staphylococcus aureus</i>
3314	S1M10000043E05	<i>Staphylococcus aureus</i>
3315	S1M10000043E07	<i>Staphylococcus aureus</i>
3316	S1M10000043E08	<i>Staphylococcus aureus</i>
3317	S1M10000043E10	<i>Staphylococcus aureus</i>
3318	S1M10000043E11	<i>Staphylococcus aureus</i>
3319	S1M10000043E12	<i>Staphylococcus aureus</i>
3320	S1M10000043F01	<i>Staphylococcus aureus</i>
3321	S1M10000043F05	<i>Staphylococcus aureus</i>
3322	S1M10000043F07	<i>Staphylococcus aureus</i>
3323	S1M10000043F08	<i>Staphylococcus aureus</i>
3324	S1M10000043F09	<i>Staphylococcus aureus</i>
3325	S1M10000043G01	<i>Staphylococcus aureus</i>
3326	S1M10000043G04	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
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3328	S1M10000043G09	<i>Staphylococcus aureus</i>
3329	S1M10000043G10	<i>Staphylococcus aureus</i>
3330	S1M10000043H01	<i>Staphylococcus aureus</i>
3331	S1M10000043H03	<i>Staphylococcus aureus</i>
3332	S1M10000043H04	<i>Staphylococcus aureus</i>
3333	S1M10000043H05	<i>Staphylococcus aureus</i>
3334	S1M10000043H06	<i>Staphylococcus aureus</i>
3335	S1M10000043H09	<i>Staphylococcus aureus</i>
3336	S1M10000043H10	<i>Staphylococcus aureus</i>
3337	S1M10000043H11	<i>Staphylococcus aureus</i>
3338	S1M10000044A02	<i>Staphylococcus aureus</i>
3339	S1M10000044A06	<i>Staphylococcus aureus</i>
3340	S1M10000044A08	<i>Staphylococcus aureus</i>
3341	S1M10000044A09	<i>Staphylococcus aureus</i>
3342	S1M10000044A11	<i>Staphylococcus aureus</i>
3343	S1M10000044A12	<i>Staphylococcus aureus</i>
3344	S1M10000044B01	<i>Staphylococcus aureus</i>
3345	S1M10000044B02	<i>Staphylococcus aureus</i>
3346	S1M10000044B05	<i>Staphylococcus aureus</i>
3347	S1M10000044B06	<i>Staphylococcus aureus</i>
3348	S1M10000044B08	<i>Staphylococcus aureus</i>
3349	S1M10000044B11	<i>Staphylococcus aureus</i>
3350	S1M10000044B12	<i>Staphylococcus aureus</i>
3351	S1M10000044C04	<i>Staphylococcus aureus</i>
3352	S1M10000044C06	<i>Staphylococcus aureus</i>
3353	S1M10000044C07	<i>Staphylococcus aureus</i>
3354	S1M10000044C08	<i>Staphylococcus aureus</i>
3355	S1M10000044C11	<i>Staphylococcus aureus</i>
3356	S1M10000044C12	<i>Staphylococcus aureus</i>
3357	S1M10000044D01	<i>Staphylococcus aureus</i>
3358	S1M10000044D04	<i>Staphylococcus aureus</i>
3359	S1M10000044D06	<i>Staphylococcus aureus</i>
3360	S1M10000044D08	<i>Staphylococcus aureus</i>
3361	S1M10000044D09	<i>Staphylococcus aureus</i>
3362	S1M10000044D10	<i>Staphylococcus aureus</i>
3363	S1M10000044D11	<i>Staphylococcus aureus</i>
3364	S1M10000044D12	<i>Staphylococcus aureus</i>
3365	S1M10000044E01	<i>Staphylococcus aureus</i>
3366	S1M10000044E02	<i>Staphylococcus aureus</i>
3367	S1M10000044E06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3368	S1M10000044E07	<i>Staphylococcus aureus</i>
3369	S1M10000044E09	<i>Staphylococcus aureus</i>
3370	S1M10000044E10	<i>Staphylococcus aureus</i>
3371	S1M10000044E11	<i>Staphylococcus aureus</i>
3372	S1M10000044F02	<i>Staphylococcus aureus</i>
3373	S1M10000044F06	<i>Staphylococcus aureus</i>
3374	S1M10000044F08	<i>Staphylococcus aureus</i>
3375	S1M10000044F10	<i>Staphylococcus aureus</i>
3376	S1M10000044G02	<i>Staphylococcus aureus</i>
3377	S1M10000044G05	<i>Staphylococcus aureus</i>
3378	S1M10000044G08	<i>Staphylococcus aureus</i>
3379	S1M10000044G10	<i>Staphylococcus aureus</i>
3380	S1M10000044G11	<i>Staphylococcus aureus</i>
3381	S1M10000044H06	<i>Staphylococcus aureus</i>
3382	S1M10000044H07	<i>Staphylococcus aureus</i>
3383	S1M10000044H08	<i>Staphylococcus aureus</i>
3384	S1M10000044H09	<i>Staphylococcus aureus</i>
3385	S1M10000044H10	<i>Staphylococcus aureus</i>
3386	S1M10000044H11	<i>Staphylococcus aureus</i>
3387	S1M10000045A02	<i>Staphylococcus aureus</i>
3388	S1M10000045A06	<i>Staphylococcus aureus</i>
3389	S1M10000045A07	<i>Staphylococcus aureus</i>
3390	S1M10000045A08	<i>Staphylococcus aureus</i>
3391	S1M10000045A12	<i>Staphylococcus aureus</i>
3392	S1M10000045B01	<i>Staphylococcus aureus</i>
3393	S1M10000045B02	<i>Staphylococcus aureus</i>
3394	S1M10000045B03	<i>Staphylococcus aureus</i>
3395	S1M10000045B07	<i>Staphylococcus aureus</i>
3396	S1M10000045B10	<i>Staphylococcus aureus</i>
3397	S1M10000045B11	<i>Staphylococcus aureus</i>
3398	S1M10000045B12	<i>Staphylococcus aureus</i>
3399	S1M10000045C02	<i>Staphylococcus aureus</i>
3400	S1M10000045C03	<i>Staphylococcus aureus</i>
3401	S1M10000045C04	<i>Staphylococcus aureus</i>
3402	S1M10000045C05	<i>Staphylococcus aureus</i>
3403	S1M10000045C07	<i>Staphylococcus aureus</i>
3404	S1M10000045C09	<i>Staphylococcus aureus</i>
3405	S1M10000045D01	<i>Staphylococcus aureus</i>
3406	S1M10000045D03	<i>Staphylococcus aureus</i>
3407	S1M10000045D07	<i>Staphylococcus aureus</i>
3408	S1M10000045D08	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3409	S1M10000045D09	<i>Staphylococcus aureus</i>
3410	S1M10000045D10	<i>Staphylococcus aureus</i>
3411	S1M10000045D11	<i>Staphylococcus aureus</i>
3412	S1M10000045D12	<i>Staphylococcus aureus</i>
3413	S1M10000045E04	<i>Staphylococcus aureus</i>
3414	S1M10000045E05	<i>Staphylococcus aureus</i>
3415	S1M10000045E08	<i>Staphylococcus aureus</i>
3416	S1M10000045E09	<i>Staphylococcus aureus</i>
3417	S1M10000045E10	<i>Staphylococcus aureus</i>
3418	S1M10000045E11	<i>Staphylococcus aureus</i>
3419	S1M10000045E12	<i>Staphylococcus aureus</i>
3420	S1M10000045F04	<i>Staphylococcus aureus</i>
3421	S1M10000045F05	<i>Staphylococcus aureus</i>
3422	S1M10000045F08	<i>Staphylococcus aureus</i>
3423	S1M10000045F11	<i>Staphylococcus aureus</i>
3424	S1M10000045F12	<i>Staphylococcus aureus</i>
3425	S1M10000045G03	<i>Staphylococcus aureus</i>
3426	S1M10000045G06	<i>Staphylococcus aureus</i>
3427	S1M10000045G07	<i>Staphylococcus aureus</i>
3428	S1M10000045G08	<i>Staphylococcus aureus</i>
3429	S1M10000045G10	<i>Staphylococcus aureus</i>
3430	S1M10000045G12	<i>Staphylococcus aureus</i>
3431	S1M10000045H06	<i>Staphylococcus aureus</i>
3432	S1M10000045H10	<i>Staphylococcus aureus</i>
3433	S1M10000045H11	<i>Staphylococcus aureus</i>
3434	S1M10000046A03	<i>Staphylococcus aureus</i>
3435	S1M10000046A04	<i>Staphylococcus aureus</i>
3436	S1M10000046A06	<i>Staphylococcus aureus</i>
3437	S1M10000046A08	<i>Staphylococcus aureus</i>
3438	S1M10000046A09	<i>Staphylococcus aureus</i>
3439	S1M10000046A11	<i>Staphylococcus aureus</i>
3440	S1M10000046A12	<i>Staphylococcus aureus</i>
3441	S1M10000046B01	<i>Staphylococcus aureus</i>
3442	S1M10000046B03	<i>Staphylococcus aureus</i>
3443	S1M10000046B04	<i>Staphylococcus aureus</i>
3444	S1M10000046B05	<i>Staphylococcus aureus</i>
3445	S1M10000046B07	<i>Staphylococcus aureus</i>
3446	S1M10000046B08	<i>Staphylococcus aureus</i>
3447	S1M10000046B09	<i>Staphylococcus aureus</i>
3448	S1M10000046B11	<i>Staphylococcus aureus</i>
3449	S1M10000046B12	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3450	S1M10000046C02	<i>Staphylococcus aureus</i>
3451	S1M10000046C04	<i>Staphylococcus aureus</i>
3452	S1M10000046C05	<i>Staphylococcus aureus</i>
3453	S1M10000046C06	<i>Staphylococcus aureus</i>
3454	S1M10000046C07	<i>Staphylococcus aureus</i>
3455	S1M10000046C08	<i>Staphylococcus aureus</i>
3456	S1M10000046C11	<i>Staphylococcus aureus</i>
3457	S1M10000046C12	<i>Staphylococcus aureus</i>
3458	S1M10000046D01	<i>Staphylococcus aureus</i>
3459	S1M10000046D02	<i>Staphylococcus aureus</i>
3460	S1M10000046D03	<i>Staphylococcus aureus</i>
3461	S1M10000046D04	<i>Staphylococcus aureus</i>
3462	S1M10000046D05	<i>Staphylococcus aureus</i>
3463	S1M10000046D08	<i>Staphylococcus aureus</i>
3464	S1M10000046D09	<i>Staphylococcus aureus</i>
3465	S1M10000046D10	<i>Staphylococcus aureus</i>
3466	S1M10000046D11	<i>Staphylococcus aureus</i>
3467	S1M10000046D12	<i>Staphylococcus aureus</i>
3468	S1M10000046E01	<i>Staphylococcus aureus</i>
3469	S1M10000046E02	<i>Staphylococcus aureus</i>
3470	S1M10000046E04	<i>Staphylococcus aureus</i>
3471	S1M10000046E07	<i>Staphylococcus aureus</i>
3472	S1M10000046E08	<i>Staphylococcus aureus</i>
3473	S1M10000046E10	<i>Staphylococcus aureus</i>
3474	S1M10000046F01	<i>Staphylococcus aureus</i>
3475	S1M10000046F02	<i>Staphylococcus aureus</i>
3476	S1M10000046F05	<i>Staphylococcus aureus</i>
3477	S1M10000046F06	<i>Staphylococcus aureus</i>
3478	S1M10000046F08	<i>Staphylococcus aureus</i>
3479	S1M10000046F09	<i>Staphylococcus aureus</i>
3480	S1M10000046F10	<i>Staphylococcus aureus</i>
3481	S1M10000046F12	<i>Staphylococcus aureus</i>
3482	S1M10000046G01	<i>Staphylococcus aureus</i>
3483	S1M10000046G02	<i>Staphylococcus aureus</i>
3484	S1M10000046G03	<i>Staphylococcus aureus</i>
3485	S1M10000046G04	<i>Staphylococcus aureus</i>
3486	S1M10000046G07	<i>Staphylococcus aureus</i>
3487	S1M10000046G09	<i>Staphylococcus aureus</i>
3488	S1M10000046G10	<i>Staphylococcus aureus</i>
3489	S1M10000046H01	<i>Staphylococcus aureus</i>
3490	S1M10000046H10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3491	S1M10000047A03	<i>Staphylococcus aureus</i>
3492	S1M10000047A04	<i>Staphylococcus aureus</i>
3493	S1M10000047A05	<i>Staphylococcus aureus</i>
3494	S1M10000047A06	<i>Staphylococcus aureus</i>
3495	S1M10000047A07	<i>Staphylococcus aureus</i>
3496	S1M10000047A08	<i>Staphylococcus aureus</i>
3497	S1M10000047A09	<i>Staphylococcus aureus</i>
3498	S1M10000047A10	<i>Staphylococcus aureus</i>
3499	S1M10000047A11	<i>Staphylococcus aureus</i>
3500	S1M10000047A12	<i>Staphylococcus aureus</i>
3501	S1M10000047B02	<i>Staphylococcus aureus</i>
3502	S1M10000047B04	<i>Staphylococcus aureus</i>
3503	S1M10000047B05	<i>Staphylococcus aureus</i>
3504	S1M10000047B06	<i>Staphylococcus aureus</i>
3505	S1M10000047B08	<i>Staphylococcus aureus</i>
3506	S1M10000047B09	<i>Staphylococcus aureus</i>
3507	S1M10000047B10	<i>Staphylococcus aureus</i>
3508	S1M10000047B12	<i>Staphylococcus aureus</i>
3509	S1M10000047C01	<i>Staphylococcus aureus</i>
3510	S1M10000047C02	<i>Staphylococcus aureus</i>
3511	S1M10000047C03	<i>Staphylococcus aureus</i>
3512	S1M10000047C04	<i>Staphylococcus aureus</i>
3513	S1M10000047C06	<i>Staphylococcus aureus</i>
3514	S1M10000047C08	<i>Staphylococcus aureus</i>
3515	S1M10000047C09	<i>Staphylococcus aureus</i>
3516	S1M10000047C11	<i>Staphylococcus aureus</i>
3517	S1M10000047C12	<i>Staphylococcus aureus</i>
3518	S1M10000047D02	<i>Staphylococcus aureus</i>
3519	S1M10000047D03	<i>Staphylococcus aureus</i>
3520	S1M10000047D04	<i>Staphylococcus aureus</i>
3521	S1M10000047D05	<i>Staphylococcus aureus</i>
3522	S1M10000047D09	<i>Staphylococcus aureus</i>
3523	S1M10000047D10	<i>Staphylococcus aureus</i>
3524	S1M10000047D11	<i>Staphylococcus aureus</i>
3525	S1M10000047D12	<i>Staphylococcus aureus</i>
3526	S1M10000047E01	<i>Staphylococcus aureus</i>
3527	S1M10000047E02	<i>Staphylococcus aureus</i>
3528	S1M10000047E03	<i>Staphylococcus aureus</i>
3529	S1M10000047E04	<i>Staphylococcus aureus</i>
3530	S1M10000047E05	<i>Staphylococcus aureus</i>
3531	S1M10000047E06	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3532	S1M10000047E08	<i>Staphylococcus aureus</i>
3533	S1M10000047E09	<i>Staphylococcus aureus</i>
3534	S1M10000047E10	<i>Staphylococcus aureus</i>
3535	S1M10000047E11	<i>Staphylococcus aureus</i>
3536	S1M10000047E12	<i>Staphylococcus aureus</i>
3537	S1M10000047F02	<i>Staphylococcus aureus</i>
3538	S1M10000047F03	<i>Staphylococcus aureus</i>
3539	S1M10000047F04	<i>Staphylococcus aureus</i>
3540	S1M10000047F05	<i>Staphylococcus aureus</i>
3541	S1M10000047F06	<i>Staphylococcus aureus</i>
3542	S1M10000047F07	<i>Staphylococcus aureus</i>
3543	S1M10000047F08	<i>Staphylococcus aureus</i>
3544	S1M10000047F09	<i>Staphylococcus aureus</i>
3545	S1M10000047F10	<i>Staphylococcus aureus</i>
3546	S1M10000047F11	<i>Staphylococcus aureus</i>
3547	S1M10000047F12	<i>Staphylococcus aureus</i>
3548	S1M10000047G01	<i>Staphylococcus aureus</i>
3549	S1M10000047G02	<i>Staphylococcus aureus</i>
3550	S1M10000047G04	<i>Staphylococcus aureus</i>
3551	S1M10000047G05	<i>Staphylococcus aureus</i>
3552	S1M10000047G06	<i>Staphylococcus aureus</i>
3553	S1M10000047G07	<i>Staphylococcus aureus</i>
3554	S1M10000047G08	<i>Staphylococcus aureus</i>
3555	S1M10000047G09	<i>Staphylococcus aureus</i>
3556	S1M10000047G10	<i>Staphylococcus aureus</i>
3557	S1M10000047H03	<i>Staphylococcus aureus</i>
3558	S1M10000047H04	<i>Staphylococcus aureus</i>
3559	S1M10000047H05	<i>Staphylococcus aureus</i>
3560	S1M10000047H06	<i>Staphylococcus aureus</i>
3561	S1M10000047H07	<i>Staphylococcus aureus</i>
3562	S1M10000047H08	<i>Staphylococcus aureus</i>
3563	S1M10000047H09	<i>Staphylococcus aureus</i>
3564	S1M10000047H11	<i>Staphylococcus aureus</i>
3565	S1M10000048A02	<i>Staphylococcus aureus</i>
3566	S1M10000048A03	<i>Staphylococcus aureus</i>
3567	S1M10000048A04	<i>Staphylococcus aureus</i>
3568	S1M10000048A05	<i>Staphylococcus aureus</i>
3569	S1M10000048A06	<i>Staphylococcus aureus</i>
3570	S1M10000048A07	<i>Staphylococcus aureus</i>
3571	S1M10000048A09	<i>Staphylococcus aureus</i>
3572	S1M10000048A10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3573	S1M10000048A11	<i>Staphylococcus aureus</i>
3574	S1M10000048A12	<i>Staphylococcus aureus</i>
3575	S1M10000048B02	<i>Staphylococcus aureus</i>
3576	S1M10000048B05	<i>Staphylococcus aureus</i>
3577	S1M10000048B08	<i>Staphylococcus aureus</i>
3578	S1M10000048B10	<i>Staphylococcus aureus</i>
3579	S1M10000048B11	<i>Staphylococcus aureus</i>
3580	S1M10000048B12	<i>Staphylococcus aureus</i>
3581	S1M10000048C01	<i>Staphylococcus aureus</i>
3582	S1M10000048C02	<i>Staphylococcus aureus</i>
3583	S1M10000048C03	<i>Staphylococcus aureus</i>
3584	S1M10000048C05	<i>Staphylococcus aureus</i>
3585	S1M10000048C06	<i>Staphylococcus aureus</i>
3586	S1M10000048C07	<i>Staphylococcus aureus</i>
3587	S1M10000048C08	<i>Staphylococcus aureus</i>
3588	S1M10000048C09	<i>Staphylococcus aureus</i>
3589	S1M10000048C11	<i>Staphylococcus aureus</i>
3590	S1M10000048D02	<i>Staphylococcus aureus</i>
3591	S1M10000048D08	<i>Staphylococcus aureus</i>
3592	S1M10000048D09	<i>Staphylococcus aureus</i>
3593	S1M10000048D10	<i>Staphylococcus aureus</i>
3594	S1M10000048D12	<i>Staphylococcus aureus</i>
3595	S1M10000048E02	<i>Staphylococcus aureus</i>
3596	S1M10000048E03	<i>Staphylococcus aureus</i>
3597	S1M10000048E04	<i>Staphylococcus aureus</i>
3598	S1M10000048E06	<i>Staphylococcus aureus</i>
3599	S1M10000048E07	<i>Staphylococcus aureus</i>
3600	S1M10000048E08	<i>Staphylococcus aureus</i>
3601	S1M10000048E10	<i>Staphylococcus aureus</i>
3602	S1M10000048F02	<i>Staphylococcus aureus</i>
3603	S1M10000048F07	<i>Staphylococcus aureus</i>
3604	S1M10000048F08	<i>Staphylococcus aureus</i>
3605	S1M10000048F09	<i>Staphylococcus aureus</i>
3606	S1M10000048F11	<i>Staphylococcus aureus</i>
3607	S1M10000048F12	<i>Staphylococcus aureus</i>
3608	S1M10000048G02	<i>Staphylococcus aureus</i>
3609	S1M10000048G03	<i>Staphylococcus aureus</i>
3610	S1M10000048G04	<i>Staphylococcus aureus</i>
3611	S1M10000048G05	<i>Staphylococcus aureus</i>
3612	S1M10000048G07	<i>Staphylococcus aureus</i>
3613	S1M10000048G10	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3614	S1M10000048G11	<i>Staphylococcus aureus</i>
3615	S1M10000048H01	<i>Staphylococcus aureus</i>
3616	S1M10000048H02	<i>Staphylococcus aureus</i>
3617	S1M10000048H03	<i>Staphylococcus aureus</i>
3618	S1M10000048H04	<i>Staphylococcus aureus</i>
3619	S1M10000048H05	<i>Staphylococcus aureus</i>
3620	S1M10000048H07	<i>Staphylococcus aureus</i>
3621	S1M10000048H08	<i>Staphylococcus aureus</i>
3622	S1M10000048H09	<i>Staphylococcus aureus</i>
3623	S1M10000048H10	<i>Staphylococcus aureus</i>
3624	S1M10000048H11	<i>Staphylococcus aureus</i>
3625	S1M10000009E10	<i>Staphylococcus aureus</i>
3626	S1M10000001F01	<i>Staphylococcus aureus</i>
3627	S1M10000006B12	<i>Staphylococcus aureus</i>
3628	S1M10000003D09	<i>Staphylococcus aureus</i>
3629	S1M10000001D11	<i>Staphylococcus aureus</i>
3630	S1M10000003B07	<i>Staphylococcus aureus</i>
3631	S1M10000002A07	<i>Staphylococcus aureus</i>
3632	S1M10000003F11	<i>Staphylococcus aureus</i>
3633	S1M10000047C07	<i>Staphylococcus aureus</i>
3634	S1M10000013F10	<i>Staphylococcus aureus</i>
3635	S1M10000014D11	<i>Staphylococcus aureus</i>
3636	S1M10000015F05	<i>Staphylococcus aureus</i>
3637	S1M10000048D01	<i>Staphylococcus aureus</i>
3638	S1M10000011C03	<i>Staphylococcus aureus</i>
3639	S1M10000012F03	<i>Staphylococcus aureus</i>
3640	S1M10000002F07	<i>Staphylococcus aureus</i>
3641	S1M10000048G01	<i>Staphylococcus aureus</i>
3642	S1M10000009G12	<i>Staphylococcus aureus</i>
3643	S1M10000012D05	<i>Staphylococcus aureus</i>
3644	S1M10000014D07	<i>Staphylococcus aureus</i>
3645	S1M10000047C05	<i>Staphylococcus aureus</i>
3646	S1M10000018D08*	<i>Staphylococcus aureus</i>
3647	S1M10000047B01	<i>Staphylococcus aureus</i>
3648	S1M10000047H10	<i>Staphylococcus aureus</i>
3649	S1M10000001A04	<i>Staphylococcus aureus</i>
3650	S1M10000016E01	<i>Staphylococcus aureus</i>
3651	S1M10000017E12	<i>Staphylococcus aureus</i>
3652	S1M10000019B01	<i>Staphylococcus aureus</i>
3653	S1M10000048F03	<i>Staphylococcus aureus</i>
3654	S1M10000034A07	<i>Staphylococcus aureus</i>

SeqID	Clone name	Organism
3655	S1M10000023G01	<i>Staphylococcus aureus</i>
3656	S1M10000021G12	<i>Staphylococcus aureus</i>
3657	S1M10000024E04	<i>Staphylococcus aureus</i>
3658	S1M10000028H08	<i>Staphylococcus aureus</i>
3659	S1M10000022B07	<i>Staphylococcus aureus</i>
3660	S1M10000003A05	<i>Staphylococcus aureus</i>
3661	S1M10000003A09	<i>Staphylococcus aureus</i>
3662	S1M10000003E01	<i>Staphylococcus aureus</i>
3663	S1M10000004C11	<i>Staphylococcus aureus</i>
3664	S1M10000007E08	<i>Staphylococcus aureus</i>
3665	S1M10000021G06	<i>Staphylococcus aureus</i>
3666	S1M10000024C06	<i>Staphylococcus aureus</i>
3667	S1M10000024D01	<i>Staphylococcus aureus</i>
3668	S1M10000027D07	<i>Staphylococcus aureus</i>
3669	S1M10000027E03	<i>Staphylococcus aureus</i>
3670	S1M10000027G01	<i>Staphylococcus aureus</i>
3671	S1M10000029A03	<i>Staphylococcus aureus</i>
3672	S1M10000032B10	<i>Staphylococcus aureus</i>
3673	S1M10000032C07	<i>Staphylococcus aureus</i>
3674	S1M10000038D04	<i>Staphylococcus aureus</i>
3675	S1M10000047D07	<i>Staphylococcus aureus</i>
3676	S1M10000048B03	<i>Staphylococcus aureus</i>
3677	S1M10000048B06	<i>Staphylococcus aureus</i>
3678	S1M10000048C10	<i>Staphylococcus aureus</i>
3679	S1M10000048F05	<i>Staphylococcus aureus</i>
3680	S4M10000001C01	<i>Salmonella typhimurium</i>
3681	S4M10000002B06	<i>Salmonella typhimurium</i>
3682	S4M10000002B09	<i>Salmonella typhimurium</i>
3683	S4M10000002G04	<i>Salmonella typhimurium</i>
3684	S4M10000002G08	<i>Salmonella typhimurium</i>
3685	S4M10000005G05	<i>Salmonella typhimurium</i>
3686	S4M10000005H02	<i>Salmonella typhimurium</i>
3687	S4M10000006A06	<i>Salmonella typhimurium</i>
3688	S4M10000006A08	<i>Salmonella typhimurium</i>
3689	S4M10000006C05	<i>Salmonella typhimurium</i>
3690	S4M10000006F08	<i>Salmonella typhimurium</i>
3691	S4M10000007G01	<i>Salmonella typhimurium</i>
3692	S4M10000008C08	<i>Salmonella typhimurium</i>
3693	S4M10000008H10	<i>Salmonella typhimurium</i>
3694	S4M10000009A05	<i>Salmonella typhimurium</i>
3695	S4M10000010B05	<i>Salmonella typhimurium</i>

SeqID	Clone name	Organism
3696	S4M10000010D04	<i>Salmonella typhimurium</i>
3697	S4M10000010H04	<i>Salmonella typhimurium</i>
3698	S4M10000011D08	<i>Salmonella typhimurium</i>
3699	S4M10000011E08	<i>Salmonella typhimurium</i>
3700	S4M10000012B06	<i>Salmonella typhimurium</i>
3701	S4M10000012B12	<i>Salmonella typhimurium</i>
3702	S4M10000012D02	<i>Salmonella typhimurium</i>
3703	S4M10000013H02	<i>Salmonella typhimurium</i>
3704	S4M10000014B05	<i>Salmonella typhimurium</i>
3705	S4M10000014D04	<i>Salmonella typhimurium</i>
3706	S4M10000014D07	<i>Salmonella typhimurium</i>
3707	S4M10000014H02	<i>Salmonella typhimurium</i>
3708	S4M10000015B11	<i>Salmonella typhimurium</i>
3709	S4M10000015E09	<i>Salmonella typhimurium</i>
3710	S4M10000016A02	<i>Salmonella typhimurium</i>
3711	S4M10000018D09	<i>Salmonella typhimurium</i>
3712	S4M10000018E10	<i>Salmonella typhimurium</i>
3713	S4M10000018F10	<i>Salmonella typhimurium</i>
3714	S4M10000018G03	<i>Salmonella typhimurium</i>
3715	S4M10000018H04	<i>Salmonella typhimurium</i>
3716	S4M10000019F05	<i>Salmonella typhimurium</i>
3717	S4M10000019G04	<i>Salmonella typhimurium</i>
3718	S4M10000019G05	<i>Salmonella typhimurium</i>
3719	S4M10000019H06	<i>Salmonella typhimurium</i>
3720	S4M10000020A04	<i>Salmonella typhimurium</i>
3721	S4M10000020F05	<i>Salmonella typhimurium</i>
3722	S4M10000020G10	<i>Salmonella typhimurium</i>
3723	S4M10000022D04	<i>Salmonella typhimurium</i>
3724	S4M10000022D12	<i>Salmonella typhimurium</i>
3725	S4M10000022E12	<i>Salmonella typhimurium</i>
3726	S4M10000022G07	<i>Salmonella typhimurium</i>
3727	S4M10000022H06	<i>Salmonella typhimurium</i>
3728	S4M10000023F01	<i>Salmonella typhimurium</i>
3729	S4M10000024B02	<i>Salmonella typhimurium</i>
3730	S4M10000024C06	<i>Salmonella typhimurium</i>
3731	S4M10000024C11	<i>Salmonella typhimurium</i>
3732	S4M10000024F08	<i>Salmonella typhimurium</i>
3733	S4M10000024G01	<i>Salmonella typhimurium</i>
3734	S4M10000024G04	<i>Salmonella typhimurium</i>
3735	S4M10000024G09	<i>Salmonella typhimurium</i>
3736	S4M10000024H02	<i>Salmonella typhimurium</i>

SeqID	Clone name	Organism
3737	S4M10000025A11	<i>Salmonella typhimurium</i>
3738	S4M10000025E02	<i>Salmonella typhimurium</i>
3739	S4M10000025E05	<i>Salmonella typhimurium</i>
3740	S4M10000025H07	<i>Salmonella typhimurium</i>
3741	S4M10000026C10	<i>Salmonella typhimurium</i>
3742	S4M10000026D04	<i>Salmonella typhimurium</i>
3743	S4M10000026E06	<i>Salmonella typhimurium</i>
3744	S4M10000026E12	<i>Salmonella typhimurium</i>
3745	S4M10000027C10	<i>Salmonella typhimurium</i>
3746	S4M10000027E02	<i>Salmonella typhimurium</i>
3747	S4M10000029B12	<i>Salmonella typhimurium</i>
3748	S4M10000029D12	<i>Salmonella typhimurium</i>
3749	S4M10000030D03	<i>Salmonella typhimurium</i>
3750	S4M10000030F07	<i>Salmonella typhimurium</i>
3751	S4M10000030G11	<i>Salmonella typhimurium</i>
3752	S4M10000032B12	<i>Salmonella typhimurium</i>
3753	S4M10000033F08	<i>Salmonella typhimurium</i>
3754	S4M10000033G05	<i>Salmonella typhimurium</i>
3755	S4M10000033G09	<i>Salmonella typhimurium</i>
3756	S4M10000034A02	<i>Salmonella typhimurium</i>
3757	S4M10000034A09	<i>Salmonella typhimurium</i>
3758	S4M10000034D06	<i>Salmonella typhimurium</i>
3759	S4M10000034H05	<i>Salmonella typhimurium</i>
3760	S4M10000034H09	<i>Salmonella typhimurium</i>
3761	S4M10000035B01	<i>Salmonella typhimurium</i>
3762	S4M10000035D01	<i>Salmonella typhimurium</i>
3763	S4M10000035D02	<i>Salmonella typhimurium</i>
3764	S4M10000035E03	<i>Salmonella typhimurium</i>
3765	S4M10000035F02	<i>Salmonella typhimurium</i>
3766	S4M10000035F09	<i>Salmonella typhimurium</i>
3767	S4M10000036D07	<i>Salmonella typhimurium</i>
3768	S4M10000036F07	<i>Salmonella typhimurium</i>
3769	S4M10000037A04	<i>Salmonella typhimurium</i>
3770	S4M10000037A10	<i>Salmonella typhimurium</i>
3771	S4M10000037E10	<i>Salmonella typhimurium</i>
3772	S4M10000037H09	<i>Salmonella typhimurium</i>
3773	S4M10000001H01	<i>Salmonella typhimurium</i>
3774	S4M10000002F06	<i>Salmonella typhimurium</i>
3775	S4M10000008D01	<i>Salmonella typhimurium</i>
3776	S4M10000009G11	<i>Salmonella typhimurium</i>
3777	S4M10000011F09	<i>Salmonella typhimurium</i>

SeqID	Clone name	Organism
3778	S4M10000020F08	<i>Salmonella typhimurium</i>
3779	S4M10000021E07	<i>Salmonella typhimurium</i>
3780	S4M10000022B05	<i>Salmonella typhimurium</i>
3781	S4M10000025H11	<i>Salmonella typhimurium</i>
3782	S4M10000026B10	<i>Salmonella typhimurium</i>
3783	S4M10000026E03	<i>Salmonella typhimurium</i>
3784	S4M10000029A03	<i>Salmonella typhimurium</i>
3785	S4M10000029C11	<i>Salmonella typhimurium</i>
3786	S4M10000030F06	<i>Salmonella typhimurium</i>
3787	S4M10000032F03	<i>Salmonella typhimurium</i>
3788	S4M10000032G01	<i>Salmonella typhimurium</i>
3789	S4M10000034C05	<i>Salmonella typhimurium</i>
3790	S4M10000034H04	<i>Salmonella typhimurium</i>
3791	S4M10000035A09	<i>Salmonella typhimurium</i>
3792	S4M10000035B06	<i>Salmonella typhimurium</i>
3793	S4M10000035F01	<i>Salmonella typhimurium</i>
3794	S4M10000037A08	<i>Salmonella typhimurium</i>
3795	S4M10000037E03	<i>Salmonella typhimurium</i>

TABLE VI B

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000001A02	8	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001A06	9	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B01	10	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001B02	11	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000001B02	11	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000001B02	11	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000001B05	12	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001B06	13	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001B08	14	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001B10	15	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001C02	16	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001C09	17	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000001D02	18	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000001D04	19	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000001D04	19	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001D04	19	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000001D05	20	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000001D05	20	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000001D09	21	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001D09	21	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E01	22	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000001E01	22	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000001E02	23	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000001E03	24	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E03	24	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001E04	25	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001E08	26	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001E09	27	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001E09	27	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001F02	28	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000001F04	29	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001F06	30	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000001F07	31	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000001G02	32	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000001G03	33	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001G03	33	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001G04	34	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000001G05	35	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000001H02	36	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000001H03	37	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000001H03	37	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000001H04	38	EFA100742	4891	EFA1c0022_orf_20p	10534

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000001H04	38	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000001H04	38	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000004A04	39	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000004A04	39	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000004C03	40	EFA100478	4880	EFA1c0012_orf_2p	10486
E3M10000004D01	41	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000004D01	41	EFA101413	4938	#N/A	#N/A
E3M10000004D01	41	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000004D02	42	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000004D02	42	EFA102023	4975	EFA1c0044_orf_107p	10882
E3M10000004D10	43	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000004D10	43	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000004E11	44	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004F08	45	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004F08	45	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000004F10	46	EFA101086	4910	EFA1c0040_orf_90p	10763
E3M10000004G01	47	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000004H11	48	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000004H11	48	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005A07	49	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005B01	50	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000005B01	50	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000005B08	51	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005B08	51	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005C01	52	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005C03	53	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005C04	54	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000005C04	54	EFA102453	4993	EFA1c0045_orf_203p	10931
E3M10000005C04	54	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000005D03	55	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005D04	56	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005D10	57	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005D10	57	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E01	58	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E01	58	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E02	59	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005E02	59	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005E03	60	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000005E08	61	EFA101403	4932	EFA1c0033_orf_54p	10662
E3M10000005F07	62	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000005F10	63	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005F10	63	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000005G05	64	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000005G05	64	EFA102551	5001	EFA1c0022_orf_25p	10539

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000005H04	65	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000006B03	66	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006B03	66	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006C01	67	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000006C01	67	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006C12	68	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000006C12	68	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000006D03	69	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000006D03	69	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000006E11	70	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006E11	70	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006F04	71	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000006F04	71	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000006G04	72	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G04	72	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006G12	73	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000006G12	73	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000006H09	74	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007A02	75	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007A02	75	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B02	76	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B02	76	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007B03	77	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007B03	77	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007C03	78	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000007C03	78	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000007C04	79	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000007D03	80	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007D03	80	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007E05	81	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000007E05	81	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000007E05	81	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000007F01	82	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F01	82	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007F06	83	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007F06	83	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000007G01	84	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000007G01	84	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008C03	85	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008C08	86	EFA101536	4946	EFA1c0042_orf_46p	10823
E3M10000008C09	87	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000008D08	88	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000008E02	89	EFA100783	4895	EFA1c0042_orf_141p	10811
E3M10000008G05	90	EFA101162	4919	EFA1c0022_orf_5p	10555

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000008G05	90	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000008G09	91	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000008G09	91	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000008H02	92	EFA101695	4954	EFA1c0031_orf_6p	10629
E3M10000009C07	93	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000009C09	94	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000009D01	95	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000009E02	96	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000009E03	97	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000009E05	98	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000009G02	99	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000010C08	100	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000010D05	101	EFA100757	4894	EFA1c0044_orf_27p	10897
E3M10000010F01	102	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000010G05	103	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000010G07	104	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000010G09	105	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000010G10	106	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000010H02	107	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000011A09	108	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000011B03	109	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000011B09	110	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000011C07	111	EFA101790	4959	EFA1c0042_orf_111p	10803
E3M10000011D03	112	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000011D03	112	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000011H02	113	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000011H05	114	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012B01	115	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012B02	116	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000012B07	117	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012B07	117	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012B07	117	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000012B08	118	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000012C01	119	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000012D10	120	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000012E08	121	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000012F05	122	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000012F06	123	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000012F07	124	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000012F07	124	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000012F10	125	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012F10	125	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000012G02	126	EFA101165	4922	EFA1c0022_orf_8p	10559

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000012G07	127	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000012G07	127	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000013A06	128	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000013A07	129	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013C05	130	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013C05	130	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000013D02	131	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000013D08	132	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000013D10	133	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000013D10	133	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000013E02	134	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000013E08	135	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000013F05	136	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000013F12	137	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000013F12	137	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000013G10	138	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000013H03	139	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000013H05	140	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000013H10	141	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000014B12	142	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000014B12	142	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000014B12	142	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000014E12	143	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000014E12	143	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000014G09	144	EFA100991	4905	EFA1c0035_orf_60p	10681
E3M10000014G09	144	EFA103033	5016	EFA1c0035_orf_60p	10681
E3M10000015B04	145	EFA100065	4863	EFA1c0042_orf_14p	10813
E3M10000015B12	146	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000015E12	147	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000015E12	147	EFA100211	4871	EFA1c0022_orf_10p	10523
E3M10000016A03	148	EFA101753	4957	EFA1c0022_orf_50p	10552
E3M10000016A04	149	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000016C11	150	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000016C11	150	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000016D03	151	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000016F06	152	EFA102205	4983	EFA1c0041_orf_115p	10769
E3M10000016F10	153	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000016F10	153	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000016H05	154	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000016H10	155	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000017A09	156	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000017A09	156	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000017D09	157	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000018A07	158	EFA102091	4977	EFA1c0010_orf_3p	10481

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000018C02	159	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000018E01	160	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000018G09	161	EFA101583	4949	EFA1c0026_orf_23p	10593
E3M10000018H06	162	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000019B06	163	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000019D02	164	EFA102022	4974	EFA1c0044_orf_106p	10881
E3M10000019E03	165	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000019E03	165	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000019E04	166	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000020G04	167	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000020G04	167	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000020H05	168	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000021A08	169	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000021A08	169	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021A11	170	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000021B10	171	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021C03	172	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000021C04	173	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000021C08	174	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000021D04	175	EFA100870	4899	EFA1c0031_orf_36p	10627
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E3M10000021E10	176	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000021G04	177	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000021G10	178	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000021G11	179	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000021H11	180	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000022A04	181	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022A11	182	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000022B04	183	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022B05	184	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000022B07	185	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000022C05	186	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000022C05	186	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022C06	187	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000022C09	188	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022D04	189	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000022F05	190	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000022F06	191	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000022F06	191	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000022F08	192	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000022G02	193	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000022G12	194	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023A03	195	EFA101413	4938	#N/A	#N/A

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E3M10000023A07	197	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000023A09	198	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000023B02	199	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000023B02	199	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023B06	200	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000023C03	201	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000023C03	201	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000023C04	202	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000023C06	203	EFA101413	4938	#N/A	#N/A
E3M10000023C08	204	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000023C09	205	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000023C09	205	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023D02	206	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000023D04	207	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023D10	208	EFA101413	4938	#N/A	#N/A
E3M10000023E04	209	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023E07	210	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000023E09	211	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000023F02	212	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000023F10	213	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000023G02	214	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000023G04	215	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000023G10	216	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000023H08	217	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000024A03	218	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024A04	219	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000024A08	220	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000024A08	220	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000024C06	221	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025A06	222	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025B01	223	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000025B01	223	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B03	224	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025B03	224	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025B05	225	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000025B10	226	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025C01	227	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000025C04	228	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025C05	229	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000025C05	229	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000025C07	230	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000025C08	231	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000025C08	231	EFA102502	4995	EFA1c0031_orf_36p	10627

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000025C11	233	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000025D01	234	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025D01	234	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025D10	235	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000025E07	236	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000025E08	237	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025E12	238	EFA102728	5006	EFA1c0045_orf_93p	10948
E3M10000025F04	239	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000025F04	239	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F06	240	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000025F06	240	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000025F06	240	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000025F08	241	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000025F09	242	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000025F10	243	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000025F11	244	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000025F12	245	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000025G02	246	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000025G07	247	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000025G09	248	EFA102185	4980	EFA1c0045_orf_95p	10950
E3M10000027A02	249	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000027A07	250	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027A09	251	EFA101413	4938	#N/A	#N/A
E3M10000027A09	251	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000027B07	252	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000027B08	253	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027B09	254	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000027B09	254	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000027C02	255	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000027C03	256	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027C08	257	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000027D03	258	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000027D03	258	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000027D05	259	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000027D08	260	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000027D10	261	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000027G01	262	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000027G08	263	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000027H04	264	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000027H07	265	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000027H07	265	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000028A02	266	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000028A03	267	EFA102551	5001	EFA1c0022_orf_25p	10539

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000028A04	268	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000028A05	269	EFA101080	4909	#N/A	#N/A
E3M10000028A05	269	EFA102915	5014	EFA1c0032_orf_27p	10640
E3M10000028A06	270	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000028A08	271	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000028A08	271	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000028B01	272	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000028B02	273	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028B02	273	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028B03	274	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028B04	275	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028B05	276	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000028B05	276	EFA101425	4944	EFA1c0041_orf_40p	10785
E3M10000028B06	277	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000028B07	278	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028B08	279	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000028C01	280	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C01	280	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C02	281	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C02	281	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028C04	282	EFA101322	4927	EFA1c0030_orf_57p	10620
E3M10000028C05	283	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000028C06	284	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000028C07	285	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028C08	286	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028C08	286	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000028D01	287	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000028D01	287	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000028D02	288	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000028D05	289	EFA101080	4909	#N/A	#N/A
E3M10000028D06	290	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000028D08	291	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000028E01	292	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000028E04	293	EFA101370	4931	EFA1c0040_orf_103p	10738
E3M10000028E07	294	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000028F02	295	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000028F03	296	EFA100742	4891	EFA1c0022_orf_20p	10534
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E3M10000028F03	296	EFA102554	5002	EFA1c0022_orf_19p	10532
E3M10000028F04	297	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000028F04	297	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000028F05	298	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028F06	299	EFA101164	4921	EFA1c0022_orf_7p	10558

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000028G05	301	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000028G06	302	EFA100748	4892	EFA1c0011_orf_10p	10483
E3M10000028G07	303	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000028G07	303	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000028H04	304	EFA101409	4934	EFA1c0022_orf_11p	10524
E3M10000028H07	305	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000029A02	306	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029A04	307	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029A05	308	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029A10	309	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029A11	310	EFA101413	4938	#N/A	#N/A
E3M10000029B01	311	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000029B02	312	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029B05	313	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000029B06	314	EFA100914	4900	EFA1c0024_orf_9p	10579
E3M10000029B08	315	EFA102338	4987	EFA1c0032_orf_8p	10651
E3M10000029B11	316	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000029B12	317	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000029C01	318	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029C02	319	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000029C03	320	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000029C04	321	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029C05	322	EFA100399	4878	EFA1c0041_orf_104p	10766
E3M10000029C06	323	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000029C06	323	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000029C07	324	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029C07	324	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029C08	325	EFA101868	4966	EFA1c0042_orf_69p	10829
E3M10000029C09	326	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029C10	327	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029C12	328	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029D01	329	EFA101080	4909	#N/A	#N/A
E3M10000029D03	330	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000029D04	331	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029D05	332	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029D06	333	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000029D06	333	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000029D08	334	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000029D12	335	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000029E01	336	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000029E02	337	EFA102051	4976	#N/A	#N/A
E3M10000029E03	338	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000029E05	339	EFA101686	4953	EFA1c0045_orf_63p	10940

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000029E08	341	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000029E09	342	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029E12	343	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000029F01	344	EFA100023	4862	EFA1c0017_orf_1p	10505
E3M10000029F05	345	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000029F06	346	EFA101795	4962	EFA1c0045_orf_165p	10922
E3M10000029F09	347	EFA100689	4886	EFA1c0038_orf_54p	10717
E3M10000029F10	348	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000029F11	349	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000029F12	350	EFA102282	4985	EFA1c0038_orf_89p	10729
E3M10000029G01	351	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000029G04	352	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000029G05	353	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000029G07	354	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000029G08	355	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000029G09	356	EFA102201	4982	#N/A	#N/A
E3M10000029G10	357	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000029G11	358	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000029G12	359	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000029H02	360	EFA101339	4928	EFA1c0040_orf_13p	10743
E3M10000029H02	360	EFA101340	4929	EFA1c0040_orf_15p	10745
E3M10000029H04	361	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000029H04	361	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000029H05	362	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000029H07	363	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000029H08	364	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000029H11	365	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000030A05	366	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030A08	367	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000030A09	368	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030A11	369	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000030B03	370	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000030B04	371	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000030B05	372	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B06	373	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030B07	374	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000030B08	375	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030B10	376	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030B11	377	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000030B12	378	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000030B12	378	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000030C03	379	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000030C04	380	EFA101165	4922	EFA1c0022_orf_8p	10559

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000030D02	382	EFA102350	4988	EFA1c0032_orf_19p	10632
E3M10000030D05	383	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000030D08	384	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D09	385	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000030D10	386	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030D12	387	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030E01	388	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000030E01	388	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000030E02	389	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000030E04	390	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030E08	391	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000030E09	392	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000030E10	393	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F01	394	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000030F04	395	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F06	396	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000030F07	397	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000030F10	398	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000030F12	399	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030G01	400	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000030G03	401	EFA100023	4862	EFA1c0017_orf_1p	10505
E3M10000030G06	402	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000030G08	403	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030G09	404	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000030G12	405	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000030H03	406	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000030H04	407	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000030H06	408	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000030H07	409	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000030H08	410	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000030H10	411	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000030H11	412	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000031A02	413	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000031A06	414	EFA100970	4903	EFA1c0044_orf_98p	10906
E3M10000031A07	415	EFA102201	4982	#N/A	#N/A
E3M10000031A08	416	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031B02	417	EFA100289	4872	EFA1c0042_orf_139p	10810
E3M10000031B03	418	EFA100426	4879	EFA1c0036_orf_59p	10702
E3M10000031B04	419	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000031B09	420	EFA102183	4979	EFA1c0045_orf_97p	10952
E3M10000031B10	421	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000031B11	422	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000031B12	423	EFA100642	4884	EFA1c0041_orf_56p	10792

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000031C04	425	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000031C06	426	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000031C10	427	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000031C11	428	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000031C12	429	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000031D03	430	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031D04	431	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000031D08	432	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000031E03	433	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000031E09	434	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000031F02	435	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031F02	435	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000031F04	436	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000031F07	437	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000031F09	438	EFA102764	5008	EFA1c0008_orf_3p	10478
E3M10000031F11	439	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000031F11	439	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000031G03	440	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000031G04	441	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000031G05	442	EFA102501	4994	EFA1c0031_orf_35p	10626
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E3M10000031G07	444	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031G08	445	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000031G11	446	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000031H05	447	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000031H06	448	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000031H07	449	EFA103038	5017	EFA1c0030_orf_17p	10613
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E3M10000031H10	451	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000031H11	452	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000031H11	452	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032A02	453	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032A04	454	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A06	455	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000032A07	456	EFA101670	4950	EFA1c0019_orf_20p	10511
E3M10000032A08	457	EFA100329	4875	EFA1c0041_orf_35p	10782
E3M10000032A09	458	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000032A10	459	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000032A11	460	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032A11	460	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000032B03	461	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032B04	462	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000032B07	463	EFA101164	4921	EFA1c0022_orf_7p	10558

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000032B11	466	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000032B12	467	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000032C01	468	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000032C02	469	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032C03	470	EFA103348	5025	EFA1c0043_orf_67p	10873
E3M10000032C04	471	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000032C06	472	EFA101150	4915	EFA1c0038_orf_57p	10719
E3M10000032C09	473	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000032C11	474	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000032C12	475	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032D01	476	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000032D02	477	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000032D03	478	EFA100399	4878	EFA1c0041_orf_104p	10766
E3M10000032D06	479	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032D09	480	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000032D12	481	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032E04	482	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000032E04	482	EFA103786	5031	EFA1c0042_orf_114p	10806
E3M10000032E05	483	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000032E08	484	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000032E10	485	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032E10	485	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032E11	486	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032E12	487	EFA102326	4986	#N/A	#N/A
E3M10000032F02	488	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000032F02	488	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000032F03	489	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000032F05	490	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000032F07	491	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000032F08	492	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000032F11	493	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000032F12	494	EFA102201	4982	#N/A	#N/A
E3M10000032G01	495	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000032G02	496	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000032G04	497	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000032G05	498	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000032G06	499	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000032G07	500	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000032H05	501	EFA100200	4869	EFA1c0041_orf_88p	10798
E3M10000032H06	502	EFA101833	4965	EFA1c0038_orf_61p	10720
E3M10000032H08	503	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000032H09	504	EFA103571	5030	EFA1c0044_orf_101p	10879

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000033A03	506	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000033A04	507	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033A05	508	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033A06	509	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033A07	510	EFA102774	5009	EFA1c0044_orf_25p	10896
E3M10000033A08	511	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033A11	512	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033B01	513	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000033B02	514	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000033B04	515	EFA101765	4958	EFA1c0025_orf_33p	10587
E3M10000033B05	516	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033B06	517	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033B08	518	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033B09	519	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000033C01	520	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000033C02	521	EFA103174	5021	EFA1c0036_orf_120p	10689
E3M10000033C05	522	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033C05	522	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033C09	523	EFA100811	4898	EFA1c0022_orf_33p	10546
E3M10000033C10	524	EFA101410	4935	EFA1c0022_orf_12p	10525
E3M10000033C10	524	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000033C11	525	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000033C12	526	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000033D01	527	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033D04	528	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000033D05	529	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000033D06	530	EFA100641	4883	EFA1c0041_orf_57p	10793
E3M10000033D06	530	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033D09	531	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033D10	532	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000033D11	533	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000033E02	534	EFA101477	4945	EFA1c0043_orf_224p	10861
E3M10000033E03	535	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000033E03	535	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033E04	536	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033E05	537	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000033E07	538	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033E08	539	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000033E09	540	EFA100617	4882	EFA1c0040_orf_93p	10764
E3M10000033E11	541	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000033F01	542	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F03	543	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000033F04	544	EFA100704	4887	EFA1c0010_orf_4p	10482

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E3M10000033F07	546	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033F08	547	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000033F10	548	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000033F12	549	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000033F12	549	EFA102542	4999	EFA1c0028_orf_4p	10603
E3M10000033G01	550	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000033G02	551	EFA102813	5013	EFA1c0043_orf_9p	10878
E3M10000033G03	552	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000033G04	553	EFA102326	4986	#N/A	#N/A
E3M10000033G06	554	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000033G07	555	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000033G08	556	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000033G09	557	EFA102656	5004	EFA1c0039_orf_26p	10734
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E3M10000033H02	559	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000033H04	560	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000033H05	561	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000033H07	562	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000033H08	563	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000033H09	564	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000033H10	565	EFA101079	4908	#N/A	#N/A
E3M10000033H11	566	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034A02	567	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000034A03	568	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000034A04	569	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034B02	570	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000034B04	571	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000034C04	572	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000034D01	573	EFA100704	4887	EFA1c0010_orf_4p	10482
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E3M10000034E01	575	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034E04	576	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034F02	577	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000034F03	578	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000034F04	579	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000034G02	580	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000034G03	581	EFA100740	4889	EFA1c0022_orf_22p	10536
E3M10000034H02	582	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000034H03	583	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000035A02	584	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000035A04	585	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035A05	586	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035A06	587	EFA103571	5030	EFA1c0044_orf_101p	10879

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000035A09	589	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035A11	590	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B01	591	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035B03	592	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035B06	593	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000035B07	594	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B08	595	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000035B10	596	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000035B11	597	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035B12	598	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C01	599	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C03	600	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035C04	601	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035C05	602	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035C06	603	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000035C07	604	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035C08	605	EFA100741	4890	EFA1c0022_orf_21p	10535
E3M10000035C08	605	EFA100742	4891	EFA1c0022_orf_20p	10534
E3M10000035C09	606	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000035C11	607	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035C12	608	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035D02	609	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000035D03	610	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035D04	611	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035D05	612	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000035D10	613	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000035D11	614	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000035E03	615	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000035E04	616	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000035E05	617	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000035E07	618	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000035E08	619	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000035E09	620	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035E10	621	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000035E11	622	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000035E12	623	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F01	624	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000035F02	625	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000035F03	626	EFA100312	4874	EFA1c0032_orf_28p	10641
E3M10000035F06	627	EFA101080	4909	#N/A	#N/A
E3M10000035F07	628	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000035F08	629	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F09	630	EFA101410	4935	EFA1c0022_orf_12p	10525

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
E3M10000035F09	630	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000035F11	631	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000035F12	632	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000035G02	633	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000035G02	633	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000035G04	634	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035G05	635	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000035G08	636	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000035G09	637	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000035G09	637	EFA103508	5029	EFA1c0033_orf_95p	10672
E3M10000035G10	638	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000035G11	639	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000035H03	640	EFA101080	4909	#N/A	#N/A
E3M10000035H06	641	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000035H09	642	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000035H11	643	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000035H11	643	EFA101258	4926	EFA1c0045_orf_160p	10918
E3M10000036A03	644	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036A04	645	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000036A05	646	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000036A06	647	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036A07	648	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000036A08	649	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036A09	650	EFA101165	4922	EFA1c0022_orf_8p	10559
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E3M10000036B01	652	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036B03	653	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000036B06	654	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B07	655	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036B08	656	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036B09	657	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000036B11	658	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000036B12	659	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036B12	659	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000036C01	660	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000036C03	661	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036C06	662	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036C07	663	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000036C08	664	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000036C09	665	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C10	666	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000036C11	667	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000036D03	668	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000036D04	669	EFA102201	4982	#N/A	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000036D08	671	EFA101164	4921	EFA1c0022_orf_7p	10558
E3M10000036D09	672	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036D10	673	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036D11	674	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000036D12	675	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036E01	676	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036E04	677	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036E05	678	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000036E07	679	EFA101022	4906	EFA1c0043_orf_69p	10875
E3M10000036E08	680	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F03	681	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000036F04	682	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000036F05	683	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000036F08	684	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036F09	685	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000036F10	686	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036F12	687	EFA101163	4920	EFA1c0022_orf_6p	10557
E3M10000036G01	688	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000036G01	688	EFA102551	5001	EFA1c0022_orf_25p	10539
E3M10000036G02	689	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000036G03	690	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000036G04	691	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000036G06	692	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000036G10	693	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H02	694	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000036H03	695	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000036H04	696	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000036H05	697	EFA100194	4868	EFA1c0022_orf_26p	10540
E3M10000036H06	698	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H07	699	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000036H08	700	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000036H09	701	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000036H10	702	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000037A03	703	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037A06	704	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000037A08	705	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000037A09	706	EFA100756	4893	EFA1c0024_orf_39p	10575
E3M10000037A10	707	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000037B02	708	EFA100641	4883	EFA1c0041_orf_57p	10793
E3M10000037B02	708	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037B07	709	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000037B08	710	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000037B11	711	EFA101686	4953	EFA1c0045_orf_63p	10940

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000037C02	713	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000037C04	714	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037C05	715	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000037C07	716	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037C07	716	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037C11	717	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000037C12	718	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000037D02	719	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037D03	720	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000037D03	720	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000037D04	721	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037D05	722	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000037D06	723	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037D09	724	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000037D09	724	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000037D11	725	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E01	726	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000037E02	727	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000037E03	728	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000037E05	729	EFA101080	4909	#N/A	#N/A
E3M10000037E07	730	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037E08	731	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000037E10	732	EFA101253	4924	EFA1c0043_orf_178p	10852
E3M10000037E12	733	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037F01	734	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000037F02	735	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000037F06	736	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037F07	737	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000037F12	738	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000037G01	739	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000037G02	740	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000037G03	741	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G05	742	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000037G06	743	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000037G07	744	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000037G08	745	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000037G10	746	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000037G11	747	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000037H02	748	EFA101413	4938	#N/A	#N/A
E3M10000037H05	749	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000037H07	750	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000037H10	751	EFA101080	4909	#N/A	#N/A
E3M10000037H11	752	EFA102541	4998	EFA1c0028_orf_3p	10602

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000038A05	755	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000038A06	756	EFA102549	5000	EFA1c0022_orf_24p	10538
E3M10000038A07	757	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000038A09	758	EFA102736	5007	EFA1c0022_orf_60p	10556
E3M10000038A10	759	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000038A11	760	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038B02	761	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038B03	762	EFA102389	4992	EFA1c0044_orf_83p	10904
E3M10000038B04	763	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038B05	764	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000038B05	764	EFA103081	5020	EFA1c0043_orf_228p	10862
E3M10000038B07	765	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000038B08	766	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038B09	767	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000038B11	768	EFA102656	5004	EFA1c0039_orf_26p	10734
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E3M10000038C03	770	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038C05	771	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038C07	772	EFA101963	4972	EFA1c0043_orf_162p	10848
E3M10000038C10	773	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038C12	774	EFA101080	4909	#N/A	#N/A
E3M10000038D01	775	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D02	776	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D04	777	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038D08	778	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038D10	779	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000038D11	780	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038D12	781	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038E02	782	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038E03	783	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000038E04	784	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000038E05	785	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000038E07	786	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000038E08	787	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000038E11	788	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000038F02	789	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038F04	790	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000038F05	791	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038F05	791	EFA101161	4918	EFA1c0022_orf_4p	10551
E3M10000038F06	792	EFA103571	5030	EFA1c0044_orf_101p	10879
E3M10000038F07	793	EFA103210	5022	EFA1c0036_orf_119p	10688
E3M10000038F09	794	EFA102185	4980	EFA1c0045_orf_95p	10950

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E3M10000038G02	797	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000038G03	798	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038G06	799	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000038G07	800	EFA102352	4990	EFA1c0032_orf_21p	10635
E3M10000038G07	800	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000038G11	801	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000038H02	802	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000038H05	803	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000038H06	804	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H07	805	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000038H08	806	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000038H09	807	EFA102802	5012	EFA1c0043_orf_18p	10854
E3M10000038H10	808	EFA101541	4948	EFA1c0012_orf_5p	10488
E3M10000039A02	809	EFA101736	4955	EFA1c0041_orf_14p	10775
E3M10000039A02	809	EFA101737	4956	EFA1c0041_orf_15p	10778
E3M10000039A06	810	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039A07	811	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000039A08	812	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039A10	813	EFA101257	4925	EFA1c0045_orf_159p	10917
E3M10000039A11	814	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000039B01	815	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039B03	816	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039B04	817	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000039B04	817	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B06	818	EFA100870	4899	EFA1c0031_orf_36p	10627
E3M10000039B07	819	EFA102110	4978	EFA1c0042_orf_99p	10841
E3M10000039B08	820	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000039B09	821	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000039B11	822	EFA101080	4909	#N/A	#N/A
E3M10000039C02	823	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000039C04	824	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039C05	825	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039C06	826	EFA103504	5028	EFA1c0033_orf_94p	10671
E3M10000039C07	827	EFA101791	4960	EFA1c0042_orf_112p	10804
E3M10000039C07	827	EFA101792	4961	EFA1c0042_orf_113p	10805
E3M10000039C08	828	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000039C09	829	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000039C10	830	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039D02	831	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000039D03	832	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000039D04	833	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039D06	834	EFA101540	4947	EFA1c0012_orf_4p	10487

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E3M10000039E02	836	EFA101540	4947	EFA1c0012_orf_4p	10487
E3M10000039E03	837	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039E05	838	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039E07	839	EFA103295	5024	EFA1c0032_orf_1p	10633
E3M10000039E08	840	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000039F01	841	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000039F02	842	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000039F03	843	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000039F03	843	EFA103375	5027	EFA1c0033_orf_40p	10660
E3M10000039F06	844	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000039F07	845	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039F08	846	EFA101162	4919	EFA1c0022_orf_5p	10555
E3M10000039G01	847	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000039G02	848	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G05	849	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000039G07	850	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000039G09	851	EFA102541	4998	EFA1c0028_orf_3p	10602
E3M10000039G10	852	EFA101682	4951	EFA1c0041_orf_53p	10789
E3M10000039H02	853	EFA101160	4917	EFA1c0022_orf_3p	10549
E3M10000039H07	854	EFA101080	4909	#N/A	#N/A
E3M10000039H08	855	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000039H10	856	EFA101413	4938	#N/A	#N/A
E3M10000039H11	857	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000039H11	857	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000040A03	858	EFA101123	4913	EFA1c0040_orf_22p	10748
E3M10000040A05	859	EFA101080	4909	#N/A	#N/A
E3M10000040A07	860	EFA100157	4865	EFA1c0034_orf_63p	10673
E3M10000040A09	861	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000040A10	862	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000040A11	863	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040B01	864	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000040B02	865	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000040B05	866	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000040B05	866	EFA103268	5023	EFA1c0010_orf_1p	10479
E3M10000040B06	867	EFA102518	4997	EFA1c0032_orf_46p	10647
E3M10000040B08	868	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040B09	869	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000040B10	870	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000040B11	871	EFA102764	5008	EFA1c0008_orf_3p	10478
E3M10000040B12	872	EFA100210	4870	EFA1c0022_orf_9p	10560
E3M10000040C02	873	EFA101080	4909	#N/A	#N/A
E3M10000040C05	874	EFA102501	4994	EFA1c0031_orf_35p	10626
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000040C09	878	EFA100165	4866	EFA1c0032_orf_23p	10637
E3M10000040C09	878	EFA102353	4991	EFA1c0032_orf_22p	10636
E3M10000040C10	879	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040C11	880	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000040C12	881	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040D03	882	EFA102201	4982	#N/A	#N/A
E3M10000040D04	883	EFA101080	4909	#N/A	#N/A
E3M10000040D08	884	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040D12	885	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000040E02	886	EFA102051	4976	#N/A	#N/A
E3M10000040E10	887	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040E11	888	EFA103039	5018	EFA1c0043_orf_16p	10850
E3M10000040E12	889	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000040F01	890	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000040F03	891	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000040F08	892	EFA101080	4909	#N/A	#N/A
E3M10000040F09	893	EFA100919	4901	EFA1c0013_orf_12p	10491
E3M10000040F10	894	EFA102051	4976	#N/A	#N/A
E3M10000040G01	895	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000040G02	896	EFA101424	4943	EFA1c0041_orf_39p	10784
E3M10000040G02	896	EFA101425	4944	EFA1c0041_orf_40p	10785
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E3M10000040G05	898	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000040G07	899	EFA101079	4908	#N/A	#N/A
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E3M10000040G08	900	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000040G09	901	EFA103021	5015	EFA1c0030_orf_16p	10612
E3M10000040G11	902	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000040H02	903	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000040H03	904	EFA100394	4876	EFA1c0034_orf_6p	10675
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E3M10000040H04	905	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H05	906	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000040H05	906	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000040H09	907	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000040H09	907	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041A03	908	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000041A05	909	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041A08	910	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041A09	911	EFA101354	4930	EFA1c0032_orf_69p	10648
E3M10000041A10	912	EFA100001	4861	EFA1c0030_orf_3p	10618
E3M10000041A11	913	EFA100642	4884	EFA1c0041_orf_56p	10792

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000041B05	916	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B06	917	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041B08	918	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041B09	919	EFA101924	4970	EFA1c0044_orf_18p	10891
E3M10000041B09	919	EFA101925	4971	EFA1c0044_orf_19p	10893
E3M10000041B10	920	EFA101080	4909	#N/A	#N/A
E3M10000041B11	921	EFA101416	4941	EFA1c0022_orf_17p	10530
E3M10000041B11	921	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041B12	922	EFA101411	4936	EFA1c0022_orf_13p	10526
E3M10000041C01	923	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000041C07	924	EFA100739	4888	EFA1c0022_orf_23p	10537
E3M10000041C08	925	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000041C09	926	EFA103365	5026	EFA1c0022_orf_1p	10533
E3M10000041C10	927	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000041C11	928	EFA102655	5003	EFA1c0039_orf_25p	10733
E3M10000041C12	929	EFA100798	4897	EFA1c0042_orf_160p	10818
E3M10000041D02	930	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041D03	931	EFA101060	4907	EFA1c0038_orf_73p	10722
E3M10000041D04	932	EFA100642	4884	EFA1c0041_orf_56p	10792
E3M10000041D04	932	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041D05	933	EFA101080	4909	#N/A	#N/A
E3M10000041D06	934	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000041D08	935	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041D09	936	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000041D10	937	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000041D11	938	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041D12	939	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000041E02	940	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000041E03	941	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041E05	942	EFA101415	4940	EFA1c0022_orf_16p	10529
E3M10000041E07	943	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000041E10	944	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041E11	945	EFA100190	4867	EFA1c0010_orf_2p	10480
E3M10000041F03	946	EFA102503	4996	EFA1c0032_orf_32p	10643
E3M10000041F05	947	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000041F06	948	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000041F07	949	EFA101159	4916	EFA1c0022_orf_2p	10543
E3M10000041F08	950	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000041F09	951	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000041F10	952	EFA101079	4908	#N/A	#N/A
E3M10000041F10	952	EFA101080	4909	#N/A	#N/A

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E3M10000041G03	955	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000041G04	956	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041G06	957	EFA100978	4904	EFA1c0022_orf_27p	10541
E3M10000041G07	958	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000041G08	959	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041G09	960	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000041G10	961	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000041G12	962	EFA100394	4876	EFA1c0034_orf_6p	10675
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E3M10000041H06	965	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000041H07	966	EFA103062	5019	EFA1c0030_orf_19p	10615
E3M10000041H08	967	EFA101686	4953	EFA1c0045_orf_63p	10940
E3M10000041H09	968	EFA102788	5011	EFA1c0033_orf_41p	10661
E3M10000041H10	969	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000041H11	970	EFA102253	4984	EFA1c0038_orf_85p	10727
E3M10000042A03	971	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000042A03	971	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042A08	972	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000042A10	973	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042B01	974	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000042B02	975	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000042B04	976	EFA102186	4981	EFA1c0045_orf_94p	10949
E3M10000042B04	976	EFA102453	4993	EFA1c0045_orf_203p	10931
E3M10000042B08	977	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000042B09	978	EFA101797	4963	EFA1c0045_orf_167p	10924
E3M10000042B10	979	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042B11	980	EFA101165	4922	EFA1c0022_orf_8p	10559
E3M10000042C02	981	EFA101150	4915	EFA1c0038_orf_57p	10719
E3M10000042C03	982	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000042C04	983	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000042C10	984	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000042C10	984	EFA100295	4873	EFA1c0021_orf_15p	10517
E3M10000042D01	985	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000042D02	986	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000042D03	987	EFA100394	4876	EFA1c0034_orf_6p	10675
E3M10000042D06	988	EFA102091	4977	EFA1c0010_orf_3p	10481
E3M10000042D09	989	EFA101141	4914	EFA1c0030_orf_18p	10614
E3M10000042D11	990	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000042D12	991	EFA100795	4896	EFA1c0043_orf_229p	10863
E3M10000042E05	992	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000042E12	993	EFA102351	4989	EFA1c0032_orf_20p	10634

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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E3M10000042G01	995	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000042G05	996	EFA101685	4952	EFA1c0041_orf_55p	10791
E3M10000042G07	997	EFA101169	4923	EFA1c0024_orf_38p	10574
E3M10000042G08	998	EFA102780	5010	EFA1c0045_orf_101p	10908
E3M10000042G11	999	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000042G11	999	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000042G12	1000	EFA102501	4994	EFA1c0031_orf_35p	10626
E3M10000042H06	1001	EFA101799	4964	EFA1c0045_orf_169p	10926
E3M10000042H08	1002	EFA101120	4911	EFA1c0036_orf_113p	10687
E3M10000042H11	1003	EFA100668	4885	EFA1c0035_orf_58p	10679
E3M10000043A02	1004	EFA101799	4964	EFA1c0045_orf_169p	10926
E3M10000043A03	1005	EFA101414	4939	EFA1c0022_orf_15p	10528
E3M10000043A05	1006	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043A08	1007	EFA100689	4886	EFA1c0038_orf_54p	10717
E3M10000043A09	1008	EFA101414	4939	EFA1c0022_orf_15p	10528
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E3M10000043A10	1009	EFA101080	4909	#N/A	#N/A
E3M10000043A11	1010	EFA102006	4973	EFA1c0025_orf_17p	10580
E3M10000043B01	1011	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043B02	1012	EFA101121	4912	EFA1c0036_orf_112p	10686
E3M10000043B03	1013	EFA103038	5017	EFA1c0030_orf_17p	10613
E3M10000043B06	1014	EFA101404	4933	EFA1c0033_orf_55p	10663
E3M10000043B08	1015	EFA101123	4913	EFA1c0040_orf_22p	10748
E3M10000043B09	1016	EFA101892	4969	EFA1c0017_orf_21p	10506
E3M10000043B10	1017	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000043B11	1018	EFA100704	4887	EFA1c0010_orf_4p	10482
E3M10000043B12	1019	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043C01	1020	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000043C08	1021	EFA101412	4937	EFA1c0022_orf_14p	10527
E3M10000043C09	1022	EFA100151	4864	EFA1c0021_orf_14p	10516
E3M10000043D01	1023	EFA101417	4942	EFA1c0022_orf_18p	10531
E3M10000043D02	1024	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043D09	1025	EFA102351	4989	EFA1c0032_orf_20p	10634
E3M10000043D10	1026	EFA101872	4967	EFA1c0042_orf_152p	10815
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E3M10000043D12	1027	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043E03	1028	EFA100397	4877	EFA1c0041_orf_148p	10773
E3M10000043E07	1029	EFA101339	4928	EFA1c0040_orf_13p	10743
E3M10000043E08	1030	EFA101872	4967	EFA1c0042_orf_152p	10815
E3M10000043E08	1030	EFA101873	4968	EFA1c0042_orf_153p	10816
E3M10000043E10	1031	EFA102656	5004	EFA1c0039_orf_26p	10734
E3M10000043E11	1032	EFA102813	5013	EFA1c0043_orf_9p	10878
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E3M10000043F08	1036	EFA101121	4912	EFA1c0036_orf_112p	10686
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E3M10000043F12	1038	EFA101080	4909	#N/A	#N/A
E3M10000043G03	1039	EFA102502	4995	EFA1c0031_orf_36p	10627
E3M10000043G04	1040	EFA102502	4995	EFA1c0031_orf_36p	10627
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E3M10000043G07	1042	EFA100157	4865	EFA1c0034_orf_63p	10673
E3M10000043G08	1043	EFA101080	4909	#N/A	#N/A
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E3M10000043G11	1045	EFA101080	4909	#N/A	#N/A
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E3M10000043H02	1047	EFA101414	4939	EFA1c0022_orf_15p	10528
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E3M10000043H08	1049	EFA100615	4881	EFA1c0016_orf_29p	10501
E3M10000043H09	1050	EFA102006	4973	EFA1c0025_orf_17p	10580
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E3M10000044C02	1052	EFA100955	4902	EFA1c0022_orf_28p	10542
E3M10000044E01	1053	EFA102091	4977	EFA1c0010_orf_3p	10481
K1M10000002F02	1054	KPN101750	5037	KPN1c1723_orf_1p	11652
K1M10000003C01	1055	KPN103882	5040	KPN1c2848_orf_1p	11716
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K1M10000020B02	1065	KPN101729	5036	KPN1c1566_orf_1p	11647
K1M10000022C10	1067	KPN100854	5033	KPN1c0845_orf_1p	11630
K1M10000030C07	1070	KPN104716	5045	KPN1c3094_orf_5p	11757
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K1M10000039H03	1079	KPN106840	5050	KPN1c2087_orf_1p	11664
K1M10000043D05	1081	KPN102638	5039	KPN1c2127_orf_1p	11667
K1M10000043H10	1082	KPN105722	5046	#N/A	#N/A
K1M10000044D08	1084	KPN104430	5043	#N/A	#N/A
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K1M10000045D10	1088	KPN102638	5039	KPN1c2127_orf_1p	11667
P1M10000008C06	1092	PA2424	5107	#N/A	#N/A
P1M10000008G04	1093	PA0337	5060	#N/A	#N/A
P1M10000010C03	1094	PA4997	5202	#N/A	#N/A
P1M10000014H10	1095	PA4252	5168	#N/A	#N/A
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P1M10000015C06	1096	PA0413	5064	#N/A	#N/A
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P1M10000018B01	1099	PA4264	5177	#N/A	#N/A
P1M10000018C01	1100	PA4264	5177	#N/A	#N/A
P1M10000018E01	1101	PA4067	5151	#N/A	#N/A
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P1M10000019F01	1103	PA4271	5180	#N/A	#N/A
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P1M10000021G03	1104	PA4264	5177	#N/A	#N/A
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P1M10000022D09	1106	PA5299	5211	#N/A	#N/A
P1M10000024D06	1107	PA3160	5130	#N/A	#N/A
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P1M10000026G09	1115	PA3011	5122	#N/A	#N/A
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P1M10000027G05	1120	PA2313	5105	#N/A	#N/A
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P1M10000028B01	1122	PA4263	5176	#N/A	#N/A
P1M10000028E02	1123	PA2584	5112	#N/A	#N/A
P1M10000029A09	1124	PA3154	5129	#N/A	#N/A
P1M10000029G03	1125	PA1301	5083	#N/A	#N/A
P1M10000029H05	1126	PA0353	5061	#N/A	#N/A
P1M10000032F04	1127	PA0265	5058	#N/A	#N/A
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PIM10000037B12	1134	PA4254	5170	#N/A	#N/A
PIM10000037G12	1135	PA5076	5204	#N/A	#N/A
PIM10000038B08	1136	PA4070	5152	#N/A	#N/A
PIM10000038C03	1137	PA3931	5146	#N/A	#N/A
PIM10000038C06	1138	PA2197	5103	#N/A	#N/A
PIM10000038F04	1139	PA5207	5208	#N/A	#N/A
PIM10000038G02	1140	PA4542	5192	#N/A	#N/A
PIM10000039G05	1141	PA3764	5141	#N/A	#N/A
PIM10000039G12	1142	PA5567	5220	#N/A	#N/A
PIM10000040C01	1143	PA4105	5154	#N/A	#N/A
PIM10000040C04	1144	PA1115	5081	#N/A	#N/A
PIM10000040D04	1145	PA0378	5062	#N/A	#N/A
PIM10000040D05	1146	PA5209	5209	#N/A	#N/A
PIM10000040E10	1147	PA2128	5100	#N/A	#N/A
PIM10000040H03	1148	PA1115	5081	#N/A	#N/A
PIM10000041A12	1149	PA4254	5170	#N/A	#N/A
PIM10000041B02	1150	PA2128	5100	#N/A	#N/A
PIM10000041E01	1151	PA2398	5106	#N/A	#N/A
PIM10000041F01	1152	PA4681	5196	#N/A	#N/A
PIM10000042B12	1153	PA0642	5072	#N/A	#N/A
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PIM10000043A03	1155	PA3006	5121	#N/A	#N/A
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PIM10000044F07	1157	PA4244	5160	#N/A	#N/A
PIM10000046B03	1158	PA1462	5087	#N/A	#N/A
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PIM10000046G11	1162	PA1115	5081	#N/A	#N/A
PIM10000047B04	1163	PA3006	5121	#N/A	#N/A
PIM10000047E11	1164	PA2684	5118	#N/A	#N/A
PIM10000047F07	1165	PA4506	5190	#N/A	#N/A
PIM10000047G10	1166	PA4259	5174	#N/A	#N/A
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PIM10000049E08	1168	PA4272	5181	#N/A	#N/A
PIM10000049G10	1169	PA4027	5149	#N/A	#N/A
PIM10000050G11	1170	PA4249	5165	#N/A	#N/A
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P1M10000053F08	1179	PA1270	5082	#N/A	#N/A
P1M10000055A11	1180	PA5076	5204	#N/A	#N/A
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P1M10000055E05	1182	PA5507	5219	#N/A	#N/A
P1M10000056C07	1183	PA1360	5084	#N/A	#N/A
P1M10000056F05	1184	PA4258	5173	#N/A	#N/A
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P1M10000056F06	1185	PA2634	5114	#N/A	#N/A
P1M10000056G01	1186	PA5076	5204	#N/A	#N/A
P1M10000058B07	1187	PA5436	5215	#N/A	#N/A
P1M10000059B04	1188	PA4375	5186	#N/A	#N/A
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P1M10000059B11	1190	PA0934	5077	#N/A	#N/A
P1M10000059D11	1191	PA4027	5149	#N/A	#N/A
P1M10000059H08	1192	PA4027	5149	#N/A	#N/A
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P1M10000060H04	1196	PA4473	5189	#N/A	#N/A
P1M10000061B04	1197	PA2726	5119	#N/A	#N/A
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P1M10000061F04	1199	PA3522	5136	#N/A	#N/A
P1M10000062A12	1200	PA4598	5194	#N/A	#N/A
P1M10000062C03	1201	PA0321	5059	#N/A	#N/A
P1M10000062C04	1202	PA4254	5170	#N/A	#N/A
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P1M10000062H04	1211	PA4254	5170	#N/A	#N/A
P1M10000063F02	1212	PA2684	5118	#N/A	#N/A
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PIM10000064D03	1218	PA0129	5055	#N/A	#N/A
PIM10000064E05	1219	PA4512	5191	#N/A	#N/A
PIM10000064G12	1220	PA2147	5101	#N/A	#N/A
PIM10000064H07	1221	PA1072	5080	#N/A	#N/A
PIM10000065A04	1222	PA3522	5136	#N/A	#N/A
PIM10000065B07	1223	PA4347	5184	#N/A	#N/A
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PIM10000067C04	1236	PA3845	5142	#N/A	#N/A
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PIM10000067F05	1239	PA3643	5137	#N/A	#N/A
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PIM10000068F04	1243	PA4237	5158	#N/A	#N/A
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PIM10000068G01	1245	PA3716	5140	#N/A	#N/A
PIM10000068H05	1246	PA4268	5178	#N/A	#N/A
PIM10000069D09	1247	PA4246	5162	#N/A	#N/A
PIM10000069G06	1248	PA4246	5162	#N/A	#N/A
PIM10000069H02	1249	PA4433	5188	#N/A	#N/A
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PIM10000070C06	1252	PA4237	5158	#N/A	#N/A
PIM10000070D08	1253	PA4105	5154	#N/A	#N/A
PIM10000070E03	1254	PA4709	5197	#N/A	#N/A
PIM10000070G06	1255	PA3374	5133	#N/A	#N/A
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P1M10000071F01	1261	PA0506	5070	#N/A	#N/A
P1M10000073A06	1262	PA4246	5162	#N/A	#N/A
P1M10000073B10	1263	PA5248	5210	#N/A	#N/A
P1M10000073D04	1264	PA1115	5081	#N/A	#N/A
P1M10000073D09	1265	PA1918	5094	#N/A	#N/A
P1M10000073G03	1266	PA5248	5210	#N/A	#N/A
P1M10000074B01	1267	PA4771	5199	#N/A	#N/A
P1M10000074B04	1268	PA1684	5091	#N/A	#N/A
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P1M10000077H05	1282	PA4246	5162	#N/A	#N/A
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P1M10000083B12	1304	PA4268	5178	#N/A	#N/A
P1M10000083C11	1305	PA4242	5159	#N/A	#N/A
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P1M10000086A02	1313	PA4413	5187	#N/A	#N/A
P1M10000086B01	1314	PA4158	5157	#N/A	#N/A
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P1M10000093A03	1338	PA5088	5205	#N/A	#N/A
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PIM10000094F04	1344	PA4268	5178	#N/A	#N/A
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PIM10000095C01	1346	PA2488	5110	#N/A	#N/A
PIM10000095C09	1347	PA5443	5216	#N/A	#N/A
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SIM10000001A09	1356	SAU101907	5574	SAU1c0040_orf_79p	12442
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SIM10000001D07	1362	SAU101360	5431	SAU1c0044_orf_109p	12555
SIM10000001E02	1363	SAU102602	5708	SAU1c0032_orf_5p	12249
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SIM10000001E09	1366	SAU201752	5832	SAU2c0436_orf_19p	12963
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SIM10000002A09	1380	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000002A10	1381	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000002A10	1381	SAU202174	5845	SAU2c0412_orf_3p	12895
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SIM10000002B03	1384	SAU101034	5371	SAU1c0044_orf_27p	12608
SIM10000002B04	1385	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000002B05	1386	SAU101868	5565	SAU1c0036_orf_23p	12320
SIM10000002B06	1387	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000002B07	1388	SAU101389	5441	SAU1c0038_orf_54p	12387
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SIM10000002E11	1408	SAU102631	5721	SAU1c0045_orf_94p	12712
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SIM10000002F02	1411	SAU301620	5899	SAU3c1478_orf_2p	13140
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M1000002G05	1417	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M1000002G06	1418	SAU101907	5574	SAU1c0040_orf_79p	12442
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S1M1000002G08	1420	SAU100158	5238	SAU1c0040_orf_80p	12443
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S1M1000002G10	1422	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M1000002G11	1423	SAU102939	5747	#N/A	#N/A
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S1M1000003A01	1425	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M1000003E07	1446	SAU100964	5363	SAU1c0044_orf_86p	12641
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000004A11	1463	SAU100521	5283	SAU1c0044_orf_250p	12600
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000004D12	1487	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000004E03	1488	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000004E04	1489	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000004E06	1490	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000004E07	1491	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000004E11	1492	SAU102939	5747	#N/A	#N/A
S1M10000004E12	1493	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000004F01	1494	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000004F02	1495	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000004F06	1496	SAU201611	5825	SAU2c0440_orf_14p	12973
S1M10000004F07	1497	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000004F08	1498	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000004F08	1498	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000004F09	1499	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000004F09	1499	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000004F09	1499	SAU301148	5888	#N/A	#N/A
S1M10000004F12	1500	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000004G01	1501	SAU201810	5836	SAU2c0308_orf_2p	12769
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S1M10000004G02	1502	SAU102939	5747	#N/A	#N/A
S1M10000004G03	1503	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000004G05	1504	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000004G06	1505	SAU102939	5747	#N/A	#N/A
S1M10000004G07	1506	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000004G07	1506	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000004G09	1507	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000004G12	1508	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000005A01	1509	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A01	1509	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A01	1509	SAU301148	5888	#N/A	#N/A
S1M10000005A03	1510	SAU101090	5380	SAU1c0028_orf_8p	12191
S1M10000005A05	1511	SAU102939	5747	#N/A	#N/A
S1M10000005A06	1512	SAU102939	5747	#N/A	#N/A
S1M10000005A07	1513	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000005A08	1514	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000005A08	1514	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000005A08	1514	SAU301148	5888	#N/A	#N/A
S1M10000005A09	1515	SAU103038	5757	#N/A	#N/A
S1M10000005A10	1516	SAU101239	5402	SAU1c0044_orf_15p	12570
S1M10000005A10	1516	SAU101240	5403	SAU1c0044_orf_16p	12573

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000005B02	1518	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000005B04	1519	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000005B07	1520	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000005B07	1520	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000005B07	1520	SAU301148	5888	#N/A	#N/A
SIM10000005B08	1521	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000005B09	1522	SAU102422	5666	SAU1c0030_orf_22p	12207
SIM10000005B12	1523	SAU102284	5635	SAU1c0038_orf_5p	12389
SIM10000005B12	1523	SAU201469	5816	SAU2c0438_orf_6p	12967
SIM10000005C01	1524	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000005C01	1524	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000005C01	1524	SAU301148	5888	#N/A	#N/A
SIM10000005C05	1525	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000005C06	1526	SAU100885	5348	SAU1c0038_orf_38p	12376
SIM10000005C09	1527	SAU302513	5906	SAU3c1298_orf_1p	13085
SIM10000005C11	1528	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000005D01	1529	SAU103038	5757	#N/A	#N/A
SIM10000005D02	1530	SAU102007	5590	SAU1c0040_orf_108p	12428
SIM10000005D03	1531	SAU101907	5574	SAU1c0040_orf_79p	12442
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SIM10000005D04	1532	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000005D05	1533	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000005D06	1534	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000005D06	1534	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000005D07	1535	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000005D08	1536	SAU101624	5497	SAU1c0040_orf_25p	12429
SIM10000005D09	1537	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000005D11	1538	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000005D12	1539	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000005E01	1540	SAU100542	5288	SAU1c0043_orf_210p	12532
SIM10000005E02	1541	SAU102631	5721	SAU1c0045_orf_94p	12712
SIM10000005E05	1542	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000005E05	1542	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000005E05	1542	SAU301148	5888	#N/A	#N/A
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SIM10000005E07	1544	SAU102939	5747	#N/A	#N/A
SIM10000005E08	1545	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000005E08	1545	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000005E08	1545	SAU301148	5888	#N/A	#N/A
SIM10000005E10	1546	SAU102939	5747	#N/A	#N/A
SIM10000005E11	1547	SAU100381	5265	SAU1c0033_orf_9p	12276
SIM10000005E12	1548	SAU102939	5747	#N/A	#N/A
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000005F03	1550	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000005F03	1550	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000005F04	1551	SAU102044	5593	SAU1c0039_orf_65p	12414
SIM10000005F04	1551	SAU102046	5594	SAU1c0039_orf_66p	12415
SIM10000005F04	1551	SAU201961	5840	#N/A	#N/A
SIM10000006A03	1552	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006A03	1552	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000006A03	1552	SAU301148	5888	#N/A	#N/A
SIM10000006A04	1553	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000006A05	1554	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000006A05	1554	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000006A07	1555	SAU100952	5358	SAU1c0043_orf_182p	12523
SIM10000006A08	1556	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006A08	1556	SAU202174	5845	SAU2c0412_orf_3p	12895
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SIM10000006A10	1557	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006A10	1557	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000006A10	1557	SAU301148	5888	#N/A	#N/A
SIM10000006A12	1558	SAU101907	5574	SAU1c0040_orf_79p	12442
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SIM10000006B04	1561	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006B04	1561	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000006B04	1561	SAU301148	5888	#N/A	#N/A
SIM10000006B07	1562	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000006B10	1563	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000006B11	1564	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000006C02	1565	SAU102939	5747	#N/A	#N/A
SIM10000006C04	1566	SAU102287	5637	SAU1c0038_orf_7p	12398
SIM10000006C06	1567	SAU102486	5687	SAU1c0039_orf_93p	12420
SIM10000006C06	1567	SAU102487	5688	SAU1c0039_orf_92p	12419
SIM10000006C07	1568	SAU100157	5237	SAU1c0040_orf_81p	12444
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SIM10000006C10	1570	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006C10	1570	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000006C10	1570	SAU301148	5888	#N/A	#N/A
SIM10000006D03	1571	SAU100608	5297	SAU1c0034_orf_69p	12293
SIM10000006D05	1572	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006D05	1572	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000006D05	1572	SAU301148	5888	#N/A	#N/A
SIM10000006D06	1573	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000006D06	1573	SAU202174	5845	SAU2c0412_orf_3p	12895
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000006D08	1575	SAU102939	5747	#N/A	#N/A
S1M10000006E02	1576	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006E02	1576	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E02	1576	SAU301148	5888	#N/A	#N/A
S1M10000006E03	1577	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000006E04	1578	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000006E07	1579	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000006E07	1579	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000006E07	1579	SAU301148	5888	#N/A	#N/A
S1M10000006E08	1580	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000006F01	1581	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000006F02	1582	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000006F03	1583	SAU102294	5639	SAU1c0044_orf_288p	12610
S1M10000006F03	1583	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000006F04	1584	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000006F06	1585	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000006G02	1586	SAU101833	5555	SAU1c0038_orf_34p	12373
S1M10000006G03	1587	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000006G05	1588	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000006G06	1589	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000006G07	1590	SAU101612	5493	SAU1c0044_orf_7p	12637
S1M10000006G07	1590	SAU202945	5857	SAU2c0394_orf_7p	12868
S1M10000006G09	1591	SAU102939	5747	#N/A	#N/A
S1M10000006G10	1592	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000006G11	1593	SAU101438	5450	SAU1c0038_orf_40p	12379
S1M10000007A02	1594	SAU102939	5747	#N/A	#N/A
S1M10000007A03	1595	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000007B02	1596	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000007B02	1596	SAU202872	5854	SAU2c0393_orf_6p	12866
S1M10000007B11	1597	SAU101476	5459	SAU1c0032_orf_69p	12254
S1M10000007C02	1598	SAU102939	5747	#N/A	#N/A
S1M10000007C04	1599	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000007C05	1600	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000007C06	1601	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000007C07	1602	SAU101266	5408	SAU1c0042_orf_117p	12490
S1M10000007C08	1603	SAU101717	5513	SAU1c0016_orf_16p	12131
S1M10000007C09	1604	SAU102939	5747	#N/A	#N/A
S1M10000007D03	1605	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000007D03	1605	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000007D03	1605	SAU301148	5888	#N/A	#N/A
S1M10000007D06	1606	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000007D08	1607	SAU102939	5747	#N/A	#N/A
S1M10000007D10	1608	SAU100300	5253	SAU1c0040_orf_90p	12451

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000007E04	1610	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000007E04	1610	SAU301148	5888	#N/A	#N/A
SIM10000007E06	1611	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000007E07	1612	SAU101365	5432	SAU1c0044_orf_112p	12556
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SIM10000007F02	1614	SAU101685	5512	SAU1c0023_orf_11p	12152
SIM10000007F04	1615	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000007F08	1616	SAU100794	5330	SAU1c0028_orf_53p	12189
SIM10000007F09	1617	SAU202930	5856	SAU2c0396_orf_3p	12871
SIM10000007F10	1618	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000007F11	1619	SAU102939	5747	#N/A	#N/A
SIM10000007F12	1620	SAU102939	5747	#N/A	#N/A
SIM10000007G02	1621	SAU101270	5410	SAU1c0037_orf_89p	12365
SIM10000007G03	1622	SAU100952	5358	SAU1c0043_orf_182p	12523
SIM10000007G05	1623	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000007G07	1624	SAU102652	5725	SAU1c0045_orf_115p	12653
SIM10000007G08	1625	SAU103038	5757	#N/A	#N/A
SIM10000008A03	1626	SAU101476	5459	SAU1c0032_orf_69p	12254
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SIM10000008A05	1628	SAU102939	5747	#N/A	#N/A
SIM10000008A08	1629	SAU102905	5742	SAU1c0033_orf_45p	12273
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SIM10000008A09	1630	SAU100741	5318	SAU1c0039_orf_48p	12409
SIM10000008A12	1631	SAU100608	5297	SAU1c0034_orf_69p	12293
SIM10000008B03	1632	SAU103144	5761	SAU1c0045_orf_15p	12663
SIM10000008B04	1633	SAU201810	5836	SAU2c0308_orf_2p	12769
SIM10000008B04	1633	SAU202174	5845	SAU2c0412_orf_3p	12895
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SIM10000008B06	1634	SAU101806	5546	SAU1c0032_orf_25p	12230
SIM10000008B08	1635	SAU101652	5503	SAU1c0042_orf_123p	12492
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SIM10000008B10	1637	SAU100608	5297	SAU1c0034_orf_69p	12293
SIM10000008C05	1638	SAU102939	5747	#N/A	#N/A
SIM10000008C06	1639	SAU102939	5747	#N/A	#N/A
SIM10000008C07	1640	SAU102939	5747	#N/A	#N/A
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SIM10000008C09	1642	SAU101793	5534	SAU1c0032_orf_14p	12218
SIM10000008D05	1643	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000008D09	1644	SAU103038	5757	#N/A	#N/A
SIM10000008E05	1645	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000008E08	1646	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000008E09	1647	SAU101343	5425	SAU1c0044_orf_40p	12619

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000008F01	1649	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000008F02	1650	SAU102007	5590	SAU1c0040_orf_108p	12428
S1M10000008F03	1651	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000008F06	1652	SAU100741	5318	SAU1c0039_orf_48p	12409
S1M10000008F08	1653	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000008F09	1654	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000008F09	1654	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000008F09	1654	SAU301148	5888	#N/A	#N/A
S1M10000008F10	1655	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000008F11	1656	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000008G02	1657	SAU201167	5803	SAU2c0407_orf_5p	12887
S1M10000008G03	1658	SAU101637	5500	SAU1c0029_orf_8p	12201
S1M10000008G05	1659	SAU102870	5738	SAU1c0026_orf_17p	12170
S1M10000009A02	1660	SAU101159	5387	SAU1c0036_orf_46p	12331
S1M10000009A04	1661	SAU102979	5750	SAU1c0043_orf_227p	12536
S1M10000009A07	1662	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000009A08	1663	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000009A08	1663	SAU100659	5304	SAU1c0038_orf_60p	12390
S1M10000009A09	1664	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000009A10	1665	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000009A11	1666	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000009B01	1667	SAU201506	5818	SAU2c0432_orf_18p	12946
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S1M10000009B03	1669	SAU201506	5818	SAU2c0432_orf_18p	12946
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S1M10000009B05	1671	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000009B06	1672	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000009B07	1673	SAU201952	5839	SAU2c0457_orf_10p	13020
S1M10000009B10	1674	SAU100141	5236	SAU1c0032_orf_8p	12259
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S1M10000009B11	1675	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000009B12	1676	SAU102433	5668	SAU1c0045_orf_37p	12701
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S1M10000009C02	1678	SAU102418	5664	SAU1c0030_orf_18p	12205
S1M10000009C05	1679	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000009C06	1680	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000009C07	1681	SAU102460	5678	SAU1c0026_orf_18p	12171
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S1M10000009C09	1683	SAU102129	5604	SAU1c0027_orf_17p	12176
S1M10000009C10	1684	SAU102336	5646	SAU1c0045_orf_146p	12659
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000009D04	1689	SAU102979	5750	SAU1c0043_orf_227p	12536
SIM10000009D05	1690	SAU100799	5331	SAU1c0045_orf_243p	12682
SIM10000009D07	1691	SAU200994	5802	SAU2c0428_orf_4p	12935
SIM10000009D09	1692	SAU101681	5510	SAU1c0044_orf_220p	12592
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SIM10000009E02	1694	SAU101572	5484	SAU1c0044_orf_211p	12586
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SIM10000009E06	1695	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000009E08	1696	SAU201539	5821	SAU2c0431_orf_15p	12943
SIM10000009E09	1697	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000009E11	1698	SAU101801	5541	#N/A	#N/A
SIM10000009E12	1699	SAU101572	5484	SAU1c0044_orf_211p	12586
SIM10000009F01	1700	SAU101452	5455	SAU1c0045_orf_247p	12684
SIM10000009F02	1701	SAU101818	5553	SAU1c0038_orf_20p	12369
SIM10000009F03	1702	SAU101488	5463	SAU1c0025_orf_18p	12164
SIM10000009F05	1703	SAU101752	5522	SAU1c0040_orf_85p	12447
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SIM10000009F07	1705	SAU102607	5712	SAU1c0041_orf_51p	12472
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SIM10000009F09	1706	SAU202176	5846	SAU2c0412_orf_3p	12895
SIM10000009F09	1706	SAU302805	5911	SAU3c1458_orf_1p	13133
SIM10000009F10	1707	SAU102392	5658	SAU1c0033_orf_40p	12270
SIM10000009F10	1707	SAU201541	5822	SAU2c0431_orf_14p	12942
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SIM10000009G02	1708	SAU101573	5485	SAU1c0044_orf_212p	12587
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SIM10000009G09	1713	SAU102693	5731	SAU1c0044_orf_58p	12627
SIM10000009G10	1714	SAU100646	5302	SAU1c0025_orf_5p	12168
SIM10000009G11	1715	SAU100131	5232	SAU1c0043_orf_156p	12517
SIM10000009H01	1716	SAU201506	5818	SAU2c0432_orf_18p	12946
SIM10000009H02	1717	SAU102658	5726	SAU1c0045_orf_121p	12654
SIM10000009H03	1718	SAU201654	5829	SAU2c0442_orf_12p	12982
SIM10000009H05	1719	SAU100582	5292	SAU1c0042_orf_21p	12503
SIM10000009H05	1719	SAU102165	5610	SAU1c0041_orf_25p	12460
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000009H11	1722	SAU101801	5541	#N/A	#N/A
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SIM10000011A03	1724	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000011A04	1725	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000011A06	1726	SAU101574	5486	SAU1c0044_orf_213p	12588
SIM10000011A06	1726	SAU101575	5487	SAU1c0044_orf_214p	12589
SIM10000011B01	1727	SAU102881	5740	SAU1c0032_orf_4p	12242
SIM10000011B02	1728	SAU101541	5472	SAU1c0037_orf_128p	12344
SIM10000011B03	1729	SAU101849	5559	SAU1c0044_orf_148p	12567
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SIM10000011B05	1731	SAU200934	5799	SAU2c0375_orf_9p	12842
SIM10000011C01	1732	SAU101447	5454	SAU1c0045_orf_244p	12683
SIM10000011C05	1733	SAU100432	5271	SAU1c0040_orf_88p	12450
SIM10000011C05	1733	SAU202756	5852	SAU2c0470_orf_1p	13027
SIM10000011C06	1734	SAU102350	5649	SAU1c0040_orf_36p	12433
SIM10000011D01	1735	SAU101293	5414	SAU1c0044_orf_61p	12631
SIM10000011D02	1736	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000011D04	1737	SAU102280	5632	SAU1c0038_orf_3p	12378
SIM10000011D06	1738	SAU102942	5748	SAU1c0035_orf_103p	12296
SIM10000011E02	1739	SAU101966	5580	SAU1c0028_orf_41p	12186
SIM10000011E03	1740	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000011E04	1741	SAU101572	5484	SAU1c0044_orf_211p	12586
SIM10000011F01	1742	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000011F03	1743	SAU102350	5649	SAU1c0040_orf_36p	12433
SIM10000011F04	1744	SAU101155	5385	SAU1c0036_orf_11p	12310
SIM10000011F06	1745	SAU101481	5460	SAU1c0015_orf_9p	12130
SIM10000011F06	1745	SAU101482	5461	SAU1c0015_orf_10p	12123
SIM10000011G01	1746	SAU301465	5896	SAU3c1429_orf_4p	13121
SIM10000011G03	1747	SAU302626	5907	SAU3c1367_orf_3p	13105
SIM10000011G04	1748	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000011G05	1749	SAU102350	5649	SAU1c0040_orf_36p	12433
SIM10000011G06	1750	SAU102298	5641	SAU1c0045_orf_42p	12705
SIM10000011H01	1751	SAU201558	5823	SAU2c0434_orf_5p	12954
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SIM10000012A06	1755	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000012A08	1756	SAU101630	5498	SAU1c0039_orf_4p	12410
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012A11	1759	SAU100390	5267	#N/A	#N/A
S1M10000012A11	1759	SAU200028	5771	SAU2c0145_orf_1p	12721
S1M10000012B01	1760	SAU100751	5321	SAU1c0036_orf_59p	12335
S1M10000012B05	1761	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000012B06	1762	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000012B07	1763	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000012B07	1763	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000012B11	1764	SAU102551	5698	SAU1c0045_orf_206p	12672
S1M10000012C01	1765	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000012C03	1766	SAU100776	5327	SAU1c0041_orf_72p	12482
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S1M10000012C05	1768	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000012C06	1769	SAU101570	5482	SAU1c0044_orf_209p	12584
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S1M10000012C12	1771	SAU101781	5528	SAU1c0037_orf_43p	12353
S1M10000012D04	1772	SAU201952	5839	SAU2c0457_orf_10p	13020
S1M10000012D06	1773	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000012D07	1774	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000012D08	1775	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000012D09	1776	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000012D12	1777	SAU102620	5718	SAU1c0041_orf_62p	12479
S1M10000012D12	1777	SAU102621	5719	SAU1c0041_orf_63p	12480
S1M10000012D12	1777	SAU202006	5842	SAU2c0456_orf_20p	13018
S1M10000012E01	1778	SAU100733	5314	SAU1c0044_orf_254p	12602
S1M10000012E01	1778	SAU100734	5315	SAU1c0044_orf_255p	12603
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S1M10000012E12	1783	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000012E12	1783	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000012E12	1783	SAU301148	5888	#N/A	#N/A
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S1M10000012F07	1785	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000012F07	1785	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000012F08	1786	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000012F09	1787	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000012F10	1788	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000012F11	1789	SAU101781	5528	SAU1c0037_orf_43p	12353

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000012G02	1792	SAU301758	5900	SAU3c1508_orf_5p	13156
S1M10000012G03	1793	SAU201301	5809	SAU2c0416_orf_17p	12899
S1M10000012G06	1794	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000012G07	1795	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000012G07	1795	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000012G08	1796	SAU102593	5704	SAU1c0041_orf_39p	12463
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S1M10000012H05	1798	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000012H08	1799	SAU202186	5847	SAU2c0222_orf_1p	12731
S1M10000012H09	1800	SAU100227	5244	SAU1c0043_orf_188p	12525
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S1M10000012H10	1801	SAU101751	5521	SAU1c0040_orf_86p	12448
S1M10000012H11	1802	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000013A02	1803	SAU102674	5730	SAU1c0024_orf_12p	12156
S1M10000013A03	1804	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000013A05	1805	SAU102450	5675	SAU1c0045_orf_21p	12675
S1M10000013A07	1806	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000013A08	1807	SAU101143	5383	SAU1c0042_orf_159p	12502
S1M10000013A09	1808	SAU101567	5481	SAU1c0022_orf_10p	12144
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S1M10000013A11	1810	SAU101573	5485	SAU1c0044_orf_212p	12587
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S1M10000013B02	1812	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000013B03	1813	SAU201236	5808	SAU2c0409_orf_10p	12891
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S1M10000013B05	1815	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013B06	1816	SAU100118	5229	SAU1c0015_orf_13p	12125
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S1M10000013B11	1819	SAU103042	5758	#N/A	#N/A
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S1M10000013C07	1822	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000013C08	1823	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000013C09	1824	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000013C10	1825	SAU100736	5316	SAU1c0038_orf_64p	12391
S1M10000013C11	1826	SAU102059	5597	SAU1c0034_orf_51p	12286

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000013D09	1829	SAU102669	5728	SAU1c0024_orf_7p	12160
S1M10000013D09	1829	SAU302956	5915	SAU3c1513_orf_9p	13161
S1M10000013D11	1830	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000013E01	1831	SAU102674	5730	SAU1c0024_orf_12p	12156
S1M10000013E02	1832	SAU101184	5391	SAU1c0035_orf_80p	12305
S1M10000013E04	1833	SAU101802	5542	SAU1c0032_orf_22p	12227
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S1M10000013E08	1835	SAU100831	5335	SAU1c0038_orf_93p	12403
S1M10000013E09	1836	SAU101571	5483	SAU1c0044_orf_210p	12585
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S1M10000013F12	1844	SAU102437	5670	SAU1c0045_orf_33p	12695
S1M10000013G01	1845	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000013G04	1846	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000013G05	1847	SAU102241	5617	SAU1c0043_orf_25p	12539
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S1M10000014A07	1863	SAU101526	5470	SAU1c0027_orf_32p	12179
S1M10000014A08	1864	SAU103038	5757	#N/A	#N/A
S1M10000014A11	1865	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000014A12	1866	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000014B01	1867	SAU100547	5290	SAU1c0032_orf_3p	12240

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
S1M10000014B02	1868	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000014B02	1868	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000014B03	1869	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000014B04	1870	SAU100778	5328	SAU1c0043_orf_140p	12514
S1M10000014B05	1871	SAU102476	5682	SAU1c0026_orf_33p	12175
S1M10000014B06	1872	SAU101199	5395	SAU1c0035_orf_62p	12302
S1M10000014B07	1873	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000014B08	1874	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000014B10	1875	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000014B11	1876	SAU102534	5696	#N/A	#N/A
S1M10000014B12	1877	SAU102534	5696	#N/A	#N/A
S1M10000014C01	1878	SAU101575	5487	SAU1c0044_orf_214p	12589
S1M10000014C05	1879	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014C06	1880	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014C07	1881	SAU101801	5541	#N/A	#N/A
S1M10000014C09	1882	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000014C09	1882	SAU102881	5740	SAU1c0032_orf_4p	12242
S1M10000014C10	1883	SAU302901	5912	SAU3c1497_orf_8p	13146
S1M10000014C11	1884	SAU100514	5281	SAU1c0044_orf_57p	12626
S1M10000014C12	1885	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000014C12	1885	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000014D03	1886	SAU100885	5348	SAU1c0038_orf_38p	12376
S1M10000014D06	1887	SAU100305	5256	SAU1c0038_orf_77p	12397
S1M10000014D08	1888	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000014D09	1889	SAU100808	5332	SAU1c0037_orf_12p	12345
S1M10000014D10	1890	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000014E01	1891	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000014E01	1891	SAU101794	5535	#N/A	#N/A
S1M10000014E04	1892	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000014E05	1893	SAU101565	5480	SAU1c0022_orf_8p	12151
S1M10000014E07	1894	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000014E07	1894	SAU100659	5304	SAU1c0038_orf_60p	12390
S1M10000014E08	1895	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000014E09	1896	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014E09	1896	SAU300269	5869	#N/A	#N/A
S1M10000014E10	1897	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000014E12	1898	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000014E12	1898	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000014F02	1899	SAU100128	5231	#N/A	#N/A
S1M10000014F02	1899	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000014F02	1899	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000014F03	1900	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000014F03	1900	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000014F04	1901	SAU102449	5674	SAU1c0045_orf_22p	12677

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000014F08	1903	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000014F09	1904	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000014F09	1904	SAU300269	5869	#N/A	#N/A
S1M10000014F10	1905	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000014G02	1906	SAU102054	5596	SAU1c0039_orf_74p	12417
S1M10000014G04	1907	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000014G06	1908	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014G07	1909	SAU201620	5827	#N/A	#N/A
S1M10000014G08	1910	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014G12	1911	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000014H02	1912	SAU100242	5246	SAU1c0036_orf_5p	12336
S1M10000014H03	1913	SAU102264	5628	SAU1c0032_orf_60p	12250
S1M10000014H04	1914	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H05	1915	SAU102116	5602	SAU1c0027_orf_5p	12180
S1M10000014H06	1916	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000014H07	1917	SAU103038	5757	#N/A	#N/A
S1M10000014H08	1918	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000014H11	1919	SAU102534	5696	#N/A	#N/A
S1M10000015A02	1920	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000015A03	1921	SAU102388	5655	SAU1c0033_orf_35p	12267
S1M10000015A05	1922	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000015A06	1923	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000015A09	1924	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000015A10	1925	SAU103038	5757	#N/A	#N/A
S1M10000015A11	1926	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015A12	1927	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015B02	1928	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015B05	1929	SAU103038	5757	#N/A	#N/A
S1M10000015B08	1930	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000015B08	1930	SAU101792	5533	SAU1c0032_orf_13p	12217
S1M10000015B09	1931	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000015B09	1931	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000015B09	1931	SAU302685	5908	SAU3c1403_orf_1p	13113
S1M10000015B10	1932	SAU102308	5642	SAU1c0045_orf_50p	12706
S1M10000015C01	1933	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000015C02	1934	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000015C03	1935	SAU102390	5657	SAU1c0033_orf_38p	12269
S1M10000015C03	1935	SAU201333	5810	SAU2c0418_orf_8p	12905
S1M10000015C05	1936	SAU100690	5309	#N/A	#N/A
S1M10000015C06	1937	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000015C08	1938	SAU100133	5233	SAU1c0044_orf_170p	12574
S1M10000015C08	1938	SAU100323	5261	SAU1c0044_orf_171p	12575
S1M10000015C10	1939	SAU100414	5270	SAU1c0022_orf_24p	12148

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000015D02	1941	SAU100794	5330	SAU1c0028_orf_53p	12189
SIM10000015D03	1942	SAU102032	5591	SAU1c0029_orf_47p	12198
SIM10000015D04	1943	SAU100131	5232	SAU1c0043_orf_156p	12517
SIM10000015D05	1944	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000015D06	1945	SAU100736	5316	SAU1c0038_orf_64p	12391
SIM10000015D12	1946	SAU101814	5551	SAU1c0032_orf_32p	12237
SIM10000015E02	1947	SAU102390	5657	SAU1c0033_orf_38p	12269
SIM10000015E02	1947	SAU201333	5810	SAU2c0418_orf_8p	12905
SIM10000015E03	1948	SAU200468	5781	SAU2c0429_orf_19p	12937
SIM10000015E06	1949	SAU101320	5420	SAU1c0015_orf_16p	12128
SIM10000015E07	1950	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000015E09	1951	SAU102433	5668	SAU1c0045_orf_37p	12701
SIM10000015E10	1952	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000015E11	1953	SAU102286	5636	SAU1c0038_orf_6p	12393
SIM10000015E11	1953	SAU102287	5637	SAU1c0038_orf_7p	12398
SIM10000015E12	1954	SAU102352	5650	SAU1c0040_orf_38p	12434
SIM10000015F01	1955	SAU100123	5230	SAU1c0043_orf_189p	12526
SIM10000015F01	1955	SAU102001	5586	SAU1c0040_orf_102p	12424
SIM10000015F01	1955	SAU103159	5762	SAU1c0045_orf_204p	12670
SIM10000015F01	1955	SAU201827	5837	SAU2c0449_orf_21p	13002
SIM10000015F02	1956	SAU101561	5479	SAU1c0022_orf_4p	12149
SIM10000015F03	1957	SAU201403	5815	SAU2c0423_orf_3p	12913
SIM10000015F04	1958	SAU201403	5815	SAU2c0423_orf_3p	12913
SIM10000015F06	1959	SAU201385	5814	#N/A	#N/A
SIM10000015F07	1960	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000015F08	1961	SAU102102	5600	SAU1c0045_orf_340p	12696
SIM10000015F09	1962	SAU101800	5540	SAU1c0032_orf_20p	12225
SIM10000015F09	1962	SAU101801	5541	#N/A	#N/A
SIM10000015F10	1963	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000015G01	1964	SAU102481	5685	SAU1c0039_orf_99p	12422
SIM10000015G02	1965	SAU200058	5773	SAU2c0134_orf_1p	12719
SIM10000015G02	1965	SAU200059	5774	SAU2c0134_orf_3p	12720
SIM10000015G03	1966	SAU101070	5376	SAU1c0034_orf_60p	12291
SIM10000015G04	1967	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000015G05	1968	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000015G06	1969	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000015G07	1970	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000015G08	1971	SAU101814	5551	SAU1c0032_orf_32p	12237
SIM10000015G09	1972	SAU102143	5607	SAU1c0041_orf_14p	12458
SIM10000015G09	1972	SAU102144	5608	SAU1c0041_orf_15p	12459
SIM10000015G10	1973	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000015G11	1974	SAU100275	5252	SAU1c0036_orf_15p	12314
SIM10000015H04	1975	SAU101801	5541	#N/A	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000015H06	1976	SAU201385	5814	#N/A	#N/A
S1M10000016A03	1977	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000016A03	1977	SAU101804	5544	#N/A	#N/A
S1M10000016A04	1978	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016A04	1978	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000016A06	1979	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000016A07	1980	SAU100932	5356	SAU1c0044_orf_308p	12615
S1M10000016A09	1981	SAU101067	5375	SAU1c0034_orf_58p	12290
S1M10000016A09	1981	SAU300732	5877	SAU3c1116_orf_1p	13061
S1M10000016A10	1982	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000016A12	1983	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000016B02	1984	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000016B05	1985	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000016B06	1986	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000016B06	1986	SAU100433	5272	SAU1c0040_orf_87p	12449
S1M10000016B07	1987	SAU103077	5759	SAU1c0039_orf_44p	12408
S1M10000016B08	1988	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016B09	1989	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000016B10	1990	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000016B11	1991	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000016B12	1992	SAU101794	5535	#N/A	#N/A
S1M10000016B12	1992	SAU101795	5536	SAU1c0032_orf_15p	12219
S1M10000016C01	1993	SAU100845	5340	SAU1c0036_orf_41p	12329
S1M10000016C02	1994	SAU102049	5595	SAU1c0039_orf_68p	12416
S1M10000016C04	1995	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016C05	1996	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000016C06	1997	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000016C06	1997	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000016C06	1997	SAU301148	5888	#N/A	#N/A
S1M10000016C08	1998	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000016C09	1999	SAU102233	5616	SAU1c0043_orf_20p	12531
S1M10000016C10	2000	SAU201513	5820	SAU2c0432_orf_10p	12944
S1M10000016C10	2000	SAU203196	5861	SAU2c0432_orf_11p	12945
S1M10000016C11	2001	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000016C12	2002	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000016D01	2003	SAU102355	5651	SAU1c0040_orf_40p	12435
S1M10000016D02	2004	SAU200242	5777	SAU2c0250_orf_2p	12734
S1M10000016D04	2005	SAU100921	5355	SAU1c0038_orf_76p	12396
S1M10000016D05	2006	SAU100770	5324	#N/A	#N/A
S1M10000016D06	2007	SAU100952	5358	SAU1c0043_orf_182p	12523
S1M10000016D08	2008	SAU101070	5376	SAU1c0034_orf_60p	12291
S1M10000016D09	2009	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000016D10	2010	SAU201513	5820	SAU2c0432_orf_10p	12944

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000016D11	2011	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000016E04	2012	SAU101371	5435	SAU1c0033_orf_7p	12275
SIM10000016E05	2013	SAU101320	5420	SAU1c0015_orf_16p	12128
SIM10000016E06	2014	SAU102639	5724	#N/A	#N/A
SIM10000016E07	2015	SAU102636	5722	SAU1c0045_orf_101p	12650
SIM10000016E07	2015	SAU102637	5723	SAU1c0045_orf_102p	12651
SIM10000016E08	2016	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000016E09	2017	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000016E10	2018	SAU102983	5751	SAU1c0045_orf_224p	12676
SIM10000016E11	2019	SAU102281	5633	SAU1c0038_orf_4p	12384
SIM10000016E12	2020	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000016F02	2021	SAU102113	5601	SAU1c0027_orf_2p	12178
SIM10000016F02	2021	SAU301223	5889	SAU3c1345_orf_3p	13090
SIM10000016F03	2022	SAU101864	5562	SAU1c0044_orf_163p	12572
SIM10000016F05	2023	SAU201168	5804	SAU2c0407_orf_8p	12889
SIM10000016F06	2024	SAU102407	5662	#N/A	#N/A
SIM10000016F08	2025	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000016F09	2026	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000016F11	2027	SAU102113	5601	SAU1c0027_orf_2p	12178
SIM10000016F11	2027	SAU301223	5889	SAU3c1345_orf_3p	13090
SIM10000016G01	2028	SAU102434	5669	SAU1c0045_orf_36p	12700
SIM10000016G03	2029	SAU101300	5415	SAU1c0044_orf_113p	12557
SIM10000016G03	2029	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000016G04	2030	SAU102450	5675	SAU1c0045_orf_21p	12675
SIM10000016G05	2031	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000016H03	2032	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000016H04	2033	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000016H08	2034	SAU101067	5375	SAU1c0034_orf_58p	12290
SIM10000016H08	2034	SAU300732	5877	SAU3c1116_orf_1p	13061
SIM10000016H10	2035	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000017A02	2036	SAU101866	5564	SAU1c0036_orf_21p	12319
SIM10000017A03	2037	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000017A03	2037	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000017A04	2038	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000017A08	2039	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000017A11	2040	SAU102437	5670	SAU1c0045_orf_33p	12695
SIM10000017A12	2041	SAU301357	5893	SAU3c1394_orf_2p	13111
SIM10000017B02	2042	SAU102242	5618	SAU1c0043_orf_26p	12540
SIM10000017B05	2043	SAU302513	5906	SAU3c1298_orf_1p	13085
SIM10000017B07	2044	SAU101806	5546	SAU1c0032_orf_25p	12230
SIM10000017B08	2045	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000017B09	2046	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000017B10	2047	SAU101754	5523	SAU1c0040_orf_84p	12446

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000017B12	2049	SAU201375	5811	SAU2c0426_orf_4p	12926
S1M10000017C01	2050	SAU101224	5397	SAU1c0044_orf_98p	12647
S1M10000017C03	2051	SAU101910	5576	SAU1c0040_orf_76p	12440
S1M10000017C05	2052	SAU200657	5789	#N/A	#N/A
S1M10000017C08	2053	SAU101890	5570	SAU1c0034_orf_29p	12280
S1M10000017C09	2054	SAU101398	5442	SAU1c0036_orf_33p	12324
S1M10000017C10	2055	SAU102614	5716	SAU1c0041_orf_56p	12476
S1M10000017C10	2055	SAU102615	5717	SAU1c0041_orf_57p	12477
S1M10000017C11	2056	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000017C11	2056	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000017C12	2057	SAU101782	5529	SAU1c0037_orf_44p	12354
S1M10000017C12	2057	SAU200994	5802	SAU2c0428_orf_4p	12935
S1M10000017D03	2058	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000017D09	2059	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000017D09	2059	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000017D10	2060	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000017E04	2061	SAU101801	5541	#N/A	#N/A
S1M10000017E05	2062	SAU102334	5645	SAU1c0045_orf_144p	12658
S1M10000017E08	2063	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000017E11	2064	SAU102883	5741	SAU1c0045_orf_38p	12702
S1M10000017F01	2065	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000017F04	2066	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000017F04	2066	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000017F05	2067	SAU102541	5697	SAU1c0045_orf_195p	12668
S1M10000017F06	2068	SAU102356	5652	SAU1c0040_orf_41p	12436
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S1M10000017G02	2070	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000017G05	2071	SAU102259	5624	SAU1c0032_orf_55p	12245
S1M10000017G06	2072	SAU200565	5785	SAU2c0324_orf_7p	12781
S1M10000018A03	2073	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A03	2073	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A04	2074	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A05	2075	SAU100886	5349	SAU1c0018_orf_16p	12139
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S1M10000018A06	2076	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000018A08	2077	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000018A08	2077	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000018A09	2078	SAU102142	5606	SAU1c0041_orf_13p	12457
S1M10000018A10	2079	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000018A11	2080	SAU100139	5234	SAU1c0032_orf_6p	12255
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S1M10000018B02	2081	SAU100886	5349	SAU1c0018_orf_16p	12139
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000018B10	2085	SAU100401	5268	SAU1c0044_orf_174p	12576
S1M10000018B10	2085	SAU300335	5870	#N/A	#N/A
S1M10000018B11	2086	SAU100658	5303	SAU1c0038_orf_59p	12388
S1M10000018C01	2087	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000018C02	2088	SAU102447	5672	SAU1c0045_orf_24p	12685
S1M10000018C03	2089	SAU100778	5328	SAU1c0043_orf_140p	12514
S1M10000018C04	2090	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000018C05	2091	SAU103038	5757	#N/A	#N/A
S1M10000018C06	2092	SAU100684	5306	SAU1c0044_orf_68p	12632
S1M10000018C08	2093	SAU102256	5622	SAU1c0032_orf_52p	12243
S1M10000018C08	2093	SAU102257	5623	SAU1c0032_orf_53p	12244
S1M10000018C09	2094	SAU101065	5374	SAU1c0034_orf_56p	12289
S1M10000018C09	2094	SAU102068	5599	SAU1c0034_orf_55p	12288
S1M10000018C10	2095	SAU100112	5227	SAU1c0044_orf_70p	12634
S1M10000018C11	2096	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000018C12	2097	SAU101948	5579	SAU1c0045_orf_69p	12709
S1M10000018D01	2098	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000018D02	2099	SAU102284	5635	SAU1c0038_orf_5p	12389
S1M10000018D02	2099	SAU201469	5816	SAU2c0438_orf_6p	12967
S1M10000018D03	2100	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000018D04	2101	SAU101798	5538	SAU1c0032_orf_18p	12222
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S1M10000018D10	2103	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000018D11	2104	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000018D12	2105	SAU100866	5344	SAU1c0044_orf_100p	12553
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S1M10000018E02	2107	SAU100265	5249	SAU1c0014_orf_11p	12122
S1M10000018E03	2108	SAU102420	5665	SAU1c0030_orf_20p	12206
S1M10000018E04	2109	SAU102035	5592	SAU1c0029_orf_50p	12199
S1M10000018E05	2110	SAU100596	5295	SAU1c0043_orf_63p	12548
S1M10000018E08	2111	SAU100793	5329	SAU1c0028_orf_52p	12188
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S1M10000018E11	2113	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000018E12	2114	SAU200914	5796	SAU2c0373_orf_2p	12837
S1M10000018F03	2115	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000018F04	2116	SAU102396	5660	SAU1c0033_orf_43p	12272
S1M10000018F04	2116	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000018F07	2117	SAU102629	5720	SAU1c0041_orf_71p	12481
S1M10000018F09	2118	SAU101810	5549	SAU1c0032_orf_28p	12233

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000018F10	2119	SAU100432	5271	SAU1c0040_orf_88p	12450
SIM10000018F10	2119	SAU100433	5272	SAU1c0040_orf_87p	12449
SIM10000018F12	2120	SAU201469	5816	SAU2c0438_orf_6p	12967
SIM10000018G03	2121	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000018G05	2122	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000018G07	2123	SAU101727	5516	SAU1c0016_orf_6p	12133
SIM10000018G08	2124	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000018G08	2124	SAU102201	5612	SAU1c0045_orf_169p	12666
SIM10000018G09	2125	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000018G09	2125	SAU102201	5612	SAU1c0045_orf_169p	12666
SIM10000018G10	2126	SAU100141	5236	SAU1c0032_orf_8p	12259
SIM10000018G10	2126	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000018G12	2127	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000018H01	2128	SAU101663	5506	SAU1c0033_orf_14p	12261
SIM10000018H02	2129	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000018H02	2129	SAU101653	5504	SAU1c0042_orf_124p	12493
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SIM10000018H09	2131	SAU101622	5496	SAU1c0040_orf_27p	12430
SIM10000018H10	2132	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000019A02	2133	SAU103077	5759	SAU1c0039_orf_44p	12408
SIM10000019A03	2134	SAU102352	5650	SAU1c0040_orf_38p	12434
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SIM10000019A07	2137	SAU101728	5517	SAU1c0016_orf_5p	12132
SIM10000019A09	2138	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000019A11	2139	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000019A12	2140	SAU102693	5731	SAU1c0044_orf_58p	12627
SIM10000019A12	2140	SAU102694	5732	SAU1c0044_orf_59p	12628
SIM10000019B03	2141	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000019B04	2142	SAU100899	5351	SAU1c0034_orf_11p	12277
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SIM10000019B07	2143	SAU100300	5253	SAU1c0040_orf_90p	12451
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SIM10000019B08	2144	SAU102423	5667	SAU1c0030_orf_23p	12208
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SIM10000019B10	2146	SAU101570	5482	SAU1c0044_orf_209p	12584
SIM10000019B11	2147	SAU100879	5345	SAU1c0041_orf_82p	12483
SIM10000019B12	2148	SAU101793	5534	SAU1c0032_orf_14p	12218
SIM10000019C01	2149	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000019C04	2150	SAU103175	5764	SAU1c0045_orf_269p	12687
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000019C06	2152	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000019C07	2153	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000019C08	2154	SAU202126	5844	SAU2c0045_orf_1p	12714
S1M10000019C11	2155	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000019C12	2156	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000019D01	2157	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000019D02	2158	SAU101145	5384	SAU1c0035_orf_43p	12299
S1M10000019D04	2159	SAU102292	5638	SAU1c0038_orf_10p	12368
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S1M10000019D06	2161	SAU102526	5692	SAU1c0045_orf_299p	12691
S1M10000019D07	2162	SAU301898	5904	SAU3c1079_orf_1p	13057
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S1M10000019E07	2167	SAU102352	5650	SAU1c0040_orf_38p	12434
S1M10000019F01	2168	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000019F05	2169	SAU101612	5493	SAU1c0044_orf_7p	12637
S1M10000019F05	2169	SAU202945	5857	SAU2c0394_orf_7p	12868
S1M10000019F06	2170	SAU101864	5562	SAU1c0044_orf_163p	12572
S1M10000019F08	2171	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000019F09	2172	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000019F11	2173	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000019G04	2174	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000019G07	2175	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000019G09	2176	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000019G10	2177	SAU101235	5400	SAU1c0044_orf_11p	12561
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S1M10000019G11	2178	SAU101802	5542	SAU1c0032_orf_22p	12227
S1M10000019H05	2179	SAU101802	5542	SAU1c0032_orf_22p	12227
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S1M10000020A12	2185	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000020B02	2186	SAU100475	5276	SAU1c0036_orf_61p	12337
S1M10000020B03	2187	SAU100059	5224	SAU1c0045_orf_10p	12652
S1M10000020B05	2188	SAU301133	5887	SAU3c1311_orf_3p	13087

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000020B07	2190	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000020B09	2191	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000020B12	2192	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000020C09	2193	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000020C10	2194	SAU101799	5539	SAU1c0032_orf_19p	12223
S1M10000020C10	2194	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000020C11	2195	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000020D03	2196	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000020D04	2197	SAU102481	5685	SAU1c0039_orf_99p	12422
S1M10000020D06	2198	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000020D07	2199	SAU100198	5243	SAU1c0009_orf_1p	12120
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S1M10000020E06	2206	SAU102162	5609	SAU1c0041_orf_27p	12462
S1M10000020E08	2207	SAU101756	5524	SAU1c0040_orf_82p	12445
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S1M10000020F06	2212	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000020F07	2213	SAU200731	5793	SAU2c0352_orf_2p	12808
S1M10000020F09	2214	SAU100114	5228	SAU1c0043_orf_225p	12535
S1M10000020F11	2215	SAU101663	5506	SAU1c0033_orf_14p	12261
S1M10000020F11	2215	SAU101664	5507	SAU1c0033_orf_15p	12262
S1M10000020F12	2216	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000020G01	2217	SAU102905	5742	SAU1c0033_orf_45p	12273
S1M10000020G05	2218	SAU100114	5228	SAU1c0043_orf_225p	12535
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S1M10000020G11	2223	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000020G12	2224	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000020H01	2225	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000020H02	2226	SAU101754	5523	SAU1c0040_orf_84p	12446
S1M10000020H04	2227	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000020H06	2228	SAU101541	5472	SAU1c0037_orf_128p	12344

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000020H11	2231	SAU100053	5222	SAU1c0020_orf_1p	12143
S1M10000021A04	2232	SAU200752	5795	SAU2c0354_orf_5p	12809
S1M10000021A04	2232	SAU300975	5880	SAU3c1240_orf_3p	13075
S1M10000021A05	2233	SAU101408	5445	SAU1c0035_orf_93p	12308
S1M10000021A06	2234	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000021A07	2235	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000021A07	2235	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000021A08	2236	SAU101183	5390	SAU1c0035_orf_79p	12304
S1M10000021A09	2237	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000021A09	2237	SAU201184	5805	SAU2c0351_orf_19p	12807
S1M10000021A10	2238	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000021B05	2239	SAU100139	5234	SAU1c0032_orf_6p	12255
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S1M10000021C04	2243	SAU200928	5798	SAU2c0365_orf_5p	12815
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S1M10000021C07	2245	SAU202968	5858	SAU2c0407_orf_2p	12886
S1M10000021C08	2246	SAU102575	5700	SAU1c0044_orf_283p	12609
S1M10000021C10	2247	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000021C11	2248	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021C12	2249	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000021D01	2250	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000021D03	2251	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000021D03	2251	SAU101286	5413	SAU1c0034_orf_67p	12292
S1M10000021D04	2252	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000021D04	2252	SAU100859	5342	SAU1c0038_orf_87p	12402
S1M10000021D06	2253	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000021D09	2254	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000021D10	2255	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000021E01	2256	SAU101655	5505	SAU1c0042_orf_125p	12494
S1M10000021E02	2257	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000021E02	2257	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000021E03	2258	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000021E05	2259	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000021E06	2260	SAU102663	5727	SAU1c0024_orf_2p	12158
S1M10000021E09	2261	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000021E12	2262	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000021F02	2263	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F04	2264	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021F04	2264	SAU102602	5708	SAU1c0032_orf_5p	12249

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000021F06	2266	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000021F07	2267	SAU101383	5438	SAU1c0022_orf_20p	12147
S1M10000021F09	2268	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021F09	2268	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000021F11	2269	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000021G01	2270	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000021G03	2271	SAU301357	5893	SAU3c1394_orf_2p	13111
S1M10000021G08	2272	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000021H04	2273	SAU100139	5234	SAU1c0032_orf_6p	12255
S1M10000021H04	2273	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000021H05	2274	SAU300131	5866	SAU3c0560_orf_2p	13034
S1M10000021H07	2275	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000021H08	2276	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000021H11	2277	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000022A02	2278	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000022A02	2278	SAU301230	5890	SAU3c1347_orf_6p	13092
S1M10000022A03	2279	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000022A05	2280	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000022A08	2281	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000022A09	2282	SAU102939	5747	#N/A	#N/A
S1M10000022A12	2283	SAU101868	5565	SAU1c0036_orf_23p	12320
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S1M10000022B02	2284	SAU301230	5890	SAU3c1347_orf_6p	13092
S1M10000022B03	2285	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022B05	2286	SAU100920	5354	SAU1c0038_orf_75p	12395
S1M10000022B06	2287	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022B08	2288	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000022B09	2289	SAU102939	5747	#N/A	#N/A
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S1M10000022B11	2291	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022B12	2292	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022C02	2293	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000022C03	2294	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000022C04	2295	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000022C06	2296	SAU100246	5247	SAU1c0042_orf_130p	12496
S1M10000022C06	2296	SAU300998	5881	SAU3c1253_orf_3p	13077
S1M10000022C07	2297	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022C08	2298	SAU100528	5286	SAU1c0042_orf_87p	12507
S1M10000022C08	2298	SAU103115	5760	SAU1c0042_orf_88p	12508
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S1M10000022D05	2301	SAU101777	5527	SAU1c0037_orf_39p	12352
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000022D09	2305	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000022D11	2306	SAU101447	5454	SAU1c0045_orf_244p	12683
S1M10000022E01	2307	SAU200601	5787	#N/A	#N/A
S1M10000022E03	2308	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000022E05	2309	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000022E09	2310	SAU101235	5400	SAU1c0044_orf_11p	12561
S1M10000022E09	2310	SAU101236	5401	SAU1c0044_orf_12p	12564
S1M10000022F04	2311	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000022F06	2312	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000022F07	2313	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000022F08	2314	SAU100414	5270	SAU1c0022_orf_24p	12148
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S1M10000022G03	2316	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000022G04	2317	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000022G07	2318	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000022G08	2319	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000022G12	2320	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000022H03	2321	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000022H05	2322	SAU101814	5551	SAU1c0032_orf_32p	12237
S1M10000022H06	2323	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000022H07	2324	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000022H08	2325	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000022H11	2326	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000023A05	2327	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000023A09	2328	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023A11	2329	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000023A12	2330	SAU101651	5502	SAU1c0042_orf_122p	12491
S1M10000023A12	2330	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000023B01	2331	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000023B03	2332	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000023B03	2332	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000023B07	2333	SAU101857	5560	SAU1c0044_orf_156p	12569
S1M10000023B08	2334	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023B08	2334	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023B09	2335	SAU101340	5423	SAU1c0038_orf_82p	12400
S1M10000023B10	2336	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000023B11	2337	SAU102613	5715	SAU1c0041_orf_55p	12475
S1M10000023B12	2338	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000023B12	2338	SAU301148	5888	#N/A	#N/A
S1M10000023C02	2339	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000023C02	2339	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000023C10	2340	SAU102554	5699	SAU1c0045_orf_209p	12673

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000023D01	2343	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000023D03	2344	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000023D04	2345	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000023D07	2346	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000023D08	2347	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000023D09	2348	SAU100547	5290	SAU1c0032_orf_3p	12240
SIM10000023D10	2349	SAU100963	5362	SAU1c0044_orf_85p	12640
SIM10000023D12	2350	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000023E01	2351	SAU101752	5522	SAU1c0040_orf_85p	12447
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SIM10000023E07	2353	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000023E10	2354	SAU203293	5862	SAU2c0441_orf_21p	12979
SIM10000023E11	2355	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000023F04	2356	SAU101736	5518	SAU1c0043_orf_166p	12519
SIM10000023F04	2356	SAU101737	5519	SAU1c0043_orf_165p	12518
SIM10000023F07	2357	SAU100546	5289	SAU1c0032_orf_2p	12235
SIM10000023F08	2358	SAU102883	5741	SAU1c0045_orf_38p	12702
SIM10000023F10	2359	SAU102352	5650	SAU1c0040_orf_38p	12434
SIM10000023F11	2360	SAU100617	5300	SAU1c0035_orf_102p	12295
SIM10000023F12	2361	SAU102352	5650	SAU1c0040_orf_38p	12434
SIM10000023G02	2362	SAU301465	5896	SAU3c1429_orf_4p	13121
SIM10000023G03	2363	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000023G06	2364	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000023G07	2365	SAU301054	5884	#N/A	#N/A
SIM10000023G08	2366	SAU100964	5363	SAU1c0044_orf_86p	12641
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SIM10000023G11	2368	SAU102613	5715	SAU1c0041_orf_55p	12475
SIM10000023H02	2369	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000023H06	2370	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000023H07	2371	SAU100300	5253	SAU1c0040_orf_90p	12451
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SIM10000023H10	2373	SAU101365	5432	SAU1c0044_orf_112p	12556
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SIM10000024A04	2375	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000024A07	2376	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000024A08	2377	SAU101231	5399	SAU1c0035_orf_6p	12303
SIM10000024A11	2378	SAU103226	5768	SAU1c0045_orf_95p	12713
SIM10000024B05	2379	SAU102418	5664	SAU1c0030_orf_18p	12205
SIM10000024B06	2380	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000024B08	2381	SAU100601	5296	SAU1c0044_orf_313p	12616
SIM10000024B09	2382	SAU200468	5781	SAU2c0429_orf_19p	12937
SIM10000024B10	2383	SAU101265	5407	#N/A	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000024C04	2385	SAU101862	5561	SAU1c0044_orf_161p	12571
S1M10000024C07	2386	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000024D02	2387	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024D03	2388	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000024D10	2389	SAU100140	5235	SAU1c0032_orf_7p	12258
S1M10000024D10	2389	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000024D11	2390	SAU101198	5394	SAU1c0035_orf_61p	12301
S1M10000024E03	2391	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024E05	2392	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000024E05	2392	SAU101801	5541	#N/A	#N/A
S1M10000024E06	2393	SAU102418	5664	SAU1c0030_orf_18p	12205
S1M10000024E07	2394	SAU101039	5373	SAU1c0043_orf_181p	12522
S1M10000024E08	2395	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000024F02	2396	SAU101447	5454	SAU1c0045_orf_244p	12683
S1M10000024F03	2397	SAU102992	5752	SAU1c0044_orf_60p	12630
S1M10000024F05	2398	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000024F08	2399	SAU101726	5515	SAU1c0016_orf_7p	12134
S1M10000024F10	2400	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000024G05	2401	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000024G05	2401	SAU101801	5541	#N/A	#N/A
S1M10000024G06	2402	SAU102418	5664	SAU1c0030_orf_18p	12205
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S1M10000024G08	2404	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000024G10	2405	SAU202176	5846	SAU2c0412_orf_3p	12895
S1M10000024G12	2406	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000024H02	2407	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000024H04	2408	SAU100770	5324	#N/A	#N/A
S1M10000024H07	2409	SAU200725	5792	SAU2c0428_orf_20p	12933
S1M10000024H08	2410	SAU102002	5587	SAU1c0040_orf_103p	12425
S1M10000024H08	2410	SAU102003	5588	SAU1c0040_orf_104p	12426
S1M10000025A03	2411	SAU101247	5405	SAU1c0043_orf_136p	12512
S1M10000025A08	2412	SAU102766	5735	#N/A	#N/A
S1M10000025A08	2412	SAU201236	5808	SAU2c0409_orf_10p	12891
S1M10000025A08	2412	SAU300338	5871	#N/A	#N/A
S1M10000025A09	2413	SAU102292	5638	SAU1c0038_orf_10p	12368
S1M10000025A10	2414	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000025A10	2414	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000025A10	2414	SAU301620	5899	SAU3c1478_orf_2p	13140
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S1M10000025B03	2417	SAU101385	5439	SAU1c0038_orf_50p	12385
S1M10000025B05	2418	SAU101455	5456	SAU1c0045_orf_250p	12686
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000025B06	2419	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000025B09	2420	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000025B12	2421	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000025C01	2422	SAU102292	5638	SAU1c0038_orf_10p	12368
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SIM10000025C05	2424	SAU100139	5234	SAU1c0032_orf_6p	12255
SIM10000025C09	2425	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000025C09	2425	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000025C10	2426	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000025C11	2427	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000025D01	2428	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000025D03	2429	SAU101771	5525	SAU1c0037_orf_33p	12350
SIM10000025D03	2429	SAU101772	5526	SAU1c0037_orf_34p	12351
SIM10000025D04	2430	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000025D06	2431	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000025D08	2432	SAU102598	5705	SAU1c0041_orf_43p	12464
SIM10000025D08	2432	SAU102599	5706	SAU1c0041_orf_45p	12466
SIM10000025D08	2432	SAU103191	5765	SAU1c0041_orf_44p	12465
SIM10000025D09	2433	SAU100522	5284	SAU1c0044_orf_249p	12599
SIM10000025D10	2434	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000025D10	2434	SAU102201	5612	SAU1c0045_orf_169p	12666
SIM10000025E01	2435	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000025E04	2436	SAU100389	5266	SAU1c0034_orf_14p	12279
SIM10000025E09	2437	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000025E11	2438	SAU102437	5670	SAU1c0045_orf_33p	12695
SIM10000025F03	2439	SAU102297	5640	SAU1c0045_orf_41p	12704
SIM10000025F05	2440	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000025F05	2440	SAU102201	5612	SAU1c0045_orf_169p	12666
SIM10000025F08	2441	SAU200685	5790	SAU2c0344_orf_9p	12801
SIM10000025F09	2442	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000025F10	2443	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000025F12	2444	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000025F12	2444	SAU102201	5612	SAU1c0045_orf_169p	12666
SIM10000025G04	2445	SAU300617	5874	SAU3c1046_orf_2p	13056
SIM10000025G06	2446	SAU300617	5874	SAU3c1046_orf_2p	13056
SIM10000025G10	2447	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000025H05	2448	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000025H06	2449	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000025H07	2450	SAU200752	5795	SAU2c0354_orf_5p	12809
SIM10000025H07	2450	SAU300975	5880	SAU3c1240_orf_3p	13075
SIM10000025H10	2451	SAU100590	5293	SAU1c0013_orf_5p	12121
SIM10000025H10	2451	SAU301268	5891	SAU3c1364_orf_2p	13102
SIM10000026A02	2452	SAU101907	5574	SAU1c0040_orf_79p	12442

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000026A05	2454	SAU200934	5799	SAU2c0375_orf_9p	12842
SIM10000026A06	2455	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000026A07	2456	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000026A08	2457	SAU100266	5250	SAU1c0032_orf_75p	12256
SIM10000026A09	2458	SAU102452	5676	SAU1c0045_orf_20p	12674
SIM10000026A09	2458	SAU102453	5677	SAU1c0045_orf_19p	12669
SIM10000026A10	2459	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000026A11	2460	SAU102259	5624	SAU1c0032_orf_55p	12245
SIM10000026A11	2460	SAU102260	5625	SAU1c0032_orf_56p	12246
SIM10000026A11	2460	SAU102261	5626	SAU1c0032_orf_57p	12247
SIM10000026A11	2460	SAU300868	5879	#N/A	#N/A
SIM10000026B02	2461	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000026B03	2462	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000026B05	2463	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000026B06	2464	SAU101570	5482	SAU1c0044_orf_209p	12584
SIM10000026B07	2465	SAU101341	5424	SAU1c0044_orf_38p	12618
SIM10000026B07	2465	SAU301275	5892	SAU3c1365_orf_2p	13103
SIM10000026B10	2466	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000026B11	2467	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000026B12	2468	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000026C01	2469	SAU100266	5250	SAU1c0032_orf_75p	12256
SIM10000026C06	2470	SAU101772	5526	SAU1c0037_orf_34p	12351
SIM10000026C07	2471	SAU101842	5557	SAU1c0042_orf_9p	12510
SIM10000026C08	2472	SAU100139	5234	SAU1c0032_orf_6p	12255
SIM10000026C11	2473	SAU200657	5789	#N/A	#N/A
SIM10000026C12	2474	SAU101726	5515	SAU1c0016_orf_7p	12134
SIM10000026D04	2475	SAU100658	5303	SAU1c0038_orf_59p	12388
SIM10000026D05	2476	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000026D06	2477	SAU100139	5234	SAU1c0032_orf_6p	12255
SIM10000026D07	2478	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000026D08	2479	SAU100690	5309	#N/A	#N/A
SIM10000026D10	2480	SAU203296	5863	SAU2c0442_orf_18p	12983
SIM10000026D12	2481	SAU100546	5289	SAU1c0032_orf_2p	12235
SIM10000026E01	2482	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000026E07	2483	SAU102939	5747	#N/A	#N/A
SIM10000026E09	2484	SAU102001	5586	SAU1c0040_orf_102p	12424
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SIM10000026E11	2486	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000026E12	2487	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000026F01	2488	SAU101784	5530	SAU1c0037_orf_46p	12355
SIM10000026F03	2489	SAU102200	5611	SAU1c0045_orf_168p	12665
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000026F06	2492	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000026F07	2493	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000026F08	2494	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000026F09	2495	SAU102939	5747	#N/A	#N/A
SIM10000026F10	2496	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000026F11	2497	SAU102939	5747	#N/A	#N/A
SIM10000026F12	2498	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000026G01	2499	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000026G03	2500	SAU100547	5290	SAU1c0032_orf_3p	12240
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SIM10000026G05	2502	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000026G06	2503	SAU101784	5530	SAU1c0037_orf_46p	12355
SIM10000026G07	2504	SAU100886	5349	SAU1c0018_orf_16p	12139
SIM10000026G09	2505	SAU100542	5288	SAU1c0043_orf_210p	12532
SIM10000026G10	2506	SAU100613	5299	SAU1c0015_orf_14p	12126
SIM10000026G10	2506	SAU102812	5736	SAU1c0015_orf_15p	12127
SIM10000026G12	2507	SAU101551	5477	SAU1c0043_orf_67p	12550
SIM10000026H01	2508	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000026H02	2509	SAU102355	5651	SAU1c0040_orf_40p	12435
SIM10000026H03	2510	SAU101801	5541	#N/A	#N/A
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SIM10000026H07	2513	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000026H09	2514	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000026H09	2514	SAU301148	5888	#N/A	#N/A
SIM10000026H10	2515	SAU102479	5683	SAU1c0039_orf_101p	12405
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SIM10000027A05	2517	SAU101805	5545	SAU1c0032_orf_24p	12229
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SIM10000027A11	2519	SAU101551	5477	SAU1c0043_orf_67p	12550
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SIM10000027B06	2521	SAU100275	5252	SAU1c0036_orf_15p	12314
SIM10000027B07	2522	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000027B08	2523	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000027B09	2524	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000027B11	2525	SAU101265	5407	#N/A	#N/A
SIM10000027C02	2526	SAU101327	5421	SAU1c0044_orf_296p	12612
SIM10000027C04	2527	SAU201236	5808	SAU2c0409_orf_10p	12891
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000027C09	2531	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000027D02	2532	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000027D02	2532	SAU101653	5504	SAU1c0042_orf_124p	12493
S1M10000027D03	2533	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000027D05	2534	SAU101554	5478	SAU1c0043_orf_70p	12551
S1M10000027D06	2535	SAU202708	5849	SAU2c0385_orf_1p	12855
S1M10000027D08	2536	SAU100714	5312	SAU1c0044_orf_74p	12635
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S1M10000027D10	2538	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000027D11	2539	SAU101996	5584	SAU1c0040_orf_99p	12456
S1M10000027E05	2540	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000027E05	2540	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000027E06	2541	SAU100690	5309	#N/A	#N/A
S1M10000027E07	2542	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000027E08	2543	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000027E09	2544	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027E11	2545	SAU101551	5477	SAU1c0043_orf_67p	12550
S1M10000027F01	2546	SAU103038	5757	#N/A	#N/A
S1M10000027F02	2547	SAU101491	5464	SAU1c0025_orf_20p	12165
S1M10000027F05	2548	SAU100882	5347	SAU1c0038_orf_35p	12374
S1M10000027F06	2549	SAU100690	5309	#N/A	#N/A
S1M10000027F08	2550	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000027F09	2551	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000027G03	2552	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000027G04	2553	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000027G05	2554	SAU102526	5692	SAU1c0045_orf_299p	12691
S1M10000027G06	2555	SAU202708	5849	SAU2c0385_orf_1p	12855
S1M10000027G07	2556	SAU102265	5629	SAU1c0032_orf_61p	12251
S1M10000027G09	2557	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000027G11	2558	SAU102533	5695	#N/A	#N/A
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S1M10000027H04	2560	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000027H05	2561	SAU102526	5692	SAU1c0045_orf_299p	12691
S1M10000027H06	2562	SAU100690	5309	#N/A	#N/A
S1M10000027H07	2563	SAU100542	5288	SAU1c0043_orf_210p	12532
S1M10000027H08	2564	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000027H09	2565	SAU101382	5437	SAU1c0022_orf_19p	12146
S1M10000027H10	2566	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000027H11	2567	SAU102533	5695	#N/A	#N/A
S1M10000027H11	2567	SAU102534	5696	#N/A	#N/A
S1M10000028A02	2568	SAU101085	5378	SAU1c0034_orf_42p	12284

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000028A06	2570	SAU100478	5277	SAU1c0044_orf_265p	12605
S1M10000028A06	2570	SAU100996	5366	SAU1c0044_orf_266p	12606
S1M10000028A08	2571	SAU102054	5596	SAU1c0039_orf_74p	12417
S1M10000028B01	2572	SAU101085	5378	SAU1c0034_orf_42p	12284
S1M10000028B01	2572	SAU101086	5379	SAU1c0034_orf_43p	12285
S1M10000028B02	2573	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000028B02	2573	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000028B03	2574	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000028B04	2575	SAU102764	5734	SAU1c0044_orf_56p	12625
S1M10000028B05	2576	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000028B06	2577	SAU201558	5823	SAU2c0434_orf_5p	12954
S1M10000028B08	2578	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028B09	2579	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028C02	2580	SAU203296	5863	SAU2c0442_orf_18p	12983
S1M10000028C04	2581	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028C05	2582	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000028C05	2582	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000028C05	2582	SAU200297	5778	SAU2c0274_orf_2p	12739
S1M10000028C06	2583	SAU103226	5768	SAU1c0045_orf_95p	12713
S1M10000028C08	2584	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000028D03	2585	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000028D04	2586	SAU101381	5436	SAU1c0022_orf_18p	12145
S1M10000028D06	2587	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000028D07	2588	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000028D08	2589	SAU100858	5341	SAU1c0038_orf_86p	12401
S1M10000028D09	2590	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000028E01	2591	SAU100062	5225	SAU1c0035_orf_98p	12309
S1M10000028E01	2591	SAU100231	5245	#N/A	#N/A
S1M10000028E03	2592	SAU100770	5324	#N/A	#N/A
S1M10000028E08	2593	SAU101865	5563	SAU1c0036_orf_20p	12318
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S1M10000028F03	2595	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000028F04	2596	SAU100301	5254	SAU1c0040_orf_91p	12452
S1M10000028F04	2596	SAU100302	5255	SAU1c0040_orf_92p	12453
S1M10000028F05	2597	SAU100301	5254	SAU1c0040_orf_91p	12452
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S1M10000028F06	2598	SAU100432	5271	SAU1c0040_orf_88p	12450
S1M10000028F06	2598	SAU202756	5852	SAU2c0470_orf_1p	13027
S1M10000028F07	2599	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000028G01	2600	SAU102554	5699	SAU1c0045_orf_209p	12673
S1M10000028G02	2601	SAU201236	5808	SAU2c0409_orf_10p	12891

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000028G04	2603	SAU301620	5899	SAU3c1478_orf_2p	13140
S1M10000028G05	2604	SAU100690	5309	#N/A	#N/A
S1M10000028G06	2605	SAU101865	5563	SAU1c0036_orf_20p	12318
S1M10000028G08	2606	SAU101341	5424	SAU1c0044_orf_38p	12618
S1M10000028G08	2606	SAU301275	5892	SAU3c1365_orf_2p	13103
S1M10000028H03	2607	SAU101815	5552	SAU1c0032_orf_33p	12238
S1M10000028H04	2608	SAU103038	5757	#N/A	#N/A
S1M10000028H05	2609	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000029A02	2610	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000029A04	2611	SAU100489	5278	SAU1c0044_orf_133p	12566
S1M10000029A04	2611	SAU100557	5291	SAU1c0044_orf_132p	12565
S1M10000029A09	2612	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029A10	2613	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000029A11	2614	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000029A12	2615	SAU100865	5343	SAU1c0044_orf_99p	12648
S1M10000029B02	2616	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000029B03	2617	SAU201225	5807	SAU2c0412_orf_5p	12896
S1M10000029B04	2618	SAU201621	5828	SAU2c0437_orf_4p	12966
S1M10000029B05	2619	SAU100355	5263	SAU1c0023_orf_6p	12155
S1M10000029B06	2620	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000029B08	2621	SAU101360	5431	SAU1c0044_orf_109p	12555
S1M10000029B10	2622	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000029C02	2623	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029C03	2624	SAU100690	5309	#N/A	#N/A
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S1M10000029C07	2626	SAU102222	5613	SAU1c0043_orf_12p	12511
S1M10000029C09	2627	SAU101495	5467	SAU1c0037_orf_65p	12360
S1M10000029C10	2628	SAU101995	5583	SAU1c0040_orf_98p	12455
S1M10000029C12	2629	SAU100859	5342	SAU1c0038_orf_87p	12402
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S1M10000029E05	2636	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000029E10	2637	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029E11	2638	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000029F01	2639	SAU101803	5543	SAU1c0032_orf_23p	12228
S1M10000029F01	2639	SAU101804	5544	#N/A	#N/A
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SIM10000029F04	2641	SAU102639	5724	#N/A	#N/A
SIM10000029F09	2642	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000029F09	2642	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000029F10	2643	SAU102621	5719	SAU1c0041_orf_63p	12480
SIM10000029F11	2644	SAU102883	5741	SAU1c0045_orf_38p	12702
SIM10000029F12	2645	SAU102603	5709	SAU1c0041_orf_48p	12469
SIM10000029F12	2645	SAU102609	5713	SAU1c0041_orf_52p	12473
SIM10000029G01	2646	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000029G02	2647	SAU101622	5496	SAU1c0040_orf_27p	12430
SIM10000029G03	2648	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000029G05	2649	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000029G07	2650	SAU101622	5496	SAU1c0040_orf_27p	12430
SIM10000029G08	2651	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000029G12	2652	SAU101270	5410	SAU1c0037_orf_89p	12365
SIM10000029H01	2653	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000029H05	2654	SAU102613	5715	SAU1c0041_orf_55p	12475
SIM10000029H06	2655	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000029H08	2656	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000029H09	2657	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000029H10	2658	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000030A02	2659	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000030A05	2660	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000030A09	2661	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000030A10	2662	SAU101092	5381	SAU1c0028_orf_9p	12192
SIM10000030A10	2662	SAU202882	5855	SAU2c0381_orf_3p	12848
SIM10000030A11	2663	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000030B02	2664	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000030B05	2665	SAU100275	5252	SAU1c0036_orf_15p	12314
SIM10000030B07	2666	SAU101180	5389	SAU1c0045_orf_126p	12656
SIM10000030B09	2667	SAU301898	5904	SAU3c1079_orf_1p	13057
SIM10000030C02	2668	SAU102531	5694	SAU1c0045_orf_186p	12667
SIM10000030C03	2669	SAU102629	5720	SAU1c0041_orf_71p	12481
SIM10000030C04	2670	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000030C05	2671	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000030C08	2672	SAU101175	5388	SAU1c0031_orf_1p	12213
SIM10000030C09	2673	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000030C10	2674	SAU301592	5898	SAU3c1467_orf_2p	13137
SIM10000030C12	2675	SAU100961	5360	SAU1c0044_orf_83p	12638
SIM10000030C12	2675	SAU100962	5361	SAU1c0044_orf_84p	12639
SIM10000030D01	2676	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000030D02	2677	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000030D03	2678	SAU100731	5313	SAU1c0044_orf_252p	12601
SIM10000030D05	2679	SAU102222	5613	SAU1c0043_orf_12p	12511

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000030D07	2681	SAU102392	5658	SAU1c0033_orf_40p	12270
S1M10000030D07	2681	SAU201541	5822	SAU2c0431_orf_14p	12942
S1M10000030D09	2682	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000030D10	2683	SAU100313	5259	SAU1c0045_orf_153p	12661
S1M10000030D10	2683	SAU100359	5264	SAU1c0032_orf_35p	12239
S1M10000030D11	2684	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000030E02	2685	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030E06	2686	SAU102909	5743	SAU1c0036_orf_16p	12315
S1M10000030E07	2687	SAU102939	5747	#N/A	#N/A
S1M10000030E11	2688	SAU101790	5531	SAU1c0032_orf_11p	12215
S1M10000030E12	2689	SAU100300	5253	SAU1c0040_orf_90p	12451
S1M10000030F01	2690	SAU100731	5313	SAU1c0044_orf_252p	12601
S1M10000030F07	2691	SAU102939	5747	#N/A	#N/A
S1M10000030F08	2692	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000030F08	2692	SAU101801	5541	#N/A	#N/A
S1M10000030F09	2693	SAU101266	5408	SAU1c0042_orf_117p	12490
S1M10000030F10	2694	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000030G03	2695	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030G05	2696	SAU102246	5619	SAU1c0043_orf_30p	12542
S1M10000030G05	2696	SAU102247	5620	SAU1c0043_orf_31p	12543
S1M10000030G07	2697	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000030G08	2698	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000030G09	2699	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000030G10	2700	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000030G11	2701	SAU101529	5471	SAU1c0043_orf_39p	12544
S1M10000030G12	2702	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000030H01	2703	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000030H02	2704	SAU200392	5780	SAU2c0298_orf_3p	12755
S1M10000030H03	2705	SAU102162	5609	SAU1c0041_orf_27p	12462
S1M10000030H05	2706	SAU102380	5654	SAU1c0033_orf_29p	12265
S1M10000030H07	2707	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000030H07	2707	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000030H07	2707	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000030H07	2707	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000030H09	2708	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000031A03	2709	SAU100546	5289	SAU1c0032_orf_2p	12235
S1M10000031A08	2710	SAU101641	5501	SAU1c0029_orf_12p	12193
S1M10000031A10	2711	SAU102242	5618	SAU1c0043_orf_26p	12540
S1M10000031B01	2712	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000031B02	2713	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000031B04	2714	SAU200928	5798	SAU2c0365_orf_5p	12815
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000031C04	2717	SAU100231	5245	#N/A	#N/A
S1M10000031C07	2718	SAU102059	5597	SAU1c0034_orf_51p	12286
S1M10000031C09	2719	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000031C11	2720	SAU102935	5745	#N/A	#N/A
S1M10000031D06	2721	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000031D07	2722	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000031D08	2723	SAU101891	5571	SAU1c0034_orf_30p	12281
S1M10000031D09	2724	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000031E02	2725	SAU101350	5429	SAU1c0042_orf_109p	12487
S1M10000031E03	2726	SAU101267	5409	SAU1c0037_orf_86p	12364
S1M10000031E03	2726	SAU300719	5876	SAU3c1108_orf_3p	13059
S1M10000031E04	2727	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000031E07	2728	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000031E08	2729	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000031E10	2730	SAU102433	5668	SAU1c0045_orf_37p	12701
S1M10000031E12	2731	SAU101400	5444	SAU1c0036_orf_35p	12326
S1M10000031F02	2732	SAU101800	5540	SAU1c0032_orf_20p	12225
S1M10000031F02	2732	SAU101801	5541	#N/A	#N/A
S1M10000031F03	2733	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000031F04	2734	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000031F04	2734	SAU101572	5484	SAU1c0044_orf_211p	12586
S1M10000031F05	2735	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000031F08	2736	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000031F10	2737	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031F11	2738	SAU102469	5679	SAU1c0026_orf_25p	12172
S1M10000031F12	2739	SAU102593	5704	SAU1c0041_orf_39p	12463
S1M10000031G02	2740	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000031G03	2741	SAU101679	5509	SAU1c0044_orf_222p	12593
S1M10000031G04	2742	SAU103198	5766	#N/A	#N/A
S1M10000031G06	2743	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000031G09	2744	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000031G10	2745	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000031G11	2746	SAU100118	5229	SAU1c0015_orf_13p	12125
S1M10000031H01	2747	SAU103144	5761	SAU1c0045_orf_15p	12663
S1M10000031H02	2748	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000031H06	2749	SAU100690	5309	#N/A	#N/A
S1M10000031H09	2750	SAU201743	5831	#N/A	#N/A
S1M10000031H11	2751	SAU100077	5226	SAU1c0043_orf_178p	12520
S1M10000032A03	2752	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000032A05	2753	SAU100275	5252	SAU1c0036_orf_15p	12314
S1M10000032A06	2754	SAU100610	5298	SAU1c0034_orf_71p	12294
S1M10000032A07	2755	SAU102059	5597	SAU1c0034_orf_51p	12286

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000032A08	2756	SAU102143	5607	SAU1c0041_orf_14p	12458
S1M10000032A10	2757	SAU101777	5527	SAU1c0037_orf_39p	12352
S1M10000032B01	2758	SAU301898	5904	SAU3c1079_orf_1p	13057
S1M10000032B05	2759	SAU102607	5712	SAU1c0041_orf_51p	12472
S1M10000032B05	2759	SAU102944	5749	SAU1c0041_orf_47p	12468
S1M10000032B07	2760	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000032B08	2761	SAU100175	5240	SAU1c0044_orf_204p	12582
S1M10000032B11	2762	SAU100944	5357	SAU1c0042_orf_5p	12505
S1M10000032B12	2763	SAU102117	5603	SAU1c0027_orf_6p	12181
S1M10000032C01	2764	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C03	2765	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C04	2766	SAU102241	5617	SAU1c0043_orf_25p	12539
S1M10000032C05	2767	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000032C09	2768	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032C10	2769	SAU201615	5826	SAU2c0440_orf_10p	12972
S1M10000032C11	2770	SAU102863	5737	#N/A	#N/A
S1M10000032C12	2771	SAU102863	5737	#N/A	#N/A
S1M10000032D03	2772	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000032D06	2773	SAU101652	5503	SAU1c0042_orf_123p	12492
S1M10000032D07	2774	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000032D09	2775	SAU100128	5231	#N/A	#N/A
S1M10000032D09	2775	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000032D09	2775	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000032D11	2776	SAU100128	5231	#N/A	#N/A
S1M10000032D11	2776	SAU101549	5476	SAU1c0043_orf_64p	12549
S1M10000032D11	2776	SAU101576	5488	SAU1c0044_orf_105p	12554
S1M10000032E02	2777	SAU101784	5530	SAU1c0037_orf_46p	12355
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S1M10000032E04	2779	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000032E06	2780	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000032E08	2781	SAU102281	5633	SAU1c0038_orf_4p	12384
S1M10000032E09	2782	SAU100521	5283	SAU1c0044_orf_250p	12600
S1M10000032E10	2783	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000032E11	2784	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000032E12	2785	SAU101999	5585	SAU1c0040_orf_101p	12423
S1M10000032F01	2786	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000032F01	2786	SAU102002	5587	SAU1c0040_orf_103p	12425
S1M10000032F04	2787	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000032F05	2788	SAU101339	5422	SAU1c0038_orf_81p	12399
S1M10000032F10	2789	SAU102585	5703	SAU1c0044_orf_289p	12611
S1M10000032F10	2789	SAU201773	5834	SAU2c0446_orf_4p	12996
S1M10000032F11	2790	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000032F12	2791	SAU100964	5363	SAU1c0044_orf_86p	12641

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000032G02	2792	SAU200628	5788	SAU2c0334_orf_4p	12790
S1M10000032G03	2793	SAU100813	5334	SAU1c0036_orf_29p	12322
S1M10000032G04	2794	SAU101904	5573	SAU1c0044_orf_36p	12617
S1M10000032G06	2795	SAU101509	5469	SAU1c0039_orf_81p	12418
S1M10000032G08	2796	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000032G10	2797	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032G12	2798	SAU101084	5377	SAU1c0034_orf_41p	12283
S1M10000032H01	2799	SAU101445	5452	SAU1c0038_orf_47p	12382
S1M10000032H01	2799	SAU101446	5453	SAU1c0038_orf_48p	12383
S1M10000032H04	2800	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000032H07	2801	SAU101797	5537	SAU1c0032_orf_17p	12221
S1M10000032H07	2801	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000032H09	2802	SAU101907	5574	SAU1c0040_orf_79p	12442
S1M10000032H11	2803	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000032H11	2803	SAU301148	5888	#N/A	#N/A
S1M10000033A02	2804	SAU201775	5835	SAU2c0446_orf_4p	12996
S1M10000033A02	2804	SAU301080	5885	SAU3c1287_orf_1p	13083
S1M10000033A07	2805	SAU200949	5800	SAU2c0380_orf_11p	12846
S1M10000033A08	2806	SAU101231	5399	SAU1c0035_orf_6p	12303
S1M10000033A10	2807	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000033B02	2808	SAU101808	5548	SAU1c0032_orf_27p	12232
S1M10000033B07	2809	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033B08	2810	SAU101868	5565	SAU1c0036_orf_23p	12320
S1M10000033B11	2811	SAU100793	5329	SAU1c0028_orf_52p	12188
S1M10000033B11	2811	SAU301433	5895	SAU3c1420_orf_2p	13118
S1M10000033B12	2812	SAU101104	5382	SAU1c0029_orf_20p	12195
S1M10000033B12	2812	SAU103010	5753	SAU1c0029_orf_19p	12194
S1M10000033C04	2813	SAU102933	5744	SAU1c0039_orf_62p	12412
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S1M10000033D03	2815	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000033D04	2816	SAU100745	5319	SAU1c0044_orf_233p	12596
S1M10000033D05	2817	SAU100301	5254	SAU1c0040_orf_91p	12452
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S1M10000033D10	2819	SAU100813	5334	SAU1c0036_orf_29p	12322
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S1M10000033E10	2822	SAU100162	5239	SAU1c0044_orf_206p	12583
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S1M10000033F02	2824	SAU101724	5514	SAU1c0016_orf_9p	12136
S1M10000033F03	2825	SAU101784	5530	SAU1c0037_orf_46p	12355
S1M10000033F06	2826	SAU102449	5674	SAU1c0045_orf_22p	12677
S1M10000033F07	2827	SAU102044	5593	SAU1c0039_orf_65p	12414
S1M10000033F09	2828	SAU100414	5270	SAU1c0022_orf_24p	12148

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000033G05	2830	SAU101904	5573	SAU1c0044_orf_36p	12617
SIM10000033G07	2831	SAU101824	5554	SAU1c0038_orf_26p	12371
SIM10000033G09	2832	SAU102380	5654	SAU1c0033_orf_29p	12265
SIM10000033G10	2833	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000033G10	2833	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000033G11	2834	SAU101968	5581	SAU1c0028_orf_43p	12187
SIM10000033G12	2835	SAU100300	5253	SAU1c0040_orf_90p	12451
SIM10000033H01	2836	SAU301465	5896	SAU3c1429_orf_4p	13121
SIM10000033H02	2837	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000033H03	2838	SAU101833	5555	SAU1c0038_orf_34p	12373
SIM10000033H07	2839	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000033H08	2840	SAU101175	5388	SAU1c0031_orf_1p	12213
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SIM10000034A02	2844	SAU101197	5393	SAU1c0035_orf_60p	12300
SIM10000034A03	2845	SAU102939	5747	#N/A	#N/A
SIM10000034A04	2846	SAU102578	5701	SAU1c0039_orf_61p	12411
SIM10000034A05	2847	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000034A08	2848	SAU101020	5368	SAU1c0045_orf_86p	12710
SIM10000034A09	2849	SAU100773	5326	SAU1c0038_orf_39p	12377
SIM10000034A11	2850	SAU102389	5656	SAU1c0033_orf_36p	12268
SIM10000034A12	2851	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000034B03	2852	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000034B05	2853	SAU101630	5498	SAU1c0039_orf_4p	12410
SIM10000034B06	2854	SAU102607	5712	SAU1c0041_orf_51p	12472
SIM10000034B06	2854	SAU102944	5749	SAU1c0041_orf_47p	12468
SIM10000034B07	2855	SAU100077	5226	SAU1c0043_orf_178p	12520
SIM10000034B08	2856	SAU101341	5424	SAU1c0044_orf_38p	12618
SIM10000034B09	2857	SAU101909	5575	SAU1c0040_orf_77p	12441
SIM10000034B10	2858	SAU101882	5569	SAU1c0025_orf_15p	12163
SIM10000034B12	2859	SAU200593	5786	SAU2c0327_orf_1p	12784
SIM10000034C02	2860	SAU100557	5291	SAU1c0044_orf_132p	12565
SIM10000034C06	2861	SAU200157	5776	#N/A	#N/A
SIM10000034C07	2862	SAU101343	5425	SAU1c0044_orf_40p	12619
SIM10000034C09	2863	SAU102281	5633	SAU1c0038_orf_4p	12384
SIM10000034C12	2864	SAU100859	5342	SAU1c0038_orf_87p	12402
SIM10000034D01	2865	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000034D05	2866	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000034D06	2867	SAU200157	5776	#N/A	#N/A
SIM10000034D07	2868	SAU100745	5319	SAU1c0044_orf_233p	12596
SIM10000034D08	2869	SAU102284	5635	SAU1c0038_orf_5p	12389
SIM10000034D08	2869	SAU201469	5816	SAU2c0438_orf_6p	12967

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000034D10	2870	SAU102474	5681	SAU1c0026_orf_31p	12174
SIM10000034D11	2871	SAU101881	5568	SAU1c0025_orf_14p	12162
SIM10000034D12	2872	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000034E01	2873	SAU102433	5668	SAU1c0045_orf_37p	12701
SIM10000034E02	2874	SAU100557	5291	SAU1c0044_orf_132p	12565
SIM10000034E04	2875	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000034E05	2876	SAU100738	5317	SAU1c0044_orf_52p	12624
SIM10000034E06	2877	SAU100347	5262	SAU1c0036_orf_56p	12334
SIM10000034E06	2877	SAU100443	5274	SAU1c0036_orf_55p	12333
SIM10000034E07	2878	SAU100617	5300	SAU1c0035_orf_102p	12295
SIM10000034E10	2879	SAU102401	5661	SAU1c0030_orf_4p	12209
SIM10000034E11	2880	SAU101881	5568	SAU1c0025_orf_14p	12162
SIM10000034E12	2881	SAU200960	5801	SAU2c0377_orf_5p	12843
SIM10000034F01	2882	SAU202731	5850	#N/A	#N/A
SIM10000034F02	2883	SAU201621	5828	SAU2c0437_orf_4p	12966
SIM10000034F03	2884	SAU201971	5841	SAU2c0455_orf_17p	13015
SIM10000034F03	2884	SAU301363	5894	#N/A	#N/A
SIM10000034F04	2885	SAU301620	5899	SAU3c1478_orf_2p	13140
SIM10000034F05	2886	SAU101630	5498	SAU1c0039_orf_4p	12410
SIM10000034F07	2887	SAU101175	5388	SAU1c0031_orf_1p	12213
SIM10000034F08	2888	SAU202736	5851	SAU2c0426_orf_7p	12927
SIM10000034F09	2889	SAU101869	5566	SAU1c0036_orf_24p	12321
SIM10000034F10	2890	SAU102350	5649	SAU1c0040_orf_36p	12433
SIM10000034F12	2891	SAU100522	5284	SAU1c0044_orf_249p	12599
SIM10000034G02	2892	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000034G03	2893	SAU101198	5394	SAU1c0035_orf_61p	12301
SIM10000034G06	2894	SAU202174	5845	SAU2c0412_orf_3p	12895
SIM10000034G07	2895	SAU102380	5654	SAU1c0033_orf_29p	12265
SIM10000034G08	2896	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000034G09	2897	SAU102294	5639	SAU1c0044_orf_288p	12610
SIM10000034G09	2897	SAU201775	5835	SAU2c0446_orf_4p	12996
SIM10000034G11	2898	SAU200558	5782	SAU2c0322_orf_5p	12777
SIM10000034G12	2899	SAU100557	5291	SAU1c0044_orf_132p	12565
SIM10000034H01	2900	SAU101293	5414	SAU1c0044_orf_61p	12631
SIM10000034H02	2901	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000034H03	2902	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000034H06	2903	SAU101570	5482	SAU1c0044_orf_209p	12584
SIM10000034H07	2904	SAU100077	5226	SAU1c0043_orf_178p	12520
SIM10000034H08	2905	SAU200740	5794	SAU2c0340_orf_3p	12798
SIM10000034H09	2906	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000034H10	2907	SAU102422	5666	SAU1c0030_orf_22p	12207
SIM10000035A03	2908	SAU101360	5431	SAU1c0044_orf_109p	12555
SIM10000035A08	2909	SAU201403	5815	SAU2c0423_orf_3p	12913
SIM10000035A09	2910	SAU101350	5429	SAU1c0042_orf_109p	12487

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000035A10	2911	SAU203296	5863	SAU2c0442_orf_18p	12983
SIM10000035A11	2912	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000035A12	2913	SAU101455	5456	SAU1c0045_orf_250p	12686
SIM10000035A12	2913	SAU200916	5797	SAU2c0373_orf_4p	12838
SIM10000035A12	2913	SAU301620	5899	SAU3c1478_orf_2p	13140
SIM10000035B01	2914	SAU102584	5702	SAU1c0043_orf_239p	12537
SIM10000035B03	2915	SAU102246	5619	SAU1c0043_orf_30p	12542
SIM10000035B04	2916	SAU102246	5619	SAU1c0043_orf_30p	12542
SIM10000035B08	2917	SAU103232	5769	SAU1c0045_orf_341p	12697
SIM10000035B11	2918	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000035C01	2919	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000035C02	2920	SAU101039	5373	SAU1c0043_orf_181p	12522
SIM10000035C04	2921	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000035C06	2922	SAU101497	5468	SAU1c0037_orf_66p	12361
SIM10000035C11	2923	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000035D01	2924	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000035D04	2925	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000035D06	2926	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000035D09	2927	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000035D12	2928	SAU100608	5297	SAU1c0034_orf_69p	12293
SIM10000035E02	2929	SAU102883	5741	SAU1c0045_orf_38p	12702
SIM10000035E03	2930	SAU102447	5672	SAU1c0045_orf_24p	12685
SIM10000035E04	2931	SAU103025	5755	SAU1c0029_orf_9p	12202
SIM10000035E08	2932	SAU100690	5309	#N/A	#N/A
SIM10000035E09	2933	SAU101197	5393	SAU1c0035_orf_60p	12300
SIM10000035E12	2934	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000035F03	2935	SAU101092	5381	SAU1c0028_orf_9p	12192
SIM10000035F03	2935	SAU202882	5855	SAU2c0381_orf_3p	12848
SIM10000035F04	2936	SAU101784	5530	SAU1c0037_orf_46p	12355
SIM10000035F09	2937	SAU203296	5863	SAU2c0442_orf_18p	12983
SIM10000035F12	2938	SAU101427	5447	SAU1c0042_orf_144p	12500
SIM10000035F12	2938	SAU103204	5767	SAU1c0042_orf_143p	12499
SIM10000035G02	2939	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000035G09	2940	SAU203296	5863	SAU2c0442_orf_18p	12983
SIM10000035G11	2941	SAU101344	5426	SAU1c0044_orf_41p	12620
SIM10000035G12	2942	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000035H01	2943	SAU100140	5235	SAU1c0032_orf_7p	12258
SIM10000035H07	2944	SAU100313	5259	SAU1c0045_orf_153p	12661
SIM10000035H07	2944	SAU100359	5264	SAU1c0032_orf_35p	12239
SIM10000035H07	2944	SAU200297	5778	SAU2c0274_orf_2p	12739
SIM10000035H08	2945	SAU101772	5526	SAU1c0037_orf_34p	12351
SIM10000035H09	2946	SAU100496	5279	SAU1c0041_orf_83p	12484
SIM10000035H09	2946	SAU301004	5882	SAU3c1255_orf_1p	13079

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000035H10	2947	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000035H11	2948	SAU101344	5426	SAU1c0044_orf_41p	12620
SIM10000036A02	2949	SAU102447	5672	SAU1c0045_orf_24p	12685
SIM10000036A03	2950	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000036A04	2951	SAU200994	5802	SAU2c0428_orf_4p	12935
SIM10000036A05	2952	SAU101810	5549	SAU1c0032_orf_28p	12233
SIM10000036A05	2952	SAU101811	5550	SAU1c0032_orf_29p	12234
SIM10000036A05	2952	SAU300110	5865	SAU3c0533_orf_2p	13031
SIM10000036A08	2953	SAU101220	5396	SAU1c0044_orf_94p	12645
SIM10000036A11	2954	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000036A12	2955	SAU100813	5334	SAU1c0036_orf_29p	12322
SIM10000036B04	2956	SAU101570	5482	SAU1c0044_orf_209p	12584
SIM10000036B04	2956	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000036B06	2957	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000036B07	2958	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000036B08	2959	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000036B11	2960	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000036B12	2961	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000036C01	2962	SAU100242	5246	SAU1c0036_orf_5p	12336
SIM10000036C03	2963	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000036C04	2964	SAU102433	5668	SAU1c0045_orf_37p	12701
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SIM10000036C06	2966	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000036C07	2967	SAU101800	5540	SAU1c0032_orf_20p	12225
SIM10000036C07	2967	SAU101801	5541	#N/A	#N/A
SIM10000036C09	2968	SAU102585	5703	SAU1c0044_orf_289p	12611
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SIM10000036C09	2968	SAU302685	5908	SAU3c1403_orf_1p	13113
SIM10000036C10	2969	SAU100433	5272	SAU1c0040_orf_87p	12449
SIM10000036C10	2969	SAU101751	5521	SAU1c0040_orf_86p	12448
SIM10000036D02	2970	SAU201197	5806	SAU2c0429_orf_2p	12938
SIM10000036D03	2971	SAU103038	5757	#N/A	#N/A
SIM10000036D06	2972	SAU103024	5754	SAU1c0029_orf_6p	12200
SIM10000036D08	2973	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000036D10	2974	SAU102933	5744	SAU1c0039_orf_62p	12412
SIM10000036D11	2975	SAU101197	5393	SAU1c0035_orf_60p	12300
SIM10000036D11	2975	SAU101198	5394	SAU1c0035_orf_61p	12301
SIM10000036D12	2976	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000036E06	2977	SAU100432	5271	SAU1c0040_orf_88p	12450
SIM10000036E06	2977	SAU202756	5852	SAU2c0470_orf_1p	13027
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SIM10000036E11	2979	SAU101343	5425	SAU1c0044_orf_40p	12619
SIM10000036F06	2980	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000036F07	2981	SAU200928	5798	SAU2c0365_orf_5p	12815

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000036F08	2982	SAU200914	5796	SAU2c0373_orf_2p	12837
SIM10000036F09	2983	SAU100532	5287	SAU1c0044_orf_198p	12580
SIM10000036F10	2984	SAU101586	5489	SAU1c0044_orf_242p	12598
SIM10000036F11	2985	SAU201506	5818	SAU2c0432_orf_18p	12946
SIM10000036G03	2986	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000036G07	2987	SAU102355	5651	SAU1c0040_orf_40p	12435
SIM10000036G08	2988	SAU102336	5646	SAU1c0045_orf_146p	12659
SIM10000036G11	2989	SAU101340	5423	SAU1c0038_orf_82p	12400
SIM10000036H01	2990	SAU101793	5534	SAU1c0032_orf_14p	12218
SIM10000036H02	2991	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000036H03	2992	SAU102909	5743	SAU1c0036_orf_16p	12315
SIM10000036H04	2993	SAU102909	5743	SAU1c0036_orf_16p	12315
SIM10000036H05	2994	SAU101798	5538	SAU1c0032_orf_18p	12222
SIM10000036H06	2995	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000036H08	2996	SAU102909	5743	SAU1c0036_orf_16p	12315
SIM10000036H11	2997	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000037A02	2998	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000037A02	2998	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000037A03	2999	SAU100128	5231	#N/A	#N/A
SIM10000037A03	2999	SAU101549	5476	SAU1c0043_orf_64p	12549
SIM10000037A03	2999	SAU101576	5488	SAU1c0044_orf_105p	12554
SIM10000037A06	3000	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000037A08	3001	SAU102669	5728	SAU1c0024_orf_7p	12160
SIM10000037A09	3002	SAU101455	5456	SAU1c0045_orf_250p	12686
SIM10000037A09	3002	SAU200916	5797	SAU2c0373_orf_4p	12838
SIM10000037A11	3003	SAU101436	5449	SAU1c0028_orf_23p	12183
SIM10000037A12	3004	SAU200914	5796	SAU2c0373_orf_2p	12837
SIM10000037B03	3005	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000037B04	3006	SAU100767	5323	SAU1c0044_orf_192p	12579
SIM10000037B05	3007	SAU102578	5701	SAU1c0039_orf_61p	12411
SIM10000037B06	3008	SAU101806	5546	SAU1c0032_orf_25p	12230
SIM10000037B06	3008	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000037B07	3009	SAU101915	5577	SAU1c0040_orf_72p	12439
SIM10000037B08	3010	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000037B10	3011	SAU101346	5427	SAU1c0044_orf_43p	12621
SIM10000037B11	3012	SAU101399	5443	SAU1c0036_orf_34p	12325
SIM10000037B12	3013	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000037C05	3014	SAU101482	5461	SAU1c0015_orf_10p	12123
SIM10000037C06	3015	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000037C07	3016	SAU101641	5501	SAU1c0029_orf_12p	12193
SIM10000037C08	3017	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000037C09	3018	SAU101818	5553	SAU1c0038_orf_20p	12369
SIM10000037C10	3019	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000037D04	3020	SAU102283	5634	SAU1c0006_orf_1p	12119

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000037D05	3021	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000037D06	3022	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000037D09	3023	SAU102246	5619	SAU1c0043_orf_30p	12542
SIM10000037D12	3024	SAU101999	5585	SAU1c0040_orf_101p	12423
SIM10000037E02	3025	SAU102447	5672	SAU1c0045_orf_24p	12685
SIM10000037E02	3025	SAU102448	5673	SAU1c0045_orf_23p	12681
SIM10000037E03	3026	SAU100813	5334	SAU1c0036_orf_29p	12322
SIM10000037E06	3027	SAU100921	5355	SAU1c0038_orf_76p	12396
SIM10000037E08	3028	SAU100139	5234	SAU1c0032_orf_6p	12255
SIM10000037E08	3028	SAU100140	5235	SAU1c0032_orf_7p	12258
SIM10000037E09	3029	SAU102049	5595	SAU1c0039_orf_68p	12416
SIM10000037E10	3030	SAU101444	5451	SAU1c0038_orf_46p	12381
SIM10000037E11	3031	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000037E12	3032	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000037F02	3033	SAU100776	5327	SAU1c0041_orf_72p	12482
SIM10000037F03	3034	SAU101339	5422	SAU1c0038_orf_81p	12399
SIM10000037F04	3035	SAU200468	5781	SAU2c0429_orf_19p	12937
SIM10000037F05	3036	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000037F06	3037	SAU102585	5703	SAU1c0044_orf_289p	12611
SIM10000037F06	3037	SAU201773	5834	SAU2c0446_orf_4p	12996
SIM10000037F07	3038	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000037F07	3038	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000037F08	3039	SAU203001	5859	SAU2c0412_orf_15p	12894
SIM10000037F08	3039	SAU203007	5860	SAU2c0412_orf_10p	12893
SIM10000037F09	3040	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000037F10	3041	SAU200468	5781	SAU2c0429_orf_19p	12937
SIM10000037G01	3042	SAU102502	5690	SAU1c0045_orf_273p	12689
SIM10000037G01	3042	SAU102503	5691	SAU1c0045_orf_274p	12690
SIM10000037G02	3043	SAU100658	5303	SAU1c0038_orf_59p	12388
SIM10000037G03	3044	SAU101344	5426	SAU1c0044_orf_41p	12620
SIM10000037G06	3045	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000037G07	3046	SAU103038	5757	#N/A	#N/A
SIM10000037G08	3047	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000037G10	3048	SAU100062	5225	SAU1c0035_orf_98p	12309
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SIM10000037H05	3051	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000037H07	3052	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000037H08	3053	SAU200928	5798	SAU2c0365_orf_5p	12815
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SIM10000038A04	3056	SAU101275	5412	SAU1c0044_orf_257p	12604
SIM10000038A07	3057	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000038A08	3058	SAU102059	5597	SAU1c0034_orf_51p	12286

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000038A11	3060	SAU100547	5290	SAU1c0032_orf_3p	12240
SIM10000038A12	3061	SAU101799	5539	SAU1c0032_orf_19p	12223
SIM10000038B01	3062	SAU101483	5462	SAU1c0015_orf_11p	12124
SIM10000038B03	3063	SAU101360	5431	SAU1c0044_orf_109p	12555
SIM10000038B07	3064	SAU102433	5668	SAU1c0045_orf_37p	12701
SIM10000038B08	3065	SAU100308	5258	SAU1c0036_orf_133p	12312
SIM10000038B09	3066	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000038B09	3066	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000038B12	3067	SAU102764	5734	SAU1c0044_orf_56p	12625
SIM10000038C01	3068	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000038C02	3069	SAU200657	5789	#N/A	#N/A
SIM10000038C06	3070	SAU101320	5420	SAU1c0015_orf_16p	12128
SIM10000038C08	3071	SAU102132	5605	SAU1c0027_orf_19p	12177
SIM10000038C10	3072	SAU101346	5427	SAU1c0044_orf_43p	12621
SIM10000038C10	3072	SAU101347	5428	SAU1c0044_orf_44p	12622
SIM10000038C11	3073	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000038C12	3074	SAU101792	5533	SAU1c0032_orf_13p	12217
SIM10000038D02	3075	SAU101842	5557	SAU1c0042_orf_9p	12510
SIM10000038D05	3076	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000038D07	3077	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000038D08	3078	SAU101341	5424	SAU1c0044_orf_38p	12618
SIM10000038D08	3078	SAU301275	5892	SAU3c1365_orf_2p	13103
SIM10000038D09	3079	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000038D10	3080	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000038D11	3081	SAU101300	5415	SAU1c0044_orf_113p	12557
SIM10000038D11	3081	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000038D12	3082	SAU100752	5322	SAU1c0043_orf_183p	12524
SIM10000038D12	3082	SAU100952	5358	SAU1c0043_orf_182p	12523
SIM10000038E01	3083	SAU101814	5551	SAU1c0032_orf_32p	12237
SIM10000038E02	3084	SAU101842	5557	SAU1c0042_orf_9p	12510
SIM10000038E03	3085	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000038E04	3086	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000038E05	3087	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000038E06	3088	SAU102231	5614	SAU1c0043_orf_18p	12527
SIM10000038E06	3088	SAU102232	5615	SAU1c0043_orf_19p	12530
SIM10000038E07	3089	SAU200593	5786	SAU2c0327_orf_1p	12784
SIM10000038E10	3090	SAU201558	5823	SAU2c0434_orf_5p	12954
SIM10000038E12	3091	SAU100838	5337	SAU1c0031_orf_12p	12211
SIM10000038E12	3091	SAU100839	5338	SAU1c0031_orf_11p	12210
SIM10000038F03	3092	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000038F04	3093	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000038F04	3093	SAU100965	5364	SAU1c0044_orf_87p	12642
SIM10000038F05	3094	SAU100964	5363	SAU1c0044_orf_86p	12641

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000038F08	3096	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038F09	3097	SAU201666	5830	SAU2c0442_orf_11p	12981
S1M10000038F10	3098	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000038F11	3099	SAU100747	5320	SAU1c0044_orf_235p	12597
S1M10000038F12	3100	SAU202039	5843	SAU2c0452_orf_20p	13009
S1M10000038G01	3101	SAU101271	5411	SAU1c0037_orf_90p	12366
S1M10000038G03	3102	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000038G04	3103	SAU100475	5276	SAU1c0036_orf_61p	12337
S1M10000038G06	3104	SAU101189	5392	SAU1c0033_orf_25p	12264
S1M10000038G08	3105	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000038G10	3106	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000038G11	3107	SAU100123	5230	SAU1c0043_orf_189p	12526
S1M10000038G11	3107	SAU102001	5586	SAU1c0040_orf_102p	12424
S1M10000038G12	3108	SAU101184	5391	SAU1c0035_orf_80p	12305
S1M10000038H03	3109	SAU101798	5538	SAU1c0032_orf_18p	12222
S1M10000038H07	3110	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000038H09	3111	SAU102340	5647	SAU1c0045_orf_149p	12660
S1M10000038H11	3112	SAU101452	5455	SAU1c0045_orf_247p	12684
S1M10000039A02	3113	SAU100496	5279	SAU1c0041_orf_83p	12484
S1M10000039A02	3113	SAU301004	5882	SAU3c1255_orf_1p	13079
S1M10000039A05	3114	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000039A05	3114	SAU100965	5364	SAU1c0044_orf_87p	12642
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S1M10000039A08	3116	SAU100522	5284	SAU1c0044_orf_249p	12599
S1M10000039A11	3117	SAU100613	5299	SAU1c0015_orf_14p	12126
S1M10000039A12	3118	SAU301465	5896	SAU3c1429_orf_4p	13121
S1M10000039B02	3119	SAU101455	5456	SAU1c0045_orf_250p	12686
S1M10000039B02	3119	SAU200916	5797	SAU2c0373_orf_4p	12838
S1M10000039B06	3120	SAU102350	5649	SAU1c0040_orf_36p	12433
S1M10000039B07	3121	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000039B10	3122	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000039B12	3123	SAU301118	5886	SAU3c1305_orf_3p	13086
S1M10000039C04	3124	SAU102252	5621	SAU1c0032_orf_48p	12241
S1M10000039C06	3125	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000039C07	3126	SAU200657	5789	#N/A	#N/A
S1M10000039C08	3127	SAU200468	5781	SAU2c0429_orf_19p	12937
S1M10000039C09	3128	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000039C10	3129	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000039C11	3130	SAU200657	5789	#N/A	#N/A
S1M10000039D02	3131	SAU201403	5815	SAU2c0423_orf_3p	12913
S1M10000039D09	3132	SAU102294	5639	SAU1c0044_orf_288p	12610
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000039E01	3134	SAU102264	5628	SAU1c0032_orf_60p	12250
SIM10000039E08	3135	SAU100412	5269	SAU1c0029_orf_38p	12197
SIM10000039E09	3136	SAU100056	5223	SAU1c0044_orf_176p	12577
SIM10000039E10	3137	SAU102394	5659	SAU1c0033_orf_41p	12271
SIM10000039E10	3137	SAU301118	5886	SAU3c1305_orf_3p	13086
SIM10000039E11	3138	SAU102473	5680	SAU1c0026_orf_30p	12173
SIM10000039F02	3139	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000039F03	3140	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000039F05	3141	SAU100118	5229	SAU1c0015_orf_13p	12125
SIM10000039F07	3142	SAU102531	5694	SAU1c0045_orf_186p	12667
SIM10000039F08	3143	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000039F09	3144	SAU200157	5776	#N/A	#N/A
SIM10000039F10	3145	SAU100059	5224	SAU1c0045_orf_10p	12652
SIM10000039F12	3146	SAU101565	5480	SAU1c0022_orf_8p	12151
SIM10000039G03	3147	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000039G04	3148	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000039G07	3149	SAU100952	5358	SAU1c0043_orf_182p	12523
SIM10000039G07	3149	SAU101039	5373	SAU1c0043_orf_181p	12522
SIM10000039G10	3150	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000039H02	3151	SAU102585	5703	SAU1c0044_orf_289p	12611
SIM10000039H02	3151	SAU201773	5834	SAU2c0446_orf_4p	12996
SIM10000039H03	3152	SAU100313	5259	SAU1c0045_orf_153p	12661
SIM10000039H03	3152	SAU100359	5264	SAU1c0032_orf_35p	12239
SIM10000039H03	3152	SAU200297	5778	SAU2c0274_orf_2p	12739
SIM10000039H04	3153	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000039H06	3154	SAU102283	5634	SAU1c0006_orf_1p	12119
SIM10000039H07	3155	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000039H07	3155	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000039H08	3156	SAU102440	5671	SAU1c0045_orf_30p	12692
SIM10000040A04	3157	SAU100040	5221	SAU1c0043_orf_217p	12533
SIM10000040A05	3158	SAU102671	5729	SAU1c0024_orf_9p	12161
SIM10000040A07	3159	SAU101028	5370	SAU1c0043_orf_7p	12552
SIM10000040A08	3160	SAU200157	5776	#N/A	#N/A
SIM10000040A10	3161	SAU103038	5757	#N/A	#N/A
SIM10000040A11	3162	SAU101801	5541	#N/A	#N/A
SIM10000040B01	3163	SAU101461	5457	SAU1c0045_orf_234p	12680
SIM10000040B03	3164	SAU102102	5600	SAU1c0045_orf_340p	12696
SIM10000040B07	3165	SAU101432	5448	SAU1c0028_orf_27p	12184
SIM10000040B11	3166	SAU101198	5394	SAU1c0035_orf_61p	12301
SIM10000040C03	3167	SAU201971	5841	SAU2c0455_orf_17p	13015
SIM10000040C03	3167	SAU301363	5894	#N/A	#N/A
SIM10000040C04	3168	SAU102551	5698	SAU1c0045_orf_206p	12672
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000040C07	3171	SAU100970	5365	SAU1c0043_orf_197p	12529
S1M10000040C08	3172	SAU101197	5393	SAU1c0035_orf_60p	12300
S1M10000040C10	3173	SAU201810	5836	SAU2c0308_orf_2p	12769
S1M10000040C10	3173	SAU202174	5845	SAU2c0412_orf_3p	12895
S1M10000040C10	3173	SAU301148	5888	#N/A	#N/A
S1M10000040C11	3174	SAU101869	5566	SAU1c0036_orf_24p	12321
S1M10000040D01	3175	SAU101806	5546	SAU1c0032_orf_25p	12230
S1M10000040D01	3175	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000040D03	3176	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000040D03	3176	SAU102201	5612	SAU1c0045_orf_169p	12666
S1M10000040D08	3177	SAU100633	5301	SAU1c0043_orf_147p	12515
S1M10000040D09	3178	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040D11	3179	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E01	3180	SAU100916	5353	SAU1c0038_orf_71p	12394
S1M10000040E02	3181	SAU101845	5558	SAU1c0042_orf_7p	12506
S1M10000040E04	3182	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000040E05	3183	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000040E06	3184	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000040E07	3185	SAU101006	5367	SAU1c0028_orf_59p	12190
S1M10000040E09	3186	SAU102605	5710	SAU1c0041_orf_49p	12470
S1M10000040E10	3187	SAU100714	5312	SAU1c0044_orf_74p	12635
S1M10000040E11	3188	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040E12	3189	SAU102503	5691	SAU1c0045_orf_274p	12690
S1M10000040E12	3189	SAU201380	5812	SAU2c0426_orf_11p	12922
S1M10000040F01	3190	SAU101226	5398	SAU1c0035_orf_2p	12298
S1M10000040F02	3191	SAU101614	5494	SAU1c0044_orf_9p	12649
S1M10000040F03	3192	SAU101592	5490	SAU1c0039_orf_37p	12406
S1M10000040F04	3193	SAU100123	5230	SAU1c0043_orf_189p	12526
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S1M10000040F04	3193	SAU103159	5762	SAU1c0045_orf_204p	12670
S1M10000040F04	3193	SAU201827	5837	SAU2c0449_orf_21p	13002
S1M10000040F05	3194	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000040F06	3195	SAU100547	5290	SAU1c0032_orf_3p	12240
S1M10000040F08	3196	SAU300713	5875	SAU3c1104_orf_1p	13058
S1M10000040F09	3197	SAU101610	5492	SAU1c0044_orf_5p	12629
S1M10000040F12	3198	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G01	3199	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000040G02	3200	SAU200561	5783	SAU2c0324_orf_3p	12779
S1M10000040G02	3200	SAU301773	5901	SAU3c1509_orf_2p	13157
S1M10000040G04	3201	SAU100414	5270	SAU1c0022_orf_24p	12148
S1M10000040G07	3202	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000040G08	3203	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000040G12	3204	SAU101421	5446	SAU1c0042_orf_138p	12498

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000040H03	3206	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000040H04	3207	SAU200914	5796	SAU2c0373_orf_2p	12837
SIM10000040H05	3208	SAU101400	5444	SAU1c0036_orf_35p	12326
SIM10000040H07	3209	SAU100921	5355	SAU1c0038_orf_76p	12396
SIM10000040H10	3210	SAU202039	5843	SAU2c0452_orf_20p	13009
SIM10000041A03	3211	SAU102054	5596	SAU1c0039_orf_74p	12417
SIM10000041B02	3212	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000041B03	3213	SAU101592	5490	SAU1c0039_orf_37p	12406
SIM10000041B05	3214	SAU101798	5538	SAU1c0032_orf_18p	12222
SIM10000041B06	3215	SAU301620	5899	SAU3c1478_orf_2p	13140
SIM10000041B07	3216	SAU101145	5384	SAU1c0035_orf_43p	12299
SIM10000041B12	3217	SAU102725	5733	SAU1c0036_orf_68p	12338
SIM10000041C08	3218	SAU102607	5712	SAU1c0041_orf_51p	12472
SIM10000041C08	3218	SAU102944	5749	SAU1c0041_orf_47p	12468
SIM10000041C10	3219	SAU101784	5530	SAU1c0037_orf_46p	12355
SIM10000041C11	3220	SAU101570	5482	SAU1c0044_orf_209p	12584
SIM10000041D06	3221	SAU101777	5527	SAU1c0037_orf_39p	12352
SIM10000041D07	3222	SAU102639	5724	#N/A	#N/A
SIM10000041D08	3223	SAU200030	5772	SAU2c0282_orf_3p	12745
SIM10000041D10	3224	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000041D12	3225	SAU102658	5726	SAU1c0045_orf_121p	12654
SIM10000041E03	3226	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000041E06	3227	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000041E09	3228	SAU201236	5808	SAU2c0409_orf_10p	12891
SIM10000041E12	3229	SAU100952	5358	SAU1c0043_orf_182p	12523
SIM10000041F03	3230	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000041F03	3230	SAU101572	5484	SAU1c0044_orf_211p	12586
SIM10000041F11	3231	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000041F12	3232	SAU102480	5684	SAU1c0039_orf_100p	12404
SIM10000041F12	3232	SAU102481	5685	SAU1c0039_orf_99p	12422
SIM10000041G01	3233	SAU100532	5287	SAU1c0044_orf_198p	12580
SIM10000041G06	3234	SAU102345	5648	SAU1c0045_orf_125p	12655
SIM10000041G08	3235	SAU101546	5475	SAU1c0037_orf_133p	12349
SIM10000041G10	3236	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000041G11	3237	SAU101802	5542	SAU1c0032_orf_22p	12227
SIM10000041H01	3238	SAU101198	5394	SAU1c0035_orf_61p	12301
SIM10000041H04	3239	SAU100497	5280	SAU1c0018_orf_3p	12140
SIM10000041H05	3240	SAU100242	5246	SAU1c0036_orf_5p	12336
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SIM10000041H08	3242	SAU301133	5887	SAU3c1311_orf_3p	13087
SIM10000041H09	3243	SAU103169	5763	SAU1c0045_orf_230p	12678
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000042A07	3247	SAU100633	5301	SAU1c0043_orf_147p	12515
SIM10000042A09	3248	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000042A11	3249	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000042A12	3250	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000042B02	3251	SAU202736	5851	SAU2c0426_orf_7p	12927
SIM10000042B03	3252	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000042B06	3253	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000042B07	3254	SAU101343	5425	SAU1c0044_orf_40p	12619
SIM10000042B08	3255	SAU100443	5274	SAU1c0036_orf_55p	12333
SIM10000042B09	3256	SAU101802	5542	SAU1c0032_orf_22p	12227
SIM10000042B10	3257	SAU100141	5236	SAU1c0032_orf_8p	12259
SIM10000042B10	3257	SAU102527	5693	SAU1c0032_orf_9p	12260
SIM10000042B11	3258	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000042B12	3259	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000042C02	3260	SAU100617	5300	SAU1c0035_orf_102p	12295
SIM10000042C06	3261	SAU102032	5591	SAU1c0029_orf_47p	12198
SIM10000042C10	3262	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000042C11	3263	SAU103037	5756	SAU1c0044_orf_303p	12613
SIM10000042D04	3264	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000042D07	3265	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000042D10	3266	SAU203296	5863	SAU2c0442_orf_18p	12983
SIM10000042D11	3267	SAU102663	5727	SAU1c0024_orf_2p	12158
SIM10000042E03	3268	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000042E06	3269	SAU102433	5668	SAU1c0045_orf_37p	12701
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SIM10000042F01	3271	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000042F02	3272	SAU101891	5571	SAU1c0034_orf_30p	12281
SIM10000042F05	3273	SAU101652	5503	SAU1c0042_orf_123p	12492
SIM10000042F06	3274	SAU100773	5326	SAU1c0038_orf_39p	12377
SIM10000042F08	3275	SAU100162	5239	SAU1c0044_orf_206p	12583
SIM10000042F09	3276	SAU100246	5247	SAU1c0042_orf_130p	12496
SIM10000042F09	3276	SAU300998	5881	SAU3c1253_orf_3p	13077
SIM10000042F10	3277	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000042F11	3278	SAU101653	5504	SAU1c0042_orf_124p	12493
SIM10000042G01	3279	SAU100140	5235	SAU1c0032_orf_7p	12258
SIM10000042G03	3280	SAU101220	5396	SAU1c0044_orf_94p	12645
SIM10000042G08	3281	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000042G09	3282	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000042G12	3283	SAU100521	5283	SAU1c0044_orf_250p	12600
SIM10000042H05	3284	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000042H07	3285	SAU100433	5272	SAU1c0040_orf_87p	12449
SIM10000042H11	3286	SAU101632	5499	SAU1c0039_orf_3p	12407

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000043A02	3287	SAU203001	5859	SAU2c0412_orf_15p	12894
SIM10000043A03	3288	SAU101400	5444	SAU1c0036_orf_35p	12326
SIM10000043A04	3289	SAU200088	5775	SAU2c0159_orf_1p	12724
SIM10000043A06	3290	SAU100077	5226	SAU1c0043_orf_178p	12520
SIM10000043A07	3291	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000043A08	3292	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000043A10	3293	SAU100865	5343	SAU1c0044_orf_99p	12648
SIM10000043A11	3294	SAU100865	5343	SAU1c0044_orf_99p	12648
SIM10000043A12	3295	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000043B01	3296	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000043B02	3297	SAU100059	5224	SAU1c0045_orf_10p	12652
SIM10000043B07	3298	SAU101922	5578	SAU1c0040_orf_66p	12438
SIM10000043B07	3298	SAU200345	5779	SAU2c0292_orf_3p	12751
SIM10000043B08	3299	SAU100313	5259	SAU1c0045_orf_153p	12661
SIM10000043B08	3299	SAU100359	5264	SAU1c0032_orf_35p	12239
SIM10000043B08	3299	SAU200297	5778	SAU2c0274_orf_2p	12739
SIM10000043B09	3300	SAU100521	5283	SAU1c0044_orf_250p	12600
SIM10000043B10	3301	SAU100436	5273	SAU1c0023_orf_20p	12154
SIM10000043B12	3302	SAU102142	5606	SAU1c0041_orf_13p	12457
SIM10000043C02	3303	SAU101777	5527	SAU1c0037_orf_39p	12352
SIM10000043C07	3304	SAU101784	5530	SAU1c0037_orf_46p	12355
SIM10000043C11	3305	SAU201403	5815	SAU2c0423_orf_3p	12913
SIM10000043C12	3306	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000043D01	3307	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000043D02	3308	SAU301465	5896	SAU3c1429_orf_4p	13121
SIM10000043D04	3309	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000043D10	3310	SAU102631	5721	SAU1c0045_orf_94p	12712
SIM10000043D12	3311	SAU100496	5279	SAU1c0041_orf_83p	12484
SIM10000043D12	3311	SAU301004	5882	SAU3c1255_orf_1p	13079
SIM10000043E02	3312	SAU100793	5329	SAU1c0028_orf_52p	12188
SIM10000043E02	3312	SAU301433	5895	SAU3c1420_orf_2p	13118
SIM10000043E03	3313	SAU102032	5591	SAU1c0029_orf_47p	12198
SIM10000043E05	3314	SAU102067	5598	SAU1c0034_orf_54p	12287
SIM10000043E07	3315	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000043E08	3316	SAU101344	5426	SAU1c0044_orf_41p	12620
SIM10000043E10	3317	SAU100186	5242	SAU1c0036_orf_19p	12317
SIM10000043E11	3318	SAU102498	5689	SAU1c0045_orf_270p	12688
SIM10000043E11	3318	SAU201381	5813	SAU2c0426_orf_16p	12923
SIM10000043E12	3319	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000043F01	3320	SAU101797	5537	SAU1c0032_orf_17p	12221
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SIM10000043F05	3321	SAU101543	5473	SAU1c0037_orf_130p	12346
SIM10000043F07	3322	SAU102447	5672	SAU1c0045_orf_24p	12685
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000043F09	3324	SAU101801	5541	#N/A	#N/A
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SIM10000043G04	3326	SAU102423	5667	SAU1c0030_orf_23p	12208
SIM10000043G05	3327	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000043G09	3328	SAU102585	5703	SAU1c0044_orf_289p	12611
SIM10000043G09	3328	SAU201773	5834	SAU2c0446_orf_4p	12996
SIM10000043G10	3329	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000043H01	3330	SAU101797	5537	SAU1c0032_orf_17p	12221
SIM10000043H01	3330	SAU101798	5538	SAU1c0032_orf_18p	12222
SIM10000043H03	3331	SAU101803	5543	SAU1c0032_orf_23p	12228
SIM10000043H03	3331	SAU101804	5544	#N/A	#N/A
SIM10000043H04	3332	SAU100128	5231	#N/A	#N/A
SIM10000043H04	3332	SAU101549	5476	SAU1c0043_orf_64p	12549
SIM10000043H04	3332	SAU101576	5488	SAU1c0044_orf_105p	12554
SIM10000043H05	3333	SAU200058	5773	SAU2c0134_orf_1p	12719
SIM10000043H05	3333	SAU200059	5774	SAU2c0134_orf_3p	12720
SIM10000043H06	3334	SAU102417	5663	SAU1c0030_orf_17p	12204
SIM10000043H06	3334	SAU102863	5737	#N/A	#N/A
SIM10000043H09	3335	SAU302950	5914	SAU3c1512_orf_12p	13160
SIM10000043H10	3336	SAU101024	5369	SAU1c0045_orf_90p	12711
SIM10000043H11	3337	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000044A02	3338	SAU101092	5381	SAU1c0028_orf_9p	12192
SIM10000044A06	3339	SAU101777	5527	SAU1c0037_orf_39p	12352
SIM10000044A08	3340	SAU101175	5388	SAU1c0031_orf_1p	12213
SIM10000044A09	3341	SAU102292	5638	SAU1c0038_orf_10p	12368
SIM10000044A11	3342	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000044A12	3343	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000044B01	3344	SAU102268	5630	SAU1c0032_orf_63p	12252
SIM10000044B02	3345	SAU101968	5581	SAU1c0028_orf_43p	12187
SIM10000044B05	3346	SAU100690	5309	#N/A	#N/A
SIM10000044B06	3347	SAU100547	5290	SAU1c0032_orf_3p	12240
SIM10000044B06	3347	SAU102881	5740	SAU1c0032_orf_4p	12242
SIM10000044B08	3348	SAU101752	5522	SAU1c0040_orf_85p	12447
SIM10000044B11	3349	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000044B12	3350	SAU201197	5806	SAU2c0429_orf_2p	12938
SIM10000044C04	3351	SAU101793	5534	SAU1c0032_orf_14p	12218
SIM10000044C06	3352	SAU101614	5494	SAU1c0044_orf_9p	12649
SIM10000044C07	3353	SAU100964	5363	SAU1c0044_orf_86p	12641
SIM10000044C07	3353	SAU100965	5364	SAU1c0044_orf_87p	12642
SIM10000044C08	3354	SAU102909	5743	SAU1c0036_orf_16p	12315
SIM10000044C11	3355	SAU101793	5534	SAU1c0032_orf_14p	12218
SIM10000044C12	3356	SAU102280	5632	SAU1c0038_orf_3p	12378
SIM10000044D01	3357	SAU100546	5289	SAU1c0032_orf_2p	12235

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000044D04	3358	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000044D06	3359	SAU101300	5415	SAU1c0044_orf_113p	12557
S1M10000044D06	3359	SAU101365	5432	SAU1c0044_orf_112p	12556
S1M10000044D08	3360	SAU102270	5631	SAU1c0032_orf_65p	12253
S1M10000044D09	3361	SAU100131	5232	SAU1c0043_orf_156p	12517
S1M10000044D10	3362	SAU201197	5806	SAU2c0429_orf_2p	12938
S1M10000044D11	3363	SAU101571	5483	SAU1c0044_orf_210p	12585
S1M10000044D12	3364	SAU102231	5614	SAU1c0043_orf_18p	12527
S1M10000044D12	3364	SAU102232	5615	SAU1c0043_orf_19p	12530
S1M10000044E01	3365	SAU101371	5435	SAU1c0033_orf_7p	12275
S1M10000044E02	3366	SAU102283	5634	SAU1c0006_orf_1p	12119
S1M10000044E06	3367	SAU201571	5824	SAU2c0447_orf_17p	12997
S1M10000044E07	3368	SAU301829	5902	SAU3c1515_orf_7p	13162
S1M10000044E09	3369	SAU101320	5420	SAU1c0015_orf_16p	12128
S1M10000044E10	3370	SAU100497	5280	SAU1c0018_orf_3p	12140
S1M10000044E11	3371	SAU101270	5410	SAU1c0037_orf_89p	12365
S1M10000044F02	3372	SAU101632	5499	SAU1c0039_orf_3p	12407
S1M10000044F06	3373	SAU101756	5524	SAU1c0040_orf_82p	12445
S1M10000044F08	3374	SAU101262	5406	SAU1c0042_orf_113p	12488
S1M10000044F10	3375	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044F10	3375	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000044G02	3376	SAU102933	5744	SAU1c0039_orf_62p	12412
S1M10000044G05	3377	SAU101242	5404	SAU1c0044_orf_18p	12578
S1M10000044G08	3378	SAU102601	5707	SAU1c0041_orf_46p	12467
S1M10000044G08	3378	SAU102606	5711	SAU1c0041_orf_50p	12471
S1M10000044G10	3379	SAU101092	5381	SAU1c0028_orf_9p	12192
S1M10000044G10	3379	SAU202882	5855	SAU2c0381_orf_3p	12848
S1M10000044G11	3380	SAU101546	5475	SAU1c0037_orf_133p	12349
S1M10000044H06	3381	SAU100964	5363	SAU1c0044_orf_86p	12641
S1M10000044H06	3381	SAU100965	5364	SAU1c0044_orf_87p	12642
S1M10000044H07	3382	SAU100595	5294	SAU1c0043_orf_62p	12547
S1M10000044H08	3383	SAU101543	5473	SAU1c0037_orf_130p	12346
S1M10000044H09	3384	SAU100886	5349	SAU1c0018_orf_16p	12139
S1M10000044H09	3384	SAU100887	5350	SAU1c0018_orf_15p	12138
S1M10000044H10	3385	SAU101573	5485	SAU1c0044_orf_212p	12587
S1M10000044H11	3386	SAU102578	5701	SAU1c0039_orf_61p	12411
S1M10000045A02	3387	SAU100866	5344	SAU1c0044_orf_100p	12553
S1M10000045A06	3388	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000045A07	3389	SAU102378	5653	SAU1c0040_orf_61p	12437
S1M10000045A08	3390	SAU102336	5646	SAU1c0045_orf_146p	12659
S1M10000045A12	3391	SAU201765	5833	SAU2c0309_orf_5p	12770
S1M10000045B01	3392	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000045B02	3393	SAU100546	5289	SAU1c0032_orf_2p	12235

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
SIM10000045B03	3394	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000045B07	3395	SAU101803	5543	SAU1c0032_orf_23p	12228
SIM10000045B10	3396	SAU200468	5781	SAU2c0429_orf_19p	12937
SIM10000045B11	3397	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000045B12	3398	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000045C02	3399	SAU100690	5309	#N/A	#N/A
SIM10000045C03	3400	SAU100887	5350	SAU1c0018_orf_15p	12138
SIM10000045C04	3401	SAU102286	5636	SAU1c0038_orf_6p	12393
SIM10000045C04	3401	SAU102287	5637	SAU1c0038_orf_7p	12398
SIM10000045C05	3402	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000045C07	3403	SAU101573	5485	SAU1c0044_orf_212p	12587
SIM10000045C09	3404	SAU101744	5520	SAU1c0037_orf_94p	12367
SIM10000045C09	3404	SAU300191	5868	SAU3c0672_orf_1p	13037
SIM10000045D01	3405	SAU101893	5572	SAU1c0034_orf_32p	12282
SIM10000045D03	3406	SAU101599	5491	SAU1c0041_orf_5p	12478
SIM10000045D07	3407	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000045D08	3408	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000045D09	3409	SAU101572	5484	SAU1c0044_orf_211p	12586
SIM10000045D10	3410	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000045D11	3411	SAU101492	5465	SAU1c0025_orf_21p	12166
SIM10000045D11	3411	SAU101493	5466	SAU1c0025_orf_22p	12167
SIM10000045D12	3412	SAU101800	5540	SAU1c0032_orf_20p	12225
SIM10000045D12	3412	SAU101801	5541	#N/A	#N/A
SIM10000045E04	3413	SAU102132	5605	SAU1c0027_orf_19p	12177
SIM10000045E05	3414	SAU101491	5464	SAU1c0025_orf_20p	12165
SIM10000045E08	3415	SAU201752	5832	SAU2c0436_orf_19p	12963
SIM10000045E09	3416	SAU101794	5535	#N/A	#N/A
SIM10000045E10	3417	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000045E11	3418	SAU100970	5365	SAU1c0043_orf_197p	12529
SIM10000045E12	3419	SAU100547	5290	SAU1c0032_orf_3p	12240
SIM10000045F04	3420	SAU102241	5617	SAU1c0043_orf_25p	12539
SIM10000045F05	3421	SAU100114	5228	SAU1c0043_orf_225p	12535
SIM10000045F08	3422	SAU200657	5789	#N/A	#N/A
SIM10000045F11	3423	SAU102117	5603	SAU1c0027_orf_6p	12181
SIM10000045F12	3424	SAU101806	5546	SAU1c0032_orf_25p	12230
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SIM10000045G06	3426	SAU101400	5444	SAU1c0036_orf_35p	12326
SIM10000045G07	3427	SAU101561	5479	SAU1c0022_orf_4p	12149
SIM10000045G08	3428	SAU100690	5309	#N/A	#N/A
SIM10000045G10	3429	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000045G12	3430	SAU101400	5444	SAU1c0036_orf_35p	12326
SIM10000045H06	3431	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000045H10	3432	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000045H11	3433	SAU100414	5270	SAU1c0022_orf_24p	12148

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000046A04	3435	SAU100062	5225	SAU1c0035_orf_98p	12309
SIM10000046A04	3435	SAU100231	5245	#N/A	#N/A
SIM10000046A06	3436	SAU101383	5438	SAU1c0022_orf_20p	12147
SIM10000046A08	3437	SAU200994	5802	SAU2c0428_orf_4p	12935
SIM10000046A09	3438	SAU100315	5260	SAU1c0037_orf_62p	12358
SIM10000046A11	3439	SAU100432	5271	SAU1c0040_orf_88p	12450
SIM10000046A11	3439	SAU100433	5272	SAU1c0040_orf_87p	12449
SIM10000046A12	3440	SAU101814	5551	SAU1c0032_orf_32p	12237
SIM10000046B01	3441	SAU102334	5645	SAU1c0045_orf_144p	12658
SIM10000046B03	3442	SAU101039	5373	SAU1c0043_orf_181p	12522
SIM10000046B04	3443	SAU101797	5537	SAU1c0032_orf_17p	12221
SIM10000046B05	3444	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000046B07	3445	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000046B08	3446	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000046B09	3447	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000046B11	3448	SAU102541	5697	SAU1c0045_orf_195p	12668
SIM10000046B12	3449	SAU101400	5444	SAU1c0036_orf_35p	12326
SIM10000046C02	3450	SAU200601	5787	#N/A	#N/A
SIM10000046C04	3451	SAU100118	5229	SAU1c0015_orf_13p	12125
SIM10000046C05	3452	SAU101159	5387	SAU1c0036_orf_46p	12331
SIM10000046C06	3453	SAU102585	5703	SAU1c0044_orf_289p	12611
SIM10000046C06	3453	SAU201773	5834	SAU2c0446_orf_4p	12996
SIM10000046C07	3454	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000046C08	3455	SAU100414	5270	SAU1c0022_orf_24p	12148
SIM10000046C11	3456	SAU102144	5608	SAU1c0041_orf_15p	12459
SIM10000046C12	3457	SAU100313	5259	SAU1c0045_orf_153p	12661
SIM10000046C12	3457	SAU100359	5264	SAU1c0032_orf_35p	12239
SIM10000046D01	3458	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000046D02	3459	SAU102144	5608	SAU1c0041_orf_15p	12459
SIM10000046D03	3460	SAU101857	5560	SAU1c0044_orf_156p	12569
SIM10000046D04	3461	SAU102433	5668	SAU1c0045_orf_37p	12701
SIM10000046D05	3462	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000046D08	3463	SAU101495	5467	SAU1c0037_orf_65p	12360
SIM10000046D09	3464	SAU100679	5305	SAU1c0018_orf_14p	12137
SIM10000046D10	3465	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000046D11	3466	SAU100496	5279	SAU1c0041_orf_83p	12484
SIM10000046D11	3466	SAU301004	5882	SAU3c1255_orf_1p	13079
SIM10000046D12	3467	SAU100496	5279	SAU1c0041_orf_83p	12484
SIM10000046D12	3467	SAU301004	5882	SAU3c1255_orf_1p	13079
SIM10000046E01	3468	SAU101610	5492	SAU1c0044_orf_5p	12629
SIM10000046E02	3469	SAU101857	5560	SAU1c0044_orf_156p	12569
SIM10000046E04	3470	SAU101800	5540	SAU1c0032_orf_20p	12225
SIM10000046E04	3470	SAU101801	5541	#N/A	#N/A

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000046E08	3472	SAU102283	5634	SAU1c0006_orf_1p	12119
SIM10000046E10	3473	SAU102283	5634	SAU1c0006_orf_1p	12119
SIM10000046F01	3474	SAU101028	5370	SAU1c0043_orf_7p	12552
SIM10000046F02	3475	SAU100546	5289	SAU1c0032_orf_2p	12235
SIM10000046F02	3475	SAU102880	5739	SAU1c0032_orf_1p	12224
SIM10000046F05	3476	SAU102671	5729	SAU1c0024_orf_9p	12161
SIM10000046F06	3477	SAU100702	5310	SAU1c0029_orf_34p	12196
SIM10000046F06	3477	SAU300825	5878	SAU3c1171_orf_1p	13068
SIM10000046F08	3478	SAU102297	5640	SAU1c0045_orf_41p	12704
SIM10000046F09	3479	SAU100517	5282	#N/A	#N/A
SIM10000046F10	3480	SAU102059	5597	SAU1c0034_orf_51p	12286
SIM10000046F12	3481	SAU101365	5432	SAU1c0044_orf_112p	12556
SIM10000046G01	3482	SAU200752	5795	SAU2c0354_orf_5p	12809
SIM10000046G01	3482	SAU300975	5880	SAU3c1240_orf_3p	13075
SIM10000046G02	3483	SAU101571	5483	SAU1c0044_orf_210p	12585
SIM10000046G03	3484	SAU100773	5326	SAU1c0038_orf_39p	12377
SIM10000046G04	3485	SAU100436	5273	SAU1c0023_orf_20p	12154
SIM10000046G07	3486	SAU101866	5564	SAU1c0036_orf_21p	12319
SIM10000046G09	3487	SAU102663	5727	SAU1c0024_orf_2p	12158
SIM10000046G10	3488	SAU101756	5524	SAU1c0040_orf_82p	12445
SIM10000046H01	3489	SAU101445	5452	SAU1c0038_orf_47p	12382
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SIM10000046H10	3490	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000047A03	3491	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000047A04	3492	SAU300572	5873	SAU3c1019_orf_1p	13051
SIM10000047A05	3493	SAU101805	5545	SAU1c0032_orf_24p	12229
SIM10000047A06	3494	SAU201775	5835	SAU2c0446_orf_4p	12996
SIM10000047A06	3494	SAU301030	5883	SAU3c1268_orf_1p	13080
SIM10000047A07	3495	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000047A08	3496	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000047A09	3497	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000047A10	3498	SAU100751	5321	SAU1c0036_orf_59p	12335
SIM10000047A11	3499	SAU100131	5232	SAU1c0043_orf_156p	12517
SIM10000047A12	3500	SAU100300	5253	SAU1c0040_orf_90p	12451
SIM10000047B02	3501	SAU101791	5532	SAU1c0032_orf_12p	12216
SIM10000047B04	3502	SAU101366	5433	SAU1c0033_orf_2p	12266
SIM10000047B05	3503	SAU101545	5474	SAU1c0037_orf_132p	12348
SIM10000047B06	3504	SAU200006	5770	SAU2c0157_orf_1p	12723
SIM10000047B08	3505	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000047B09	3506	SAU100131	5232	SAU1c0043_orf_156p	12517
SIM10000047B10	3507	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000047B12	3508	SAU101868	5565	SAU1c0036_orf_23p	12320
SIM10000047C01	3509	SAU100275	5252	SAU1c0036_orf_15p	12314

Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000047C03	3511	SAU200006	5770	SAU2c0157_orf_1p	12723
SIM10000047C04	3512	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000047C06	3513	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000047C08	3514	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000047C09	3515	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000047C11	3516	SAU201775	5835	SAU2c0446_orf_4p	12996
SIM10000047C11	3516	SAU301030	5883	SAU3c1268_orf_1p	13080
SIM10000047C12	3517	SAU101868	5565	SAU1c0036_orf_23p	12320
SIM10000047D02	3518	SAU101387	5440	SAU1c0038_orf_52p	12386
SIM10000047D03	3519	SAU101868	5565	SAU1c0036_orf_23p	12320
SIM10000047D04	3520	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000047D05	3521	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000047D09	3522	SAU100921	5355	SAU1c0038_orf_76p	12396
SIM10000047D10	3523	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000047D11	3524	SAU103038	5757	#N/A	#N/A
SIM10000047D12	3525	SAU101175	5388	SAU1c0031_orf_1p	12213
SIM10000047E01	3526	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000047E02	3527	SAU100131	5232	SAU1c0043_orf_156p	12517
SIM10000047E03	3528	SAU102452	5676	SAU1c0045_orf_20p	12674
SIM10000047E04	3529	SAU101996	5584	SAU1c0040_orf_99p	12456
SIM10000047E05	3530	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000047E06	3531	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000047E08	3532	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000047E09	3533	SAU100810	5333	SAU1c0037_orf_11p	12343
SIM10000047E10	3534	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000047E11	3535	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000047E12	3536	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000047F02	3537	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000047F03	3538	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000047F04	3539	SAU300572	5873	SAU3c1019_orf_1p	13051
SIM10000047F05	3540	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000047F06	3541	SAU200928	5798	SAU2c0365_orf_5p	12815
SIM10000047F07	3542	SAU102602	5708	SAU1c0032_orf_5p	12249
SIM10000047F08	3543	SAU101242	5404	SAU1c0044_orf_18p	12578
SIM10000047F09	3544	SAU100157	5237	SAU1c0040_orf_81p	12444
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SIM10000047F11	3546	SAU101805	5545	SAU1c0032_orf_24p	12229
SIM10000047F12	3547	SAU101808	5548	SAU1c0032_orf_27p	12232
SIM10000047G01	3548	SAU101369	5434	SAU1c0033_orf_5p	12274
SIM10000047G02	3549	SAU100141	5236	SAU1c0032_orf_8p	12259
SIM10000047G04	3550	SAU101341	5424	SAU1c0044_orf_38p	12618
SIM10000047G05	3551	SAU100684	5306	SAU1c0044_orf_68p	12632
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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SIM10000047G07	3553	SAU101798	5538	SAU1c0032_orf_18p	12222
SIM10000047G08	3554	SAU101028	5370	SAU1c0043_orf_7p	12552
SIM10000047G09	3555	SAU100810	5333	SAU1c0037_orf_11p	12343
SIM10000047G10	3556	SAU102607	5712	SAU1c0041_orf_51p	12472
SIM10000047H03	3557	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000047H04	3558	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000047H05	3559	SAU102452	5676	SAU1c0045_orf_20p	12674
SIM10000047H06	3560	SAU103038	5757	#N/A	#N/A
SIM10000047H07	3561	SAU200006	5770	SAU2c0157_orf_1p	12723
SIM10000047H08	3562	SAU101798	5538	SAU1c0032_orf_18p	12222
SIM10000047H09	3563	SAU102578	5701	SAU1c0039_orf_61p	12411
SIM10000047H11	3564	SAU101028	5370	SAU1c0043_orf_7p	12552
SIM10000048A02	3565	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000048A03	3566	SAU100866	5344	SAU1c0044_orf_100p	12553
SIM10000048A04	3567	SAU103038	5757	#N/A	#N/A
SIM10000048A05	3568	SAU101868	5565	SAU1c0036_orf_23p	12320
SIM10000048A06	3569	SAU100157	5237	SAU1c0040_orf_81p	12444
SIM10000048A07	3570	SAU101156	5386	SAU1c0036_orf_12p	12311
SIM10000048A09	3571	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000048A10	3572	SAU201571	5824	SAU2c0447_orf_17p	12997
SIM10000048A11	3573	SAU101807	5547	SAU1c0032_orf_26p	12231
SIM10000048A12	3574	SAU101271	5411	SAU1c0037_orf_90p	12366
SIM10000048B02	3575	SAU100608	5297	SAU1c0034_orf_69p	12293
SIM10000048B05	3576	SAU101028	5370	SAU1c0043_orf_7p	12552
SIM10000048B08	3577	SAU102452	5676	SAU1c0045_orf_20p	12674
SIM10000048B10	3578	SAU100158	5238	SAU1c0040_orf_80p	12443
SIM10000048B11	3579	SAU103038	5757	#N/A	#N/A
SIM10000048B12	3580	SAU200916	5797	SAU2c0373_orf_4p	12838
SIM10000048B12	3580	SAU301620	5899	SAU3c1478_orf_2p	13140
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SIM10000048C03	3583	SAU102200	5611	SAU1c0045_orf_168p	12665
SIM10000048C05	3584	SAU300998	5881	SAU3c1253_orf_3p	13077
SIM10000048C06	3585	SAU100684	5306	SAU1c0044_orf_68p	12632
SIM10000048C06	3585	SAU100685	5307	SAU1c0044_orf_69p	12633
SIM10000048C07	3586	SAU102452	5676	SAU1c0045_orf_20p	12674
SIM10000048C08	3587	SAU101632	5499	SAU1c0039_orf_3p	12407
SIM10000048C09	3588	SAU101907	5574	SAU1c0040_orf_79p	12442
SIM10000048C11	3589	SAU101815	5552	SAU1c0032_orf_33p	12238
SIM10000048D02	3590	SAU100123	5230	SAU1c0043_orf_189p	12526
SIM10000048D02	3590	SAU102001	5586	SAU1c0040_orf_102p	12424
SIM10000048D02	3590	SAU103159	5762	SAU1c0045_orf_204p	12670
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S1M10000048D09	3592	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000048D10	3593	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048D12	3594	SAU102599	5706	SAU1c0041_orf_45p	12466
S1M10000048D12	3594	SAU103191	5765	SAU1c0041_orf_44p	12465
S1M10000048E02	3595	SAU101028	5370	SAU1c0043_orf_7p	12552
S1M10000048E03	3596	SAU102200	5611	SAU1c0045_orf_168p	12665
S1M10000048E04	3597	SAU101545	5474	SAU1c0037_orf_132p	12348
S1M10000048E06	3598	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000048E07	3599	SAU100959	5359	SAU1c0042_orf_102p	12485
S1M10000048E08	3600	SAU101807	5547	SAU1c0032_orf_26p	12231
S1M10000048E10	3601	SAU302950	5914	SAU3c1512_orf_12p	13160
S1M10000048F02	3602	SAU101387	5440	SAU1c0038_orf_52p	12386
S1M10000048F07	3603	SAU101175	5388	SAU1c0031_orf_1p	12213
S1M10000048F08	3604	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048F09	3605	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000048F11	3606	SAU202174	5845	SAU2c0412_orf_3p	12895
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S1M10000048F12	3607	SAU103038	5757	#N/A	#N/A
S1M10000048G02	3608	SAU102453	5677	SAU1c0045_orf_19p	12669
S1M10000048G03	3609	SAU200928	5798	SAU2c0365_orf_5p	12815
S1M10000048G04	3610	SAU102602	5708	SAU1c0032_orf_5p	12249
S1M10000048G05	3611	SAU101752	5522	SAU1c0040_orf_85p	12447
S1M10000048G07	3612	SAU102006	5589	SAU1c0040_orf_107p	12427
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S1M10000048G10	3613	SAU101793	5534	SAU1c0032_orf_14p	12218
S1M10000048G11	3614	SAU200006	5770	SAU2c0157_orf_1p	12723
S1M10000048H01	3615	SAU100608	5297	SAU1c0034_orf_69p	12293
S1M10000048H02	3616	SAU100158	5238	SAU1c0040_orf_80p	12443
S1M10000048H03	3617	SAU101815	5552	SAU1c0032_orf_33p	12238
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S1M10000048H08	3621	SAU100141	5236	SAU1c0032_orf_8p	12259
S1M10000048H09	3622	SAU100157	5237	SAU1c0040_orf_81p	12444
S1M10000048H10	3623	SAU101791	5532	SAU1c0032_orf_12p	12216
S1M10000048H11	3624	SAU101271	5411	SAU1c0037_orf_90p	12366
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K1M10000002F02	1054	ECO100252	10052	#N/A	#N/A
K1M10000007F01	1057	ECO100397	10064	#N/A	#N/A
K1M10000007F01	1057	ECO100398	10065	#N/A	#N/A
K1M10000004F06	1056	ECO100990	10120	#N/A	#N/A
K1M10000019D06	1064	ECO100990	10120	#N/A	#N/A
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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K1M10000036G08	1076	ECO102447	10247	#N/A	#N/A
K1M10000033E01	1075	ECO102539	10258	#N/A	#N/A
K1M10000043D05	1081	ECO102620	10266	#N/A	#N/A
K1M10000045D10	1088	ECO102620	10266	#N/A	#N/A
K1M10000003C01	1055	ECO103101	10315	#N/A	#N/A
K1M10000030E07	1071	ECO104120	10462	#N/A	#N/A
K1M10000045A07	1087	ECO104268	10475	#N/A	#N/A
S4M10000020F05	3721	ECO100449	#N/A	#N/A	#N/A
S4M10000026D04	3742	ECO100676	#N/A	#N/A	#N/A
S4M10000014D07	3706	ECO100757	#N/A	#N/A	#N/A
S4M10000015B11	3708	ECO100757	#N/A	#N/A	#N/A
S4M10000016A02	3710	ECO100757	#N/A	#N/A	#N/A
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S4M10000020G10	3722	ECO100796	10105	#N/A	#N/A
S4M10000023F01	3728	ECO101916	#N/A	#N/A	#N/A
S4M10000014H02	3707	ECO102028	#N/A	#N/A	#N/A
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S4M10000037H09	3772	ECO102296	#N/A	#N/A	#N/A
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S4M10000006F08	3690	ECO102541	10259	#N/A	#N/A
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S4M10000034H05	3759	ECO102900	#N/A	#N/A	#N/A
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Clone name	Clone SeqID	PathoSeq Locus	Gene SeqID (protein)	Genemarked gene	full length ORF Protein Seq ID
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S4M10000022D12	3724	ECO103238	10354	#N/A	#N/A
S4M10000033F08	3753	ECO103238	10354	#N/A	#N/A
S4M10000033G09	3755	ECO103238	10354	#N/A	#N/A
S4M10000001C01	3680	ECO103265	10365	#N/A	#N/A
S4M10000024B02	3729	ECO103280	#N/A	#N/A	#N/A
S4M10000020A04	3720	ECO103461	#N/A	#N/A	#N/A
S4M10000002B06	3681	ECO103666	#N/A	#N/A	#N/A
S4M10000019H06	3719	ECO103738	#N/A	#N/A	#N/A
S4M10000024H02	3736	ECO103738	#N/A	#N/A	#N/A
S4M10000030F07	3750	ECO103738	#N/A	#N/A	#N/A
S4M10000034H09	3760	ECO103738	#N/A	#N/A	#N/A
S4M10000032B12	3752	ECO103935	#N/A	#N/A	#N/A
S4M10000002B09	3682	ECO103936	#N/A	#N/A	#N/A
S4M10000037A10	3770	ECO103951	#N/A	#N/A	#N/A
S4M10000018D09	3711	ECO104080	#N/A	#N/A	#N/A
S4M10000035F09	3766	EFA101301	#N/A	EFA1c0040_orf_173p	#N/A
S4M10000035F09	3766	EFA102170	#N/A	EFA1c0040_orf_121p	#N/A
S4M10000001C01	3680	EFA103268	#N/A	EFA1c0010_orf_1p	10479
S4M10000036F07	3768	HPY200334	#N/A	#N/A	#N/A
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S4M10000037A10	3770	KPN100467	#N/A	KPN1c0583_orf_2p	#N/A
S4M10000030G11	3751	KPN101078	#N/A	KPN1c1190_orf_1p	#N/A
S4M10000024B02	3729	KPN101160	#N/A	KPN1c1224_orf_1p	#N/A
S4M10000032B12	3752	KPN101846	#N/A	KPN1c1681_orf_2p	#N/A
S4M10000006C05	3689	KPN102011	#N/A	KPN1c1862_orf_4p	#N/A
S4M10000035B01	3761	KPN102014	#N/A	KPN1c1786_orf_1p	11654
S4M10000012B06	3700	KPN102524	#N/A	#N/A	#N/A
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S4M10000002G04	3683	KPN102558	#N/A	KPN1c1982_orf_3p	#N/A
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S4M10000029B12	3747	KPN103641	#N/A	KPN1c2761_orf_2p	11705
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S4M10000013H02	3703	STY000753	#N/A	STYc00054_orf_91p	#N/A
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S4M10000036D07	3767	STY000817	#N/A	STYc00054_orf_145p	#N/A
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S4M10000035F09	3766	STY001185	#N/A	STYc00098_orf_2p	#N/A
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S4M10000025A11	3737	STY001582	#N/A	#N/A	#N/A
S4M10000035F09	3766	STY001619	#N/A	#N/A	#N/A
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S4M10000012D02	3702	STY003377	#N/A	#N/A	#N/A
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S4M10000008H10	3693	STY004152	#N/A	STYc00207_orf_194p	14003
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K1M10000036G08	1076	STY001867	#N/A	STYc00180_orf_50p	13948
K1M10000030C07	1070	STY002768	#N/A	#N/A	#N/A
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TABLE VI C

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KPN100432		3977	5032
KPN100854		3978	5033
KPN101022		3979	5034
KPN101026		3980	5035
KPN101729		3981	5036
KPN101750		3982	5037
KPN102057		3983	5038
KPN102638		3984	5039
KPN103882		3985	5040
KPN104183		3986	5041
KPN104281		3987	5042
KPN104430		3988	5043
KPN104538		3989	5044
KPN104716		3990	5045
KPN105722		3991	5046
KPN105779		3992	5047
KPN106044		3993	5048
KPN106659		3994	5049
KPN106840		3995	5050
KPN107626		3996	5051
KPN107776		3997	5052
PA0028		3998	5053
PA0120		3999	5054
PA0129		4000	5055
PA0141		4001	5056
PA0221		4002	5057
PA0265		4003	5058
PA0321		4004	5059
PA0337		4005	5060
PA0353		4006	5061
PA0378		4007	5062
PA0401		4008	5063
PA0413		4009	5064

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
PA0414		4010	5065
PA0419		4011	5066
PA0423		4012	5067
PA0469		4013	5068
PA0472		4014	5069
PA0506		4015	5070
PA0600		4016	5071
PA0642		4017	5072
PA0650		4018	5073
PA0715		4019	5074
PA0788		4020	5075
PA0882		4021	5076
PA0934		4022	5077
PA0938		4023	5078
PA1019		4024	5079
PA1072		4025	5080
PA1115		4026	5081
PA1270		4027	5082
PA1301		4028	5083
PA1360		4029	5084
PA1365		4030	5085
PA1398		4031	5086
PA1462		4032	5087
PA1493		4033	5088
PA1547		4034	5089
PA1636		4035	5090
PA1684		4036	5091
PA1868		4037	5092
PA1876		4038	5093
PA1918		4039	5094
PA1986		4040	5095
PA2009		4041	5096
PA2083		4042	5097
PA2101		4043	5098
PA2108		4044	5099
PA2128		4045	5100
PA2147		4046	5101
PA2196		4047	5102
PA2197		4048	5103
PA2222		4049	5104
PA2313		4050	5105

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
PA2398		4051	5106
PA2424		4052	5107
PA2461		4053	5108
PA2470		4054	5109
PA2488		4055	5110
PA2494		4056	5111
PA2584		4057	5112
PA2594		4058	5113
PA2634		4059	5114
PA2641		4060	5115
PA2671		4061	5116
PA2680		4062	5117
PA2684		4063	5118
PA2726		4064	5119
PA2742		4065	5120
PA3006		4066	5121
PA3011		4067	5122
PA3013		4068	5123
PA3041		4069	5124
PA3048		4070	5125
PA3068		4071	5126
PA3121		4072	5127
PA3153		4073	5128
PA3154		4074	5129
PA3160		4075	5130
PA3279		4076	5131
PA3280		4077	5132
PA3374		4078	5133
PA3479		4079	5134
PA3484		4080	5135
PA3522		4081	5136
PA3643		4082	5137
PA3703		4083	5138
PA3709		4084	5139
PA3716		4085	5140
PA3764		4086	5141
PA3845		4087	5142
PA3866		4088	5143
PA3876		4089	5144
PA3877		4090	5145
PA3931		4091	5146

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
PA3984		4092	5147
PA4024		4093	5148
PA4027		4094	5149
PA4037		4095	5150
PA4067		4096	5151
PA4070		4097	5152
PA4081		4098	5153
PA4105		4099	5154
PA4124		4100	5155
PA4125		4101	5156
PA4158		4102	5157
PA4237		4103	5158
PA4242		4104	5159
PA4244		4105	5160
PA4245		4106	5161
PA4246		4107	5162
PA4247		4108	5163
PA4248		4109	5164
PA4249		4110	5165
PA4250		4111	5166
PA4251		4112	5167
PA4252		4113	5168
PA4253		4114	5169
PA4254		4115	5170
PA4256		4116	5171
PA4257		4117	5172
PA4258		4118	5173
PA4259		4119	5174
PA4262		4120	5175
PA4263		4121	5176
PA4264		4122	5177
PA4268		4123	5178
PA4269		4124	5179
PA4271		4125	5180
PA4272		4126	5181
PA4316		4127	5182
PA4332		4128	5183
PA4347		4129	5184
PA4363		4130	5185
PA4375		4131	5186
PA4413		4132	5187

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
PA4433		4133	5188
PA4473		4134	5189
PA4506		4135	5190
PA4512		4136	5191
PA4542		4137	5192
PA4576		4138	5193
PA4598		4139	5194
PA4665		4140	5195
PA4681		4141	5196
PA4709		4142	5197
PA4744		4143	5198
PA4771		4144	5199
PA4888		4145	5200
PA4942		4146	5201
PA4997		4147	5202
PA5030		4148	5203
PA5076		4149	5204
PA5088		4150	5205
PA5193		4151	5206
PA5199		4152	5207
PA5207		4153	5208
PA5209		4154	5209
PA5248		4155	5210
PA5299		4156	5211
PA5316		4157	5212
PA5388		4158	5213
PA5393		4159	5214
PA5436		4160	5215
PA5443		4161	5216
PA5490		4162	5217
PA5493		4163	5218
PA5507		4164	5219
PA5567		4165	5220
SAU100040		4166	5221
SAU100053		4167	5222
SAU100056		4168	5223
SAU100059		4169	5224
SAU100062		4170	5225
SAU100077		4171	5226
SAU100112		4172	5227
SAU100114		4173	5228

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU100118		4174	5229
SAU100123		4175	5230
SAU100128		4176	5231
SAU100131		4177	5232
SAU100133		4178	5233
SAU100139		4179	5234
SAU100140		4180	5235
SAU100141		4181	5236
SAU100157		4182	5237
SAU100158		4183	5238
SAU100162		4184	5239
SAU100175		4185	5240
SAU100182		4186	5241
SAU100186		4187	5242
SAU100198		4188	5243
SAU100227		4189	5244
SAU100231		4190	5245
SAU100242		4191	5246
SAU100246		4192	5247
SAU100251		4193	5248
SAU100265		4194	5249
SAU100266		4195	5250
SAU100272		4196	5251
SAU100275		4197	5252
SAU100300		4198	5253
SAU100301		4199	5254
SAU100302		4200	5255
SAU100305		4201	5256
SAU100307		4202	5257
SAU100308		4203	5258
SAU100313		4204	5259
SAU100315		4205	5260
SAU100323		4206	5261
SAU100347		4207	5262
SAU100355		4208	5263
SAU100359		4209	5264
SAU100381		4210	5265
SAU100389		4211	5266
SAU100390		4212	5267
SAU100401		4213	5268
SAU100412		4214	5269

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU100414		4215	5270
SAU100432		4216	5271
SAU100433		4217	5272
SAU100436		4218	5273
SAU100443		4219	5274
SAU100444		4220	5275
SAU100475		4221	5276
SAU100478		4222	5277
SAU100489		4223	5278
SAU100496		4224	5279
SAU100497		4225	5280
SAU100514		4226	5281
SAU100517		4227	5282
SAU100521		4228	5283
SAU100522		4229	5284
SAU100527		4230	5285
SAU100528		4231	5286
SAU100532		4232	5287
SAU100542		4233	5288
SAU100546		4234	5289
SAU100547		4235	5290
SAU100557		4236	5291
SAU100582		4237	5292
SAU100590		4238	5293
SAU100595		4239	5294
SAU100596		4240	5295
SAU100601		4241	5296
SAU100608		4242	5297
SAU100610		4243	5298
SAU100613		4244	5299
SAU100617		4245	5300
SAU100633		4246	5301
SAU100646		4247	5302
SAU100658		4248	5303
SAU100659		4249	5304
SAU100679		4250	5305
SAU100684		4251	5306
SAU100685		4252	5307
SAU100689		4253	5308
SAU100690		4254	5309
SAU100702		4255	5310

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU100714		4257	5312
SAU100731		4258	5313
SAU100733		4259	5314
SAU100734		4260	5315
SAU100736		4261	5316
SAU100738		4262	5317
SAU100741		4263	5318
SAU100745		4264	5319
SAU100747		4265	5320
SAU100751		4266	5321
SAU100752		4267	5322
SAU100767		4268	5323
SAU100770		4269	5324
SAU100771		4270	5325
SAU100773		4271	5326
SAU100776		4272	5327
SAU100778		4273	5328
SAU100793		4274	5329
SAU100794		4275	5330
SAU100799		4276	5331
SAU100808		4277	5332
SAU100810		4278	5333
SAU100813		4279	5334
SAU100831		4280	5335
SAU100836		4281	5336
SAU100838		4282	5337
SAU100839		4283	5338
SAU100843		4284	5339
SAU100845		4285	5340
SAU100858		4286	5341
SAU100859		4287	5342
SAU100865		4288	5343
SAU100866		4289	5344
SAU100879		4290	5345
SAU100880		4291	5346
SAU100882		4292	5347
SAU100885		4293	5348
SAU100886		4294	5349
SAU100887		4295	5350
SAU100899		4296	5351

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU100916		4298	5353
SAU100920		4299	5354
SAU100921		4300	5355
SAU100932		4301	5356
SAU100944		4302	5357
SAU100952		4303	5358
SAU100959		4304	5359
SAU100961		4305	5360
SAU100962		4306	5361
SAU100963		4307	5362
SAU100964		4308	5363
SAU100965		4309	5364
SAU100970		4310	5365
SAU100996		4311	5366
SAU101006		4312	5367
SAU101020		4313	5368
SAU101024		4314	5369
SAU101028		4315	5370
SAU101034		4316	5371
SAU101038		4317	5372
SAU101039		4318	5373
SAU101065		4319	5374
SAU101067		4320	5375
SAU101070		4321	5376
SAU101084		4322	5377
SAU101085		4323	5378
SAU101086		4324	5379
SAU101090		4325	5380
SAU101092		4326	5381
SAU101104		4327	5382
SAU101143		4328	5383
SAU101145		4329	5384
SAU101155		4330	5385
SAU101156		4331	5386
SAU101159		4332	5387
SAU101175		4333	5388
SAU101180		4334	5389
SAU101183		4335	5390
SAU101184		4336	5391
SAU101189		4337	5392

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU101197		4338	5393
SAU101198		4339	5394
SAU101199		4340	5395
SAU101220		4341	5396
SAU101224		4342	5397
SAU101226		4343	5398
SAU101231		4344	5399
SAU101235		4345	5400
SAU101236		4346	5401
SAU101239		4347	5402
SAU101240		4348	5403
SAU101242		4349	5404
SAU101247		4350	5405
SAU101262		4351	5406
SAU101265		4352	5407
SAU101266		4353	5408
SAU101267		4354	5409
SAU101270		4355	5410
SAU101271		4356	5411
SAU101275		4357	5412
SAU101286		4358	5413
SAU101293		4359	5414
SAU101300		4360	5415
SAU101301		4361	5416
SAU101302		4362	5417
SAU101310		4363	5418
SAU101311		4364	5419
SAU101320		4365	5420
SAU101327		4366	5421
SAU101339		4367	5422
SAU101340		4368	5423
SAU101341		4369	5424
SAU101343		4370	5425
SAU101344		4371	5426
SAU101346		4372	5427
SAU101347		4373	5428
SAU101350		4374	5429
SAU101351		4375	5430
SAU101360		4376	5431
SAU101365		4377	5432
SAU101366		4378	5433

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU101369		4379	5434
SAU101371		4380	5435
SAU101381		4381	5436
SAU101382		4382	5437
SAU101383		4383	5438
SAU101385		4384	5439
SAU101387		4385	5440
SAU101389		4386	5441
SAU101398		4387	5442
SAU101399		4388	5443
SAU101400		4389	5444
SAU101408		4390	5445
SAU101421		4391	5446
SAU101427		4392	5447
SAU101432		4393	5448
SAU101436		4394	5449
SAU101438		4395	5450
SAU101444		4396	5451
SAU101445		4397	5452
SAU101446		4398	5453
SAU101447		4399	5454
SAU101452		4400	5455
SAU101455		4401	5456
SAU101461		4402	5457
SAU101463		4403	5458
SAU101476		4404	5459
SAU101481		4405	5460
SAU101482		4406	5461
SAU101483		4407	5462
SAU101488		4408	5463
SAU101491		4409	5464
SAU101492		4410	5465
SAU101493		4411	5466
SAU101495		4412	5467
SAU101497		4413	5468
SAU101509		4414	5469
SAU101526		4415	5470
SAU101529		4416	5471
SAU101541		4417	5472
SAU101543		4418	5473
SAU101545		4419	5474

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU101546		4420	5475
SAU101549		4421	5476
SAU101551		4422	5477
SAU101554		4423	5478
SAU101561		4424	5479
SAU101565		4425	5480
SAU101567		4426	5481
SAU101570		4427	5482
SAU101571		4428	5483
SAU101572		4429	5484
SAU101573		4430	5485
SAU101574		4431	5486
SAU101575		4432	5487
SAU101576		4433	5488
SAU101586		4434	5489
SAU101592		4435	5490
SAU101599		4436	5491
SAU101610		4437	5492
SAU101612		4438	5493
SAU101614		4439	5494
SAU101616		4440	5495
SAU101622		4441	5496
SAU101624		4442	5497
SAU101630		4443	5498
SAU101632		4444	5499
SAU101637		4445	5500
SAU101641		4446	5501
SAU101651		4447	5502
SAU101652		4448	5503
SAU101653		4449	5504
SAU101655		4450	5505
SAU101663		4451	5506
SAU101664		4452	5507
SAU101674		4453	5508
SAU101679		4454	5509
SAU101681		4455	5510
SAU101682		4456	5511
SAU101685		4457	5512
SAU101717		4458	5513
SAU101724		4459	5514
SAU101726		4460	5515

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU101727		4461	5516
SAU101728		4462	5517
SAU101736		4463	5518
SAU101737		4464	5519
SAU101744		4465	5520
SAU101751		4466	5521
SAU101752		4467	5522
SAU101754		4468	5523
SAU101756		4469	5524
SAU101771		4470	5525
SAU101772		4471	5526
SAU101777		4472	5527
SAU101781		4473	5528
SAU101782		4474	5529
SAU101784		4475	5530
SAU101790		4476	5531
SAU101791		4477	5532
SAU101792		4478	5533
SAU101793		4479	5534
SAU101794		4480	5535
SAU101795		4481	5536
SAU101797		4482	5537
SAU101798		4483	5538
SAU101799		4484	5539
SAU101800		4485	5540
SAU101801		4486	5541
SAU101802		4487	5542
SAU101803		4488	5543
SAU101804		4489	5544
SAU101805		4490	5545
SAU101806		4491	5546
SAU101807		4492	5547
SAU101808		4493	5548
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SAU101811		4495	5550
SAU101814		4496	5551
SAU101815		4497	5552
SAU101818		4498	5553
SAU101824		4499	5554
SAU101833		4500	5555
SAU101839		4501	5556

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU101842		4502	5557
SAU101845		4503	5558
SAU101849		4504	5559
SAU101857		4505	5560
SAU101862		4506	5561
SAU101864		4507	5562
SAU101865		4508	5563
SAU101866		4509	5564
SAU101868		4510	5565
SAU101869		4511	5566
SAU101876		4512	5567
SAU101881		4513	5568
SAU101882		4514	5569
SAU101890		4515	5570
SAU101891		4516	5571
SAU101893		4517	5572
SAU101904		4518	5573
SAU101907		4519	5574
SAU101909		4520	5575
SAU101910		4521	5576
SAU101915		4522	5577
SAU101922		4523	5578
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SAU101966		4525	5580
SAU101968		4526	5581
SAU101991		4527	5582
SAU101995		4528	5583
SAU101996		4529	5584
SAU101999		4530	5585
SAU102001		4531	5586
SAU102002		4532	5587
SAU102003		4533	5588
SAU102006		4534	5589
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SAU102044		4538	5593
SAU102046		4539	5594
SAU102049		4540	5595
SAU102054		4541	5596
SAU102059		4542	5597

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU102067		4543	5598
SAU102068		4544	5599
SAU102102		4545	5600
SAU102113		4546	5601
SAU102116		4547	5602
SAU102117		4548	5603
SAU102129		4549	5604
SAU102132		4550	5605
SAU102142		4551	5606
SAU102143		4552	5607
SAU102144		4553	5608
SAU102162		4554	5609
SAU102165		4555	5610
SAU102200		4556	5611
SAU102201		4557	5612
SAU102222		4558	5613
SAU102231		4559	5614
SAU102232		4560	5615
SAU102233		4561	5616
SAU102241		4562	5617
SAU102242		4563	5618
SAU102246		4564	5619
SAU102247		4565	5620
SAU102252		4566	5621
SAU102256		4567	5622
SAU102257		4568	5623
SAU102259		4569	5624
SAU102260		4570	5625
SAU102261		4571	5626
SAU102262		4572	5627
SAU102264		4573	5628
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SAU102281		4578	5633
SAU102283		4579	5634
SAU102284		4580	5635
SAU102286		4581	5636
SAU102287		4582	5637
SAU102292		4583	5638

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
SAU102294		4584	5639
SAU102297		4585	5640
SAU102298		4586	5641
SAU102308		4587	5642
SAU102318		4588	5643
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SAU102407		4607	5662
SAU102417		4608	5663
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SAU102437		4615	5670
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SAU102449		4619	5674
SAU102450		4620	5675
SAU102452		4621	5676
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SAU102460		4623	5678
SAU102469		4624	5679

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU102474		4626	5681
SAU102476		4627	5682
SAU102479		4628	5683
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SAU102481		4630	5685
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SAU102486		4632	5687
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SAU102498		4634	5689
SAU102502		4635	5690
SAU102503		4636	5691
SAU102526		4637	5692
SAU102527		4638	5693
SAU102531		4639	5694
SAU102533		4640	5695
SAU102534		4641	5696
SAU102541		4642	5697
SAU102551		4643	5698
SAU102554		4644	5699
SAU102575		4645	5700
SAU102578		4646	5701
SAU102584		4647	5702
SAU102585		4648	5703
SAU102593		4649	5704
SAU102598		4650	5705
SAU102599		4651	5706
SAU102601		4652	5707
SAU102602		4653	5708
SAU102603		4654	5709
SAU102605		4655	5710
SAU102606		4656	5711
SAU102607		4657	5712
SAU102609		4658	5713
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SAU102614		4661	5716
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SAU102620		4663	5718
SAU102621		4664	5719
SAU102629		4665	5720

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU102636		4667	5722
SAU102637		4668	5723
SAU102639		4669	5724
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SAU102658		4671	5726
SAU102663		4672	5727
SAU102669		4673	5728
SAU102671		4674	5729
SAU102674		4675	5730
SAU102693		4676	5731
SAU102694		4677	5732
SAU102725		4678	5733
SAU102764		4679	5734
SAU102766		4680	5735
SAU102812		4681	5736
SAU102863		4682	5737
SAU102870		4683	5738
SAU102880		4684	5739
SAU102881		4685	5740
SAU102883		4686	5741
SAU102905		4687	5742
SAU102909		4688	5743
SAU102933		4689	5744
SAU102935		4690	5745
SAU102936		4691	5746
SAU102939		4692	5747
SAU102942		4693	5748
SAU102944		4694	5749
SAU102979		4695	5750
SAU102983		4696	5751
SAU102992		4697	5752
SAU103010		4698	5753
SAU103024		4699	5754
SAU103025		4700	5755
SAU103037		4701	5756
SAU103038		4702	5757
SAU103042		4703	5758
SAU103077		4704	5759
SAU103115		4705	5760
SAU103144		4706	5761

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU103175		4709	5764
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SAU200006		4715	5770
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SAU200030		4717	5772
SAU200058		4718	5773
SAU200059		4719	5774
SAU200088		4720	5775
SAU200157		4721	5776
SAU200242		4722	5777
SAU200297		4723	5778
SAU200345		4724	5779
SAU200392		4725	5780
SAU200468		4726	5781
SAU200558		4727	5782
SAU200561		4728	5783
SAU200564		4729	5784
SAU200565		4730	5785
SAU200593		4731	5786
SAU200601		4732	5787
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SAU200657		4734	5789
SAU200685		4735	5790
SAU200721		4736	5791
SAU200725		4737	5792
SAU200731		4738	5793
SAU200740		4739	5794
SAU200752		4740	5795
SAU200914		4741	5796
SAU200916		4742	5797
SAU200928		4743	5798
SAU200934		4744	5799
SAU200949		4745	5800
SAU200960		4746	5801
SAU200994		4747	5802

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU201168		4749	5804
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SAU201236		4753	5808
SAU201301		4754	5809
SAU201333		4755	5810
SAU201375		4756	5811
SAU201380		4757	5812
SAU201381		4758	5813
SAU201385		4759	5814
SAU201403		4760	5815
SAU201469		4761	5816
SAU201486		4762	5817
SAU201506		4763	5818
SAU201508		4764	5819
SAU201513		4765	5820
SAU201539		4766	5821
SAU201541		4767	5822
SAU201558		4768	5823
SAU201571		4769	5824
SAU201611		4770	5825
SAU201615		4771	5826
SAU201620		4772	5827
SAU201621		4773	5828
SAU201654		4774	5829
SAU201666		4775	5830
SAU201743		4776	5831
SAU201752		4777	5832
SAU201765		4778	5833
SAU201773		4779	5834
SAU201775		4780	5835
SAU201810		4781	5836
SAU201827		4782	5837
SAU201929		4783	5838
SAU201952		4784	5839
SAU201961		4785	5840
SAU201971		4786	5841
SAU202006		4787	5842
SAU202039		4788	5843

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU202174		4790	5845
SAU202176		4791	5846
SAU202186		4792	5847
SAU202267		4793	5848
SAU202708		4794	5849
SAU202731		4795	5850
SAU202736		4796	5851
SAU202756		4797	5852
SAU202781		4798	5853
SAU202872		4799	5854
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SAU202968		4803	5858
SAU203001		4804	5859
SAU203007		4805	5860
SAU203196		4806	5861
SAU203293		4807	5862
SAU203296		4808	5863
SAU203524		4809	5864
SAU300110		4810	5865
SAU300131		4811	5866
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SAU300269		4814	5869
SAU300335		4815	5870
SAU300338		4816	5871
SAU300455		4817	5872
SAU300572		4818	5873
SAU300617		4819	5874
SAU300713		4820	5875
SAU300719		4821	5876
SAU300732		4822	5877
SAU300825		4823	5878
SAU300868		4824	5879
SAU300975		4825	5880
SAU300998		4826	5881
SAU301004		4827	5882
SAU301030		4828	5883
SAU301054		4829	5884

PathoSeq Locus	Gene	Nucleotide SeqID	Protein SeqID
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SAU301133		4832	5887
SAU301148		4833	5888
SAU301223		4834	5889
SAU301230		4835	5890
SAU301268		4836	5891
SAU301275		4837	5892
SAU301357		4838	5893
SAU301363		4839	5894
SAU301433		4840	5895
SAU301465		4841	5896
SAU301472		4842	5897
SAU301592		4843	5898
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SAU301758		4845	5900
SAU301773		4846	5901
SAU301829		4847	5902
SAU301869		4848	5903
SAU301898		4849	5904
SAU302060		4850	5905
SAU302513		4851	5906
SAU302626		4852	5907
SAU302685		4853	5908
SAU302698		4854	5909
SAU302699		4855	5910
SAU302805		4856	5911
SAU302901		4857	5912
SAU302931		4858	5913
SAU302950		4859	5914
SAU302956		4860	5915

TABLE VII

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14111	CaYDL105W	14151	CaYOL026C
14112	CaYJL090C	14152	CaYGR251W
14113	CaYLR127C	14153	CaYDR118W
14114	CaYNL151C	14154	CaYJL085W
14115	CaYPL083C	14155	CaYDR052C
14116	CaYHR036W	14156	CaYGR002C
14117	CaYNL256W	14157	CaYLL004W
14118	CaYOL149W	14158	CaYOR075W
14119	CaYDR361C	14159	CaYMR005W
14120	CaYDR407C	14160	CaYHR172W
14121	CaYBR070C	14161	CaYGL122C
14122	CaYOR148C	14162	CaYOR287C
14123	CaYJR041C	14163	CaYMR149W
14124	CaYGR090W	14164	CaYKR071C
14125	CaYBR123C	14165	CaYDR412W
14126	CaYHR118C	14166	CaYKR025W
14127	CaYKR063C	14167	CaYJR112W
14128	CaYOR004W	14168	CaYMR277W
14129	CaYML025C	14169	CaYKR083C
14130	CaYKL033W	14170	CaYNL245C
14131	CaYDR498C	14171	CaYNL181W
14132	CaYIR011C	14172	CaYNL260C
14133	CaYMR220W	14173	CaYDR365C
14134	CaYPR105C	14174	CaYNL149C
14135	CaYDL153C	14175	CaYGL029W
14136	CaYPL128C	14176	CaYOR057W
14137	CaYER026C	14177	CaYIL022W
14138	CaYKL004W	14178	CaYMR203W
14139	CaYMR200W	14179	CaYOR206W
14140	CaYPR165W	14180	CaYBR167C
14141	CaYHR007C	14181	CaYDR016C
14142	CaYJL087C	14182	CaYNL306W
14143	CaYLR229C	14183	CaYJR067C
14144	CaYER118C	14184	CaYDR362C
14145	CaYPL228W	14185	CaYLR355C
14146	CaYPL160W	14186	CaYLR105C
14147	CaYHR101C	14187	CaYML127W
14148	CaYML085C	14188	CaYPL011C
14149	CaYBR243C	14189	CaYKL108W
14150	CaYLR342W	14190	CaYCR035C

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14191	CaYML114C	14235	CaYLR002C
14192	CaYNL118C	14236	CaYJL061W
14193	CaYDR527W	14237	CaYLR071C
14194	CaYBR256C	14238	CaYML031W
14195	CaYGL233W	14239	CaYIL147C
14196	CaYLR103C	14240	CaYJL025W
14197	CaYOR340C	14241	CaYOR353C
14198	CaYPR175W	14242	CaYKR008W
14199	CaYJR093C	14243	CaYMR033W
14200	CaYCL031C	14244	CaYNL313C
14201	CaYML130C	14245	CaYGL225W
14202	CaYAL033W	14246	CaYNL308C
14203	CaYNL062C	14247	CaYDR353W
14204	CaYNL132W	14248	CaYIL068C
14205	CaYDL193W	14249	CaYPR190C
14206	CaYDR489W	14250	CaYOR174W
14207	CaYJL069C	14251	CaYDL150W
14208	CaYPL063W	14252	CaYAL041W
14209	CaYNL232W	14253	CaYMR227C
14210	CaYNR054C	14254	CaYPL043W
14211	CaYGR245C	14255	CaYDR324C
14212	CaYPR162C	14256	CaYOL022C
14213	CaYHR058C	14257	CaYOL069W
14214	CaYKR081C	14258	CaYGR156W
14215	CaYNL240C	14259	CaYDL003W
14216	CaYPR168W	14260	CaYDR228C
14217	CaYKL099C	14261	CaYKR062W
14218	CaYLR008C	14262	CaYDR398W
14219	CaYOL142W	14263	CaYNL126W
14220	CaYDL015C	14264	CaYKL089W
14221	CaYDR472W	14265	CaYMR028W
14222	CaYNR046W	14266	CaYDR299W
14223	CaYDR473C	14267	CaYOL034W
14224	CaYGL207W	14268	CaYGR119C
14225	CaYHR088W	14269	CaYDL111C
14226	CaYIR015W	14270	CaYHR052W
14227	CaYHR197W	14271	CaYKL021C
14228	CaYMR218C	14272	CaYLL031C
14229	CaYKL182W	14273	CaYHR040W
14230	CaYDR325W	14274	CaYML015C
14231	CaYLL003W	14275	CaYIL004C
14232	CaYNR026C	14276	CaYDR302W
14233	CaYNL251C	14277	CaYPR133C
14234	CaYPL126W	14278	CaYDL195W

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14279	CaYCR052W	14323	CaYBR253W
14280	CaYFR042W	14324	CaYBR254C
14281	CaYNR017W	14325	CaYCL003W
14282	CaYOR254C	14326	CaYCL017C
14283	CaYFL029C	14327	CaYCL054W
14284	CaYBR265W	14328	CaYCR012W
14285	CaYNL312W	14329	CaYCR057C
14286	CaYBR155W	14330	CaYCR072C
14287	CaYGR280C	14331	CaYDL030W
14288	CaYJL203W	14332	CaYDL043C
14289	CaYIR012W	14333	CaYDL055C
14290	CaYMR093W	14334	CaYDL060W
14291	CaYPR137W	14335	CaYDL084W
14292	CaYLR298C	14336	CaYDL087C
14293	CaYBR192W	14337	CaYDL126C
14294	CaYPR112C	14338	CaYDL132W
14295	CaYLL011W	14339	CaYDL141W
14296	CaYER082C	14340	CaYKL059C
14297	CaYDL217C	14341	CaYDL108W
14298	CaYFL035C	14342	CaYKL060C
14299	CaYOR262W	14343	CaYHR070W
14300	CaYLR323C	14344	CaYGR195W
14301	CaYAR007C	14345	CaYOL102C
14302	CaYBL023C	14346	CaYOR074C
14303	CaYBL026W	14347	CaYGL155W
14304	CaYBL030C	14348	CaYLR305C
14305	CaYBL035C	14349	CaYNL222W
14306	CaYBL040C	14350	CaYDR236C
14307	CaYBL050W	14351	CaYBL020W
14308	CaYBL076C	14352	CaYNL261W
14309	CaYBR002C	14353	CaYDR246W
14310	CaYBR029C	14354	CaYNL075W
14311	CaYBR080C	14355	CaYOR145C
14312	CaYBR091C	14356	CaYOL077C
14313	CaYBR135W	14357	CaYBR257W
14314	CaYBR142W	14358	CaYHR170W
14315	CaYBR143C	14359	CaYNL263C
14316	CaYBR160W	14360	CaYKR068C
14317	CaYBR196C	14361	CaYPR016C
14318	CaYBR198C	14362	CaYGR172C
14319	CaYBR202W	14363	CaYHR089C
14320	CaYBR234C	14364	CaYMR197C
14321	CaYBR236C	14365	CaYHR188C
14322	CaYBR237W	14366	CaYPL266W

SEQ ID NO.	Candida designation
14367	CaYBR011C
14368	CaYCL059C
14369	CaYDL008W
14370	CaYDL097C
14371	CaYDL143W
14372	CaYDL205C
14373	CaYDL208W
14374	CaYDR002W
14375	CaYDR013W
14376	CaYDR023W
14377	CaYDR037W
14378	CaYDR045C
14379	CaYDR054C
14380	CaYDR086C
14381	CaYDR087C
14382	CaYDR091C
14383	CaYDR167W
14384	CaYDR172W
14385	CaYDR189W
14386	CaYDR196C
14387	CaYDR212W
14388	CaYDR238C
14389	CaYDR280W
14390	CaYDR331W
14391	CaYDR373W
14392	CaYDR376W
14393	CaYDR390C
14394	CaYDR394W
14395	CaYDR404C
14396	CaYDR429C
14397	CaYDR454C
14398	CaYEL020W-A
14399	CaYEL026W
14400	CaYER003C
14401	CaYER006W
14402	CaYER012W
14403	CaYER021W
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14405	CaYER094C
14406	CaYER125W
14407	CaYER148W
14408	CaYER159C
14409	CaYFL002C
14410	CaYFL005W

SEQ ID NO.	Candida designation
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14412	CaYFL022C
14413	CaYFL038C
14414	CaYFL045C
14415	CaYFR004W
14416	CaYFR037C
14417	CaYFR050C
14418	CaYFR052W
14419	CaYDL029W
14420	CaYDL147W
14421	CaYDL148C
14422	CaYDR060W
14423	CaYDR062W
14424	CaYDR211W
14425	CaYDR328C
14426	CaYER025W
14427	CaYER136W
14428	CaYER171W
14429	CaYFL008W
14430	CaYGL001C
14431	CaYGL008C
14432	CaYGL011C
14433	CaYGL022W
14434	CaYGL044C
14435	CaYGL048C
14436	CaYGL068W
14437	CaYGL097W
14438	CaYGL112C
14439	CaYGL120C
14440	CaYGL130W
14441	CaYGR029W
14442	CaYGR060W
14443	CaYGR094W
14444	CaYGR103W
14445	CaYGR185C
14446	CaYGR211W
14447	CaYGR218W
14448	CaYGR246C
14449	CaYGR253C
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14451	CaYHR005C-A
14452	CaYHR019C
14453	CaYHR020W
14454	CaYHR024C

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
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14456	CaYHR072W	14500	CaYLL018C
14457	CaYHR072W-A	14501	CaYLR005W
14458	CaYHR090C	14502	CaYLR009W
14459	CaYHR122W	14503	CaYLR022C
14460	CaYHR143W-A	14504	CaYLR026C
14461	CaYHR148W	14505	CaYLR051C
14462	CaYHR165C	14506	CaYLR060W
14463	CaYHR166C	14507	CaYLR078C
14464	CaYHR169W	14508	CaYLR100W
14465	CaYHR190W	14509	CaYLR116W
14466	CaYIL003W	14510	CaYLR117C
14467	CaYIL021W	14511	CaYLR129W
14468	CaYIL075C	14512	CaYLR147C
14469	CaYIL078W	14513	CaYLR153C
14470	CaYIL142W	14514	CaYLR163C
14471	CaYIR008C	14515	CaYLR175W
14472	CaYIR022W	14516	CaYLR186W
14473	CaYJL001W	14517	CaYLR197W
14474	CaYJL014W	14518	CaYLR208W
14475	CaYJL050W	14519	CaYLR222C
14476	CaYJL074C	14520	CaYLR259C
14477	CaYJL081C	14521	CaYLR276C
14478	CaYJL104W	14522	CaYLR277C
14479	CaYJL111W	14523	CaYLR291C
14480	CaYJL143W	14524	CaYLR293C
14481	CaYJL167W	14525	CaYLR347C
14482	CaYJL194W	14526	CaYLR378C
14483	CaYJR006W	14527	CaYLR397C
14484	CaYJR017C	14528	CaYML064C
14485	CaYJR064W	14529	CaYML069W
14486	CaYJR065C	14530	CaYML092C
14487	CaYJR072C	14531	CaYML093W
14488	CaYJR123W	14532	CaYML125C
14489	CaYKL012W	14533	CaYML126C
14490	CaYKL019W	14534	CaYMR113W
14491	CaYKL028W	14535	CaYMR131C
14492	CaYKL058W	14536	CaYMR146C
14493	CaYKL104C	14537	CaYMR208W
14494	CaYKL144C	14538	CaYMR213W
14495	CaYKL145W	14539	CaYMR240C
14496	CaYKL172W	14540	CaYMR260C
14497	CaYKL210W	14541	CaYMR308C
14498	CaYKR079C	14542	CaYMR314W

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14543	CaYNL002C	14587	CaYPL211W
14544	CaYNL006W	14588	CaYPL235W
14545	CaYNL061W	14589	CaYPL252C
14546	CaYNL102W	14590	CaYPR019W
14547	CaYNL113W	14591	CaYPR025C
14548	CaYNL178W	14592	CaYPR034W
14549	CaYNL189W	14593	CaYPR055W
14550	CaYNL244C	14594	CaYPR056W
14551	CaYNL247W	14595	CaYPR082C
14552	CaYNL287W	14596	CaYPR103W
14553	CaYNR043W	14597	CaYPR107C
14554	CaYOL005C	14598	CaYPR108W
14555	CaYOL010W	14599	CaYPR110C
14556	CaYOL094C	14600	CaYPR113W
14557	CaYOL139C	14601	CaYPR176C
14558	CaYOR048C	14602	CaYPR183W
14559	CaYOR056C	14603	CaYPR186C
14560	CaYOR063W	14604	CaYPR187W
14561	CaYOR103C	14605	CaYGL123W
14562	CaYOR116C	14606	CaYHR042W
14563	CaYOR117W	14607	CaYIL062C
14564	CaYOR151C	14608	CaYJR042W
14565	CaYOR157C	14609	CaYJR063W
14566	CaYOR159C	14610	CaYJR076C
14567	CaYOR168W	14611	CaYKL013C
14568	CaYOR194C	14612	CaYLR196W
14569	CaYOR207C	14613	CaYLR272C
14570	CaYOR210W	14614	CaYNR035C
14571	CaYOR217W	14615	CaYPR088C
14572	CaYOR224C	14616	CaYDR397C
14573	CaYOR232W	14617	CaYAL032C
14574	CaYOR259C	14618	CaYBR060C
14575	CaYOR261C	14619	CaYBR154C
14576	CaYOR272W	14620	CaYDL028C
14577	CaYOR294W	14621	CaYDR088C
14578	CaYOR310C	14622	CaYDR235W
14579	CaYOR335C	14623	CaYDR267C
14580	CaYOR341W	14624	CaYDR460W
14581	CaYPL010W	14625	CaYEL032W
14582	CaYPL076W	14626	CaYER013W
14583	CaYPL094C	14627	CaYER048W-A
14584	CaYPL117C	14628	CaYER172C
14585	CaYPL122C	14629	CaYFR031C
14586	CaYPL131W	14630	CaYGL065C

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14631	CaYGL073W	14675	CaYOR249C
14632	CaYGL091C	14676	CaYOR250C
14633	CaYGL103W	14677	CaYOR257W
14634	CaYGL116W	14678	CaYOR370C
14635	CaYGL201C	14679	CaYPL151C
14636	CaYGL245W	14680	CaYPL204W
14637	CaYGL247W	14681	CaYPL209C
14638	CaYGR047C	14682	CaYPL242C
14639	CaYGR074W	14683	CaYPR048W
14640	CaYGR083C	14684	CaYPR086W
14641	CaYGR128C	14685	CaYPR178W
14642	CaYHR074W	14686	CaYIL109C
14643	CaYHR107C	14687	CaYKL045W
14644	CaYIL126W	14688	CaYLR316C
14645	CaYJL010C	14689	CaYBR087W
14646	CaYJL011C	14690	CaYGR048W
14647	CaYJL026W	14691	CaYPL169C
14648	CaYJL039C	14692	CaYGR186W
14649	CaYJL041W	14693	CaYNL131W
14650	CaYJR045C	14694	CaYLR088W
14651	CaYKL049C	14695	CaYKL193C
14652	CaYKL152C	14696	CaYJR007W
14653	CaYKL181W	14697	CaYJL034W
14654	CaYLR086W	14698	CaYDL207W
14655	CaYLR115W	14699	CaYDL017W
14656	CaYLR223C	14700	CaYAL035W
14657	CaYLR274W	14701	CaYBR038W
14658	CaYLR336C	14702	CaYBR159W
14659	CaYML065W	14703	CaYDR120C
14660	CaYML098W	14704	CaYER070W
14661	CaYMR043W	14705	CaYGL003C
14662	CaYMR112C	14706	CaYGL206C
14663	CaYMR281W	14707	CaYAL043C
14664	CaYMR288W	14708	CaYBL097W
14665	CaYMR290C	14709	CaYBL105C
14666	CaYMR309C	14710	CaYBR079C
14667	CaYNL039W	14711	CaYBR088C
14668	CaYNL110C	14712	CaYDL145C
14669	CaYNL221C	14713	CaYDL166C
14670	CaYNL317W	14714	CaYDR145W
14671	CaYNR053C	14715	CaYDR170C
14672	CaYOL038W	14716	CaYDR301W
14673	CaYOR095C	14717	CaYDR531W
14674	CaYOR204W	14718	CaYFL024C

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14719	CaYFR002W	14763	CaYPR041W
14720	CaYGR264C	14764	CaYGR255C
14721	CaYHR023W	14765	CaYBR055C
14722	CaYHR027C	14766	CaYER022W
14723	CaYJL008C	14767	CaYKL014C
14724	CaYJL033W	14768	CaYIL046W
14725	CaYJL054W	14769	CaYMR015C
14726	CaYJL109C	14770	CaYNL280C
14727	CaYJL125C	14771	CaYML075C
14728	CaYJL156C	14772	CaYCR042C
14729	CaYJR002W	14773	CaYMR235C
14730	CaYKL192C	14774	CaYIL026C
14731	CaYLL034C	14775	CaYPL085W
14732	CaYLR029C	14776	CaYGR005C
14733	CaYLR167W	14777	CaYOL144W
14734	CaYLR243W	14778	CaYHR005C
14735	CaYLR249W	14779	CaYGR013W
14736	CaYLR321C	14780	CaYIL115C
14737	CaYLR383W	14781	CaYGR147C
14738	CaYMR239C	14782	CaYOR336W
14739	CaYNL088W	14783	CaYPR159W
14740	CaYNL163C	14784	CaYJL174W
14741	CaYNR038W	14785	CaYOL130W
14742	CaYOL097C	14786	CaYNL048W
14743	CaYOR260W	14787	CaYER007W
14744	CaYPL028W	14788	CaYGL106W
14745	CaYPL153C	14789	CaYDL102W
14746	CaYPL210C	14790	CaYDL007W
14747	CaYPL217C	14791	CaYER031C
14748	CaYPR010C	14792	CaYDR226W
14749	CaYPR144C	14793	CaYOR349W
14750	CaYPR169W	14794	CaYNL148C
14751	CaYDL140C	14795	CaYPR119W
14752	CaYDL031W	14796	CaYMR055C
14753	CaYHR186C	14797	CaYFL018C
14754	CaYPL093W	14798	CaYNL238W
14755	CaYKL035W	14799	CaYPL231W
14756	CaYDL058W	14800	CaYNL025C
14757	CaYDR341C	14801	CaYJL141C
14758	CaYGL238W	14802	CaYLR306W
14759	CaYFR028C	14803	CaYLR300W
14760	CaYNL172W	14804	CaYKL046C
14761	CaYDR190C	14805	CaYDR311W
14762	CaYEL055C	14806	CaYDR449C

SEQ ID NO.	Candida designation	SEQ ID NO.	Candida designation
14807	CaYER023W	14851	orf6.5199
14808	CaYGL040C	14852	orf6.5210
14809	CaYGR009C	14853	orf6.5520
14810	CaYNR003C	14854	orf6.569
14811	CaYOL066C	14855	orf6.5739
14812	CaYOR119C	14856	orf6.6011
14813	CaYMR049C	14857	orf6.7375
14814	CaYNR050C	14858	orf6.7629
14815	CaYPL203W	14859	orf6.8025
14816	CaYER113C	14860	orf6.804
14817	CaYOR280C	14861	orf6.8362
14818	CaYGR006W	14862	orf6.8377
14819	CaYJL122W	14863	orf6.8395
14820	CaORF6_3320	14864	orf6.8482
14821	CaORF6_7574	14865	orf6.8837
14822	CaORF6_6275	14866	orf6.889
14823	CaORF6_1979	14867	orf6.8938
14824	CaORF6_8942	14868	orf6.9113
14825	CaYJL153C	14869	CaLYS4
14826	CaYNL277W	14870	CaTRP5
14827	CaYIL104C	14871	CaPRO1
14828	CaYOL027C	14872	CaPBS2
14829	CaYJL134W	14873	CaYBL041W
14830	CaYLL012W	14874	CaYBR170C
14831	CaORF6_7779	14875	CaYDR188W
14832	CaORF6_3262	14876	CaYGR098C
14833	CaORF6_7304	14877	CaYGR267C
14834	CaORF6_2028	14878	CaYGR274C
14835	CaORF6_1717	14879	CaYJL002C
14836	CaORF6_1780	14880	CaYKL125W
14837	CaORF6_1932	14881	CaYLL035W
14838	CaORF6_1934	14882	CaYPL016W
14839	CaORF6_2193	14883	CaYPL218W
14840	CaORF6_2398	14884	CaYKL141W
14841	orf6.3168	14885	CaYHR174W
14842	orf6.3295	14886	CaYDR356W
14843	orf6.3939	14887	CaYNL124W
14844	orf6.4497	14888	CaYAL015C
14845	orf6.4499	14889	CaYBR001C
14846	orf6.4537	14890	CaYCL035C
14847	orf6.4747	14891	CaYCR048W
14848	orf6.4899	14892	CaYDR379W
14849	orf6.4974	14893	CaYER059W
14850	orf6.5147	14894	CaYGR070W

SEQ ID NO.	Candida designation
14895	CaYGR209C
14896	orf6.1498
14897	orf6.2086
14898	orf6.3026
14899	orf6.3261
14900	orf6.3819
14901	orf6.3864
14902	orf6.3972
14903	orf6.4005
14904	orf6.4010
14905	orf6.4114
14906	orf6.4153
14907	orf6.4206
14908	orf6.4293
14909	orf6.4463
14910	orf6.4555
14911	orf6.4628
14912	orf6.4837
14913	orf6.4854
14914	orf6.4923
14915	orf6.4927
14916	orf6.5092
14917	orf6.5279
14918	orf6.5786
14919	orf6.5919
14920	orf6.5920
14921	orf6.6022
14922	orf6.6026
14923	orf6.6030
14924	orf6.6069
14925	orf6.6140
14926	orf6.6218
14927	orf6.6390
14928	orf6.6550
14929	orf6.6562
14930	orf6.6660
14931	orf6.6664
14932	orf6.6670
14933	orf6.6700
14934	orf6.6933
14935	orf6.6939
14936	orf6.7203
14937	orf6.7214
14938	orf6.7847

SEQ ID NO.	Candida designation
14939	orf6.7893
14940	orf6.8239
14941	orf6.8461
14942	orf6.8607
14943	orf6.8654
14944	orf6.8716

WHAT IS CLAIMED IS:

1. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain
5 in said culture overexpresses a different gene product which is essential for proliferation of said organism;

contacting said culture with a sufficient concentration of said compound
to inhibit the proliferation of strains of said organism which do not overexpress
said gene product on which said compound acts, such that strains which
10 overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which
proliferated more rapidly in said culture.

15 2. The method of Claim 1, wherein said culture includes at least one strain which does not overexpresses a gene product which is essential for proliferation of said organism.

3. The method of Claim 1, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for
20 proliferation of said organism operably linked to a regulatable promoter.

4. The method of Claim 1, wherein said strains which overexpress said gene products a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

5. The method of Claim 1, wherein said identification step comprises
25 determining the nucleotide sequence of a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said culture.

6. The method of Claim 1, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

30 7. The method of Claim 6, wherein the products of said amplification reaction are labeled with a detectable dye.

8. The method of Claim 1, wherein said identification step comprises performing a hybridization procedure.

9. The method of Claim 1, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said cell which proliferated more rapidly in said cell culture.

10. The method of Claim 1, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

11. The method of Claim 1, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

12. The method of Claim 1, wherein said compound is obtained from a library of natural compounds.

13. The method of Claim 1, wherein said compound is obtained from a library of synthetic compounds.

14. The method of Claim 1, wherein said compound is present in a crude or partially purified state.

15. The method of Claim 1, further comprising determining whether said gene product in said strain which proliferated more rapidly in said culture has a counterpart in at least one other organism.

16. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

17. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress

said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

5 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

18. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain
10 in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

15 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said
20 compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

19. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

25 obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version
30 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the

group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

20. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a

gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

21. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain in said culture overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected

from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

5 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

10 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture.

22. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

15 obtaining an array of strains on a solid growth medium wherein each strain in overexpresses a different gene product which is essential for proliferation of said organism

20 contacting said array of strains with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

 identifying the gene product which is overexpressed in a strain which proliferated more rapidly on said solid medium.

25 23. The method of Claim 21, wherein at least one strain in said array does not overexpresses a gene product which is essential for proliferation of said organism.

24. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

30 obtaining a plurality of cultures, wherein each culture comprises a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism;

contacting each of said cultures with a different concentration of said compound ; and

identifying the gene product which is overexpressed in a strain whose proliferation is inhibited by said compound.

5 25. The method of Claim 23, wherein at least one strain in said plurality of cultures does not overexpress a gene product which is essential for proliferation of said organism.

26. A method of profiling a compound's activity comprising
10 performing the method of Claim 1 on a first culture using a first compound;

performing the method of Claim 1 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

15 27. A method of profiling a first compound's activity comprising
growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein each strain in said array overexpresses a different gene product which is essential for proliferation of an organism and wherein said first compound and
20 said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

28. The method of any one of Claims 26 and 27, wherein said first compound is present in a crude or partially purified state.

25 29. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism;

30 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said

gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

5 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

30. The method of Claim 29, wherein at least one strain in said culture does not underexpresses a gene product which is essential for proliferation of said organism.

31. The method of Claim 29, wherein said strains which underexpress said
10 gene products comprise a nucleic acid complementary to at least a portion of a gene encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

32. The method of Claim 29, wherein said strains which underexpress said gene products express an antisense nucleic acid complementary to at least a portion of a gene
15 encoding said gene product which is essential for proliferation of said organism, wherein expression of said antisense nucleic acid reduces expression of said gene product in said strain.

33. The method of Claim 29, wherein said identification step comprises determining the nucleotide sequence of a nucleic acid encoding said gene product in
20 said strain which proliferated more slowly.

34. The method of Claim 29, wherein said identification step comprises performing an amplification reaction to identify the nucleic acid encoding said gene product in said cell which proliferated more slowly.

35. The method of Claim 34, wherein the products of said amplification reaction
25 are labeled with a detectable dye.

36. The method of Claim 29, wherein said identification step comprises performing a hybridization procedure.

37. The method of Claim 29, wherein said identification step comprises contacting a nucleic acid array with a nucleic acid encoding said gene product in said
30 cell which proliferated more slowly.

38. The method of Claim 29, wherein said organism is selected from the group consisting of bacteria, fungi, protozoa.

39. The method of Claim 29, wherein said compound is obtained from a library of natural compounds.

5 40. The method of Claim 29, wherein said compound is obtained from a library of synthetic compounds.

41. The method of Claim 29, wherein said compound is present in a crude or partially purified state.

10 42. The method of Claim 29, further comprising determining whether said gene product in said strain which proliferated more slowly in said culture has a counterpart in at least one other organism.

43. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

15 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed;

20 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

25 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

44. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

30 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of

said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is underexpressed;

5 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

10 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

45. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

15 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

20 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

25 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

30 46. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

47. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

5 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70%
10 nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860,
15 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed;

 contacting said culture with a sufficient concentration of said compound
20 to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

25 identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

48. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

 obtaining a culture comprising a plurality of strains wherein each strain
30 underexpresses a different gene product which is essential for proliferation of said organism wherein said culture comprises a strain in which a gene product

comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress said gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture.

49. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures, each culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism; and

contacting each of said cultures with a different concentration of said compound; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

50. A method of profiling a compound's activity comprising

performing the method of Claim 29 on a first culture using a first compound;

performing the method of Claim 29 on a second culture using a second compound; and

comparing the strains identified in said first culture to the strains identified in said second culture.

51. A method of profiling a first compound's activity comprising

growing an array of strains on a first solid medium comprising said first compound and on a second solid medium comprising a second compound, wherein said array comprises a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of an organism and wherein said first compound and said second compound inhibit the proliferation of said organism; and

comparing the pattern of strains which grow on said first solid medium with the pattern of strains which grow on said second solid medium.

52. The method of any one of Claims 49 and 50, wherein said first compound is present in a crude or partially purified state.

53. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a plurality of cultures comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism;

contacting each of said plurality of cultures with a varying concentration of a regulatory agent which regulates the level of expression of said gene products which are essential for proliferation of said organism ; and

identifying the gene product which is underexpressed in a strain whose rate of proliferation is reduced by said compound.

54. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism.

55. The culture of Claim 54, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a regulatable promoter.

56. The culture of Claim 54, wherein said strains which overexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

57. The culture of Claim 54, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*,

Bacillus anthracis, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*,
Campylobacter jejuni, *Candida albicans*, *Candida glabrata* (also called *Torulopsis*
glabrata), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida*
krusei, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*,
5 *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium*
difficile, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,
Cryptococcus neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus*
faecium, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma*
capsulatum, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*,
10 *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia*
asteroides, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*,
Proteus vulgaris, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella*
choleraesuis, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
typhimurium, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella*
15 *dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
Streptococcus pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia*
enterocolitica, and *Yersinia pestis*.

58. A culture comprising a plurality of strains wherein each strain overexpresses
 a different gene product which is essential for proliferation of said organism, wherein
 20 said culture comprises a strain in which a gene product whose activity or level is
 inhibited by a nucleic acid comprising a nucleotide sequence selected from the group
 consisting of SEQ ID NOs.: 8-3795 is overexpressed.

59. A culture comprising a plurality of strains wherein each strain overexpresses
 a different gene product which is essential for proliferation of said organism, wherein
 25 said culture comprises a strain in which a gene product encoded by a nucleic acid
 comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.:
 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed.

60. A culture comprising a plurality of strains wherein each strain overexpresses
 a different gene product which is essential for proliferation of said organism, wherein
 30 said culture comprises a strain in which a gene product comprising an amino acid

sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed.

61. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed.

62. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860,

5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide
5 sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed.

63. A culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected
10 from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-
15 15778 is overexpressed.

64. A culture comprising a a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism.

65. The culture of Claim 64, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for
20 proliferation of said organism operably linked to a regulatable promoter.

66. The culture of Claim 64, wherein said strains which underexpress said gene products comprise a nucleic acid encoding said gene product which is essential for proliferation of said organism operably linked to a constitutive promoter.

67. The culture of Claim 64, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*,
30 *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium*

difficile, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,
Cryptococcus neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus*
faecium, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma*
capsulatum, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*,
5 *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia*
asteroides, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*,
Proteus vulgaris, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella*
choleraesuis, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella*
typhimurium, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella*
10 *dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*,
Streptococcus pneumoniae, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia*
enterocolitica, and *Yersinia pestis*.

68. A culture comprising a plurality of strains wherein each strain
 underexpresses a different gene product which is essential for proliferation of said
 15 organism, wherein said culture comprises a strain in which a gene product whose
 activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected
 from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

69. A culture comprising a plurality of strains wherein each strain
 underexpresses a different gene product which is essential for proliferation of said
 20 organism, wherein said culture comprises a strain in which a gene product encoded by a
 nucleic acid comprising a nucleotide sequence selected from the group consisting of
 SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is
 underexpressed.

70. A culture comprising a plurality of strains wherein each strain
 25 underexpresses a different gene product which is essential for proliferation of said
 organism, wherein said culture comprises a strain in which a gene product comprising
 an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-
 3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed.

71. A culture comprising a plurality of strains wherein each strain
 30 underexpresses a different gene product which is essential for proliferation of said
 organism, wherein said culture comprises a strain in which a gene product selected from

the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product
5 encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using
10 FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product
15 encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

20 72. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity
25 as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a
30 nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide

sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed.

73. A culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOS.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOS: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed.

74. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

75. The method of Claim 74, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate overexpression of said gene products.

76. The method of Claim 74, wherein the nucleotide sequence of each of the genes encoding an overexpressed gene product has been altered by inserting a regulatory element into the native promoters of said genes with a promoter which facilitates overexpression of said gene products.

5 77. The method of Claim 76, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

10 78. The method of Claim 74, wherein the step of identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

15 79. The method of Claim 75, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

80. The method of Claim 75, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

20 81. The method of Claim 75, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

82. The method of Claim 75, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

25 83. The method of Claim 74, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

84. The method of Claim 74, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*,

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Chlamydia pneumoniae, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*, *Cryptococcus neoformans*, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

85. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

5 86. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used
10 to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed;

15 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said
20 compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

25 87. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used
30 to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprising an

amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

88. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected

5 from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed;

10 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

15 identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

20 89. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes;

25 contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

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identifying the gene product which is overexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

90. A method for identifying the gene product on which a compound which
5 inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain overexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the overexpressed genes has been altered so as to include a nucleotide sequence which can be used
10 to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the
15 default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid
20 comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which do not overexpress
25 said gene product on which said compound acts, such that strains which overexpress said gene product on which said compound acts proliferate more rapidly than strains which do not overexpress said gene product on which said compound acts; and

identifying the gene product which is overexpressed in a strain which
30 proliferated more rapidly in said culture by detecting the unique product corresponding to said gene, wherein said culture comprises a strain in which a

gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a
5 polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed.

91. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

10 obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the
15 overexpressed genes;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than
20 strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

25 92. The method of Claim 91, wherein the nucleotide sequence of each of the genes encoding an underexpressed gene product has been altered by replacing the native promoters of said genes with promoters which facilitate underexpression of said gene products.

93. The method of Claim 91, wherein the nucleotide sequence of each of the
30 genes encoding an underexpressed gene product has been altered by inserting a

regulatory element into the native promoters of said genes with a promoter which facilitates underexpression of said gene products.

94. The method of Claim 93, wherein said regulatory element is selected from the group consisting of a regulatable promoter, an operator which is recognized by a repressor, a nucleotide sequence which is recognized by a transcriptional activator, a transcriptional terminator, a nucleotide sequence which introduces a bend in the DNA and an upstream activating sequence.

95. The method of Claim 91, wherein the step of identifying the gene product which is underexpressed in a strain which proliferated more slowly in said culture by detecting the unique product corresponding to said gene comprises performing an amplification reaction and detecting a unique amplification product corresponding to said gene.

96. The method of Claim 92, wherein the native promoter of each of the genes encoding a gene product essential for proliferation is replaced with the same promoter.

97. The method of Claim 92, wherein the native promoters of the genes encoding gene products essential for proliferation are replaced with a plurality of promoters selected to give a desired expression level for each gene product.

98. The method of Claim 92, wherein said promoters which replaced the native promoters in each strain comprise regulatable promoters.

99. The method of Claim 92, wherein said promoters which replaced the native promoters in each strain each strain comprise constitutive promoters.

100. The method of Claim 91, wherein said organism is selected from the group consisting of bacteria, fungi, and protozoa.

101. The method of Claim 91, wherein said culture is a culture of an organism selected from the group consisting of *Anaplasma marginale*, *Aspergillus fumigatus*, *Bacillus anthracis*, *Bacterioides fragilis*, *Bordetella pertussis*, *Burkholderia cepacia*, *Campylobacter jejuni*, *Candida albicans*, *Candida glabrata* (also called *Torulopsis glabrata*), *Candida tropicalis*, *Candida parapsilosis*, *Candida guilliermondii*, *Candida krusei*, *Candida kefyr* (also called *Candida pseudotropicalis*), *Candida dubliniensis*, *Chlamydia pneumoniae*, *Chlamydia trachomatis*, *Clostridium botulinum*, *Clostridium difficile*, *Clostridium perfringens*, *Coccidioides immitis*, *Corynebacterium diphtheriae*,

Cryptococcus neoformans, *Enterobacter cloacae*, *Enterococcus faecalis*, *Enterococcus faecium*, *Escherichia coli*, *Haemophilus influenzae*, *Helicobacter pylori*, *Histoplasma capsulatum*, *Klebsiella pneumoniae*, *Listeria monocytogenes*, *Mycobacterium leprae*, *Mycobacterium tuberculosis*, *Neisseria gonorrhoeae*, *Neisseria meningitidis*, *Nocardia asteroides*, *Pasteurella haemolytica*, *Pasteurella multocida*, *Pneumocystis carinii*, *Proteus vulgaris*, *Pseudomonas aeruginosa*, *Salmonella bongori*, *Salmonella choleraesuis*, *Salmonella enterica*, *Salmonella paratyphi*, *Salmonella typhi*, *Salmonella typhimurium*, *Staphylococcus aureus*, *Moxarella catarrhalis*, *Shigella boydii*, *Shigella dysenteriae*, *Shigella flexneri*, *Shigella sonnei*, *Staphylococcus epidermidis*, *Streptococcus pneumoniae*, *Streptococcus mutans*, *Treponema pallidum*, *Yersinia enterocolitica*, and *Yersinia pestis*.

102. The method of Claim 91, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed.

103. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes and wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than

strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

104. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

105. A method for identifying the gene product on which a compound which inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence

which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is underexpressed;

contacting said culture with a sufficient concentration of said compound to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

106. A method for identifying the gene product on which a compound which
5 inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence
10 which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version
15 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic
20 acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is underexpressed;

contacting said culture with a sufficient concentration of said compound
25 to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

107. A method for identifying the gene product on which a compound which
5 inhibits proliferation of an organism acts comprising:

obtaining a culture comprising a plurality of strains wherein each strain underexpresses a different gene product which is essential for proliferation of said organism and wherein the nucleotide sequence of each of the underexpressed genes has been altered so as to include a nucleotide sequence
10 which can be used to generate a unique product corresponding to each of the overexpressed genes, wherein said culture comprises a strain in which a gene product comprises a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of
15 SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is underexpressed;

contacting said culture with a sufficient concentration of said compound
20 to inhibit the proliferation of strains of said organism which underexpress said gene product on which said compound acts, such that strains which underexpress said gene product on which said compound acts proliferate more slowly than strains which do not underexpress the gene product on which said compound acts; and

25 identifying the gene product which is underexpressed in a strain which proliferated more rapidly in said culture by detecting the unique product corresponding to said gene.

108. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

30 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a

plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

109. The method of Claim 108, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

110. The method of Claim 108 wherein:

said nucleic acid sample is divided into N aliquots;

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

111. The method of Claim 109, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

112. The method of Claim 108, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

113. The method of Claim 111, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

114. The method of Claim 111, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

5 115. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism
10 wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which
15 are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide
20 sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

25 116. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism ,
30 wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group

consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

117. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

118. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product selected from
10 the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID
15 NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence
20 selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected
25 from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a
30 nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

119. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes

which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

120. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism , wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

121. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

5 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been
10 contacted with said compound;

 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with
15 said compound;

 performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair
20 would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

 performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification
25 reaction;

 and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in
30 said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the

target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products.

122. The method of Claim 121, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

123. The method of Claim 121, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

124. The method of Claim 121, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

125. The method of Claim 121, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

126. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences

within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

127. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

128. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first

amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in
5 which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

129. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

10 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been
15 contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with
20 said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair
25 would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid
30 sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a

nucleotide sequence selected from the group consisting of SEQ ID NOs: 8-3795 is overexpressed or underexpressed.

130. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

5 obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been
10 contacted with said compound;

 obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with
15 said compound;

 performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair
20 would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

 performing a second amplification reaction on said second nucleic acid
25 sample using the same set of primer pairs used in said first amplification reaction;

 and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in
30 said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the

target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second cultures or collection of strains comprise a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

131. A method for identifying the target of a compound which inhibits the proliferation of an organism comprising:

obtaining a first nucleic acid sample comprising nucleic acids from a first culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains wherein each strain overexpresses or underexpresses a different gene product which is required for proliferation of said organism and wherein said culture or collection of strains has been contacted with said compound;

obtaining a second nucleic acid sample comprising nucleic acids from a second culture or collection of strains wherein said culture or collection of strains comprises the same strains as said first culture or collection of strains wherein said second culture or collection of strains has not been contacted with said compound;

performing a first amplification reaction on said first nucleic acid sample using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains;

performing a second amplification reaction on said second nucleic acid sample using the same set of primer pairs used in said first amplification reaction;

and comparing the amount of each amplification product in said first amplification reaction to the amount of that amplification product in said second amplification reaction, wherein an increased level of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products and a decreased level of of an amplification product in said first amplification reaction relative to said second amplification reaction indicates that the gene product corresponding to said amplification product is the target of said compound if said culture or strain overexpresses said gene products, wherein said first and second culture or collection of strains comprise a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

132. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

5 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the
10 amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction.

15 133. The method of Claim 132, wherein one member of each primer pair for each of said genes is labeled with a detectable dye.

134. The method of Claim 132 wherein:

said nucleic acid sample is divided into N aliquots;

20 said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

25 135. The method of Claim 134, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

136. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

30 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a

plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

137. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene

product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

138. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

139. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set

of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

140. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

5 performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the
10 amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene
15 product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-
20 14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-
25 4860, 5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

141. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

30 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a

plurality of strains which transcribe an antisense nucleic acid complementary to a different gene product which is required for proliferation of said organism;

performing an amplification reaction using a set of primer pairs which are complementary to nucleotide sequences within or adjacent to the nucleic acids which encode said antisense nucleic acids, wherein the members of said set of primer pairs are designed such that each primer pair would yield an amplification product having a length distinguishable from the lengths of the amplification products from the other primer pairs if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

determining the lengths of the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

142. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the basis selected from the group consisting of length, detectable label and both length

and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction.

143. The method of Claim 142, wherein said primer pairs are divided into at least two sets, each primer pair comprises a primer which is labeled with a distinguishable dye, and the distinguishable dye used to label each set of primer pairs is distinguishable from the dye used to label the other sets of primer pairs.

144. The method of Claim 142 wherein:

said nucleic acid sample is divided into N aliquots;

said amplification reaction is performed on each aliquot using primer pairs complementary to nucleotide sequences within or adjacent to 1/N of the genes which encode said gene products, wherein one of the members of each primer pair in each aliquot is labeled with a dye and wherein the dyes on the primers in each aliquot are distinguishable from one another.

145. The method of Claim 144, further comprising pooling the amplification products from each of the aliquots prior to determining the lengths of the amplification products.

146. The method of Claim 142, wherein the native promoters of said genes which encode said gene products have been replaced with a regulatable promoter and one of the primers in said primer pairs is complementary to a nucleotide sequence within said regulatable promoter.

147. The method of Claim 146, wherein the native promoters for each of said genes were replaced with the same regulatable promoter.

148. The method of Claim 146, wherein more than one regulatable promoter was used to replace the promoters of said genes such that some of said genes are under the control of a different regulatable promoter.

149. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

5 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis
10 selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification
15 reaction, wherein said culture comprises a strain in which a gene product whose activity or level is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 is overexpressed or underexpressed.

150. A method for determining the extent to which each of a plurality of
20 strains are present in a culture or collection of strains comprising:

obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

25 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis
30 selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences

complementary to said primer pair is present in said culture or collection of strains; and

5 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 is overexpressed or underexpressed.

151. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

10 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

15 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences
20 complementary to said primer pair is present in said culture or collection of strains; and

25 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product comprising an amino acid sequence selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

152. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

30 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a

plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

5 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences
10 complementary to said primer pair is present in said culture or collection of strains; and

identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product selected from the group consisting of a gene product having at least 70%
15 nucleotide sequence identity as determined using BLASTN version 2.0 with the default parameters to a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN
20 version 2.0 with the default parameters to a nucleic acid encoding a gene product whose expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product having at least 25% amino acid identity as determined using FASTA version 3.0t78 with the default parameters to a gene product whose
25 expression is inhibited by an antisense nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795, a gene product encoded by a nucleic acid which hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under stringent conditions, a gene product encoded by a nucleic acid which
30 hybridizes to a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOs.: 8-3795 under moderate conditions, and a

gene product whose activity may be complemented by the gene product whose activity is inhibited by a nucleic acid comprising a nucleotide sequence selected from the group consisting of SEQ ID NOS: 8-3795 is overexpressed or underexpressed.

5 153. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product
10 which is required for proliferation of said organism;

 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from
15 the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product encoded by a nucleic acid comprising a nucleotide sequence selected from the group consisting of a nucleic acid comprising a nucleic acid having at least 70% nucleotide sequence identity as determined using BLASTN version 2.0 with the
20 default parameters to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944, a nucleic acid comprising a nucleotide sequence which hybridizes to a sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860, 5916-10012, and 14111-14944 under stringent conditions, and a nucleic acid
25 comprising a nucleotide sequence which hybridizes to a nucleotide sequence selected from the group consisting of SEQ ID NOS.: 3796-3800, 3806-4860,
30

5916-10012, and 14111-14944 under moderate conditions is overexpressed or underexpressed.

154. A method for determining the extent to which each of a plurality of strains are present in a culture or collection of strains comprising:

5 obtaining a nucleic acid sample comprising nucleic acids from a culture or collection of strains wherein said culture or collection of strains comprises a plurality of strains which overexpress or underexpress a different gene product which is required for proliferation of said organism;

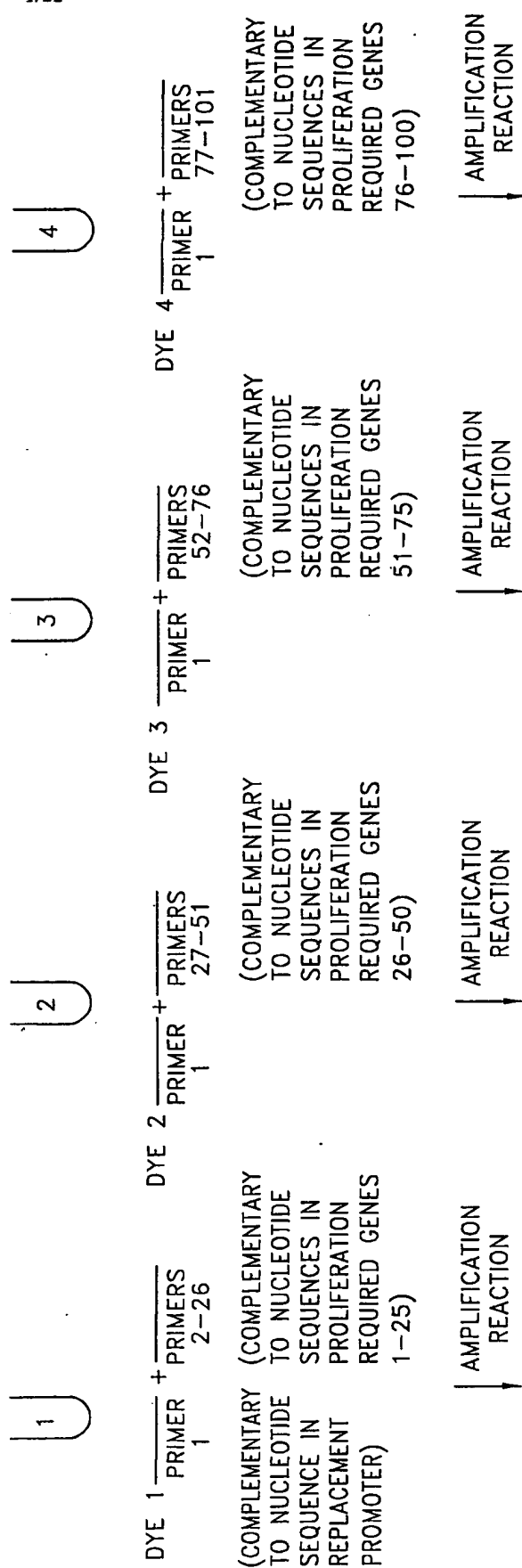
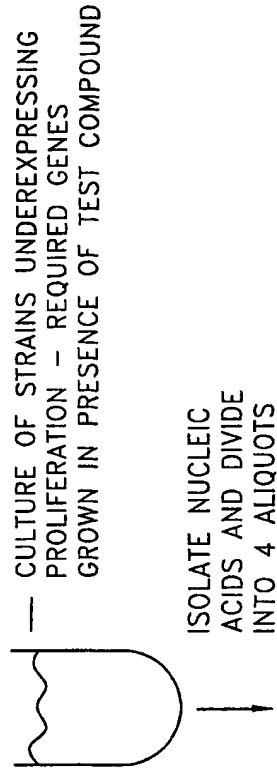
10 performing an amplification reaction using primer pairs which are complementary to nucleotide sequences within or adjacent to the genes which encode said gene products, wherein said primer pairs are designed such that each primer pair would yield an amplification product which is distinguishable from the amplification products produced by the other primer pairs on the a basis selected from the group consisting of length, detectable label and both length
15 and detectable label if a strain comprising the nucleotide sequences complementary to said primer pair is present in said culture or collection of strains; and

 identifying the amplification products obtained in said amplification reaction, wherein said culture comprises a strain in which a gene product
20 comprising a polypeptide selected from the group consisting of a polypeptide having at least 25% amino acid identity as determined using FASTA version 3.0t78 to a polypeptide selected from the group consisting of SEQ ID NOs.: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 and a polypeptide whose activity may be complemented by a polypeptide selected from the group
25 consisting of SEQ ID NOs: 3801-3805, 4861-5915, 10013-14110 and 14945-15778 is overexpressed or underexpressed.

FIG. 1

FIG. 1A
FIG. 1B

FIG. 1A



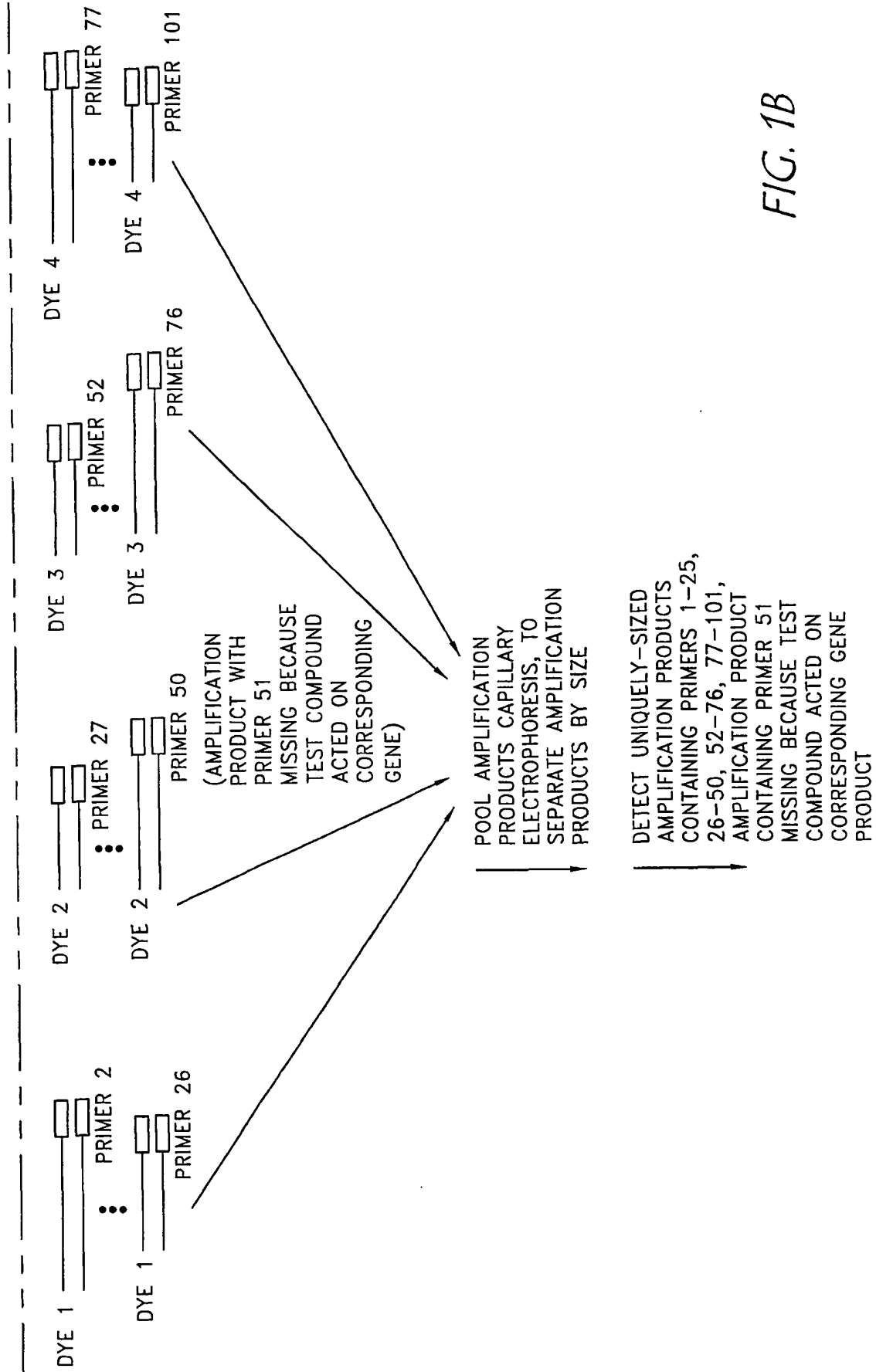
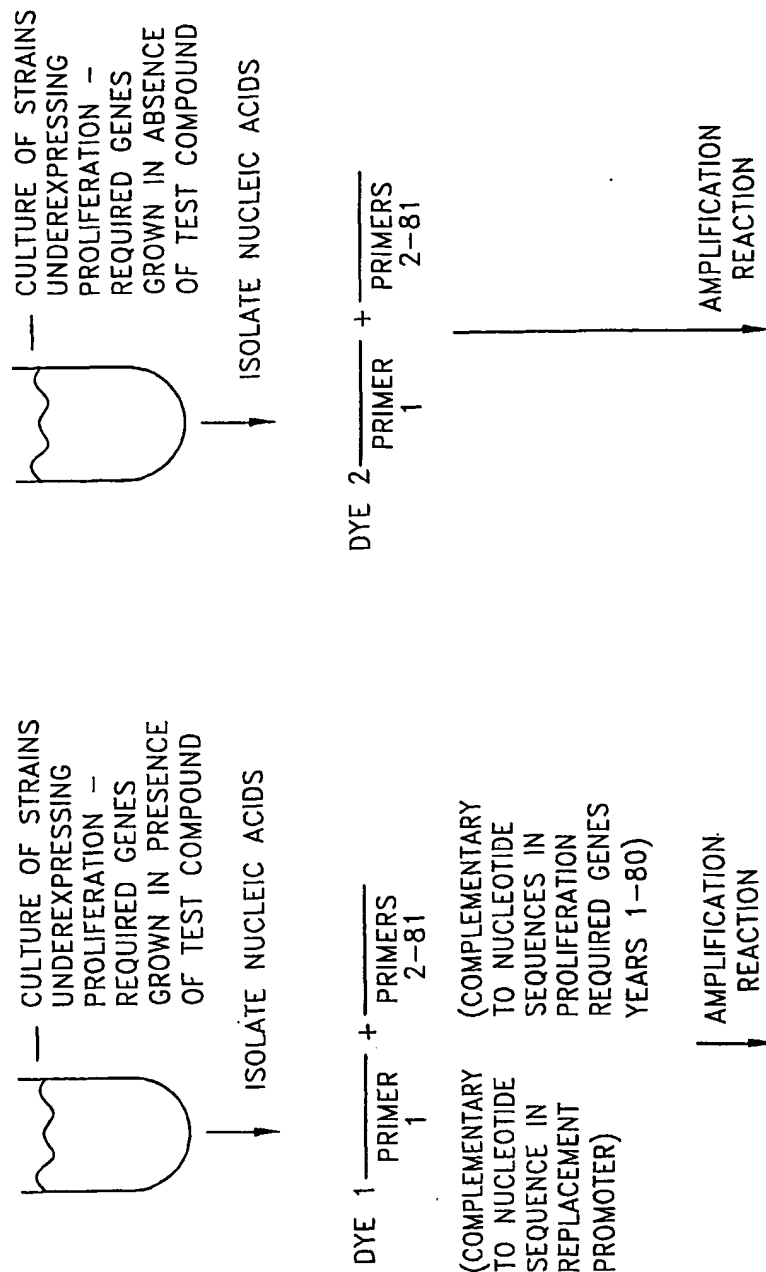


FIG. 1B

FIG. 2

FIG. 2A
FIG. 2B

FIG. 2A



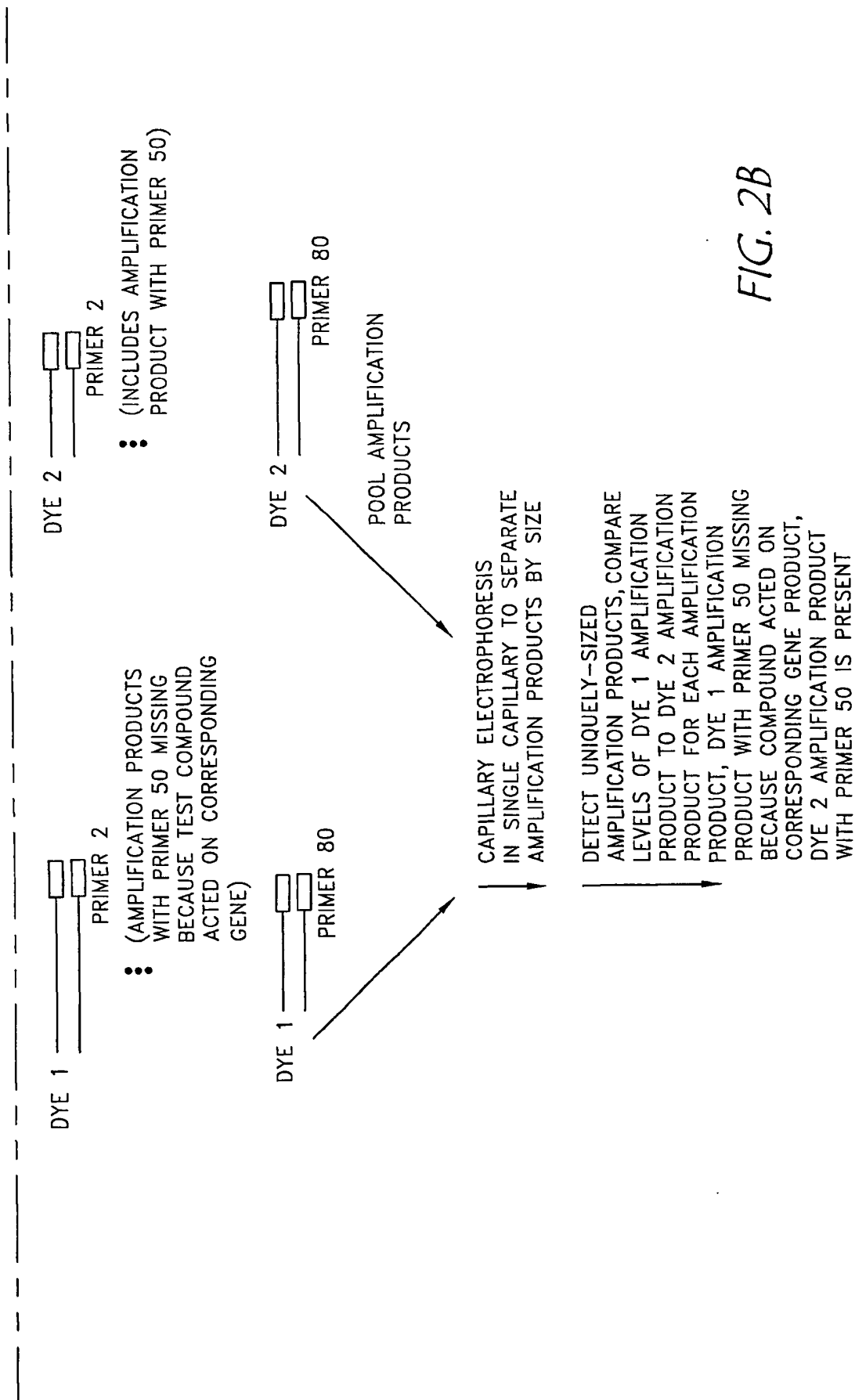


FIG. 2B

FIG. 3

Hypothetical 3 D Matrix Hybridization Results for Nonspecific Clones

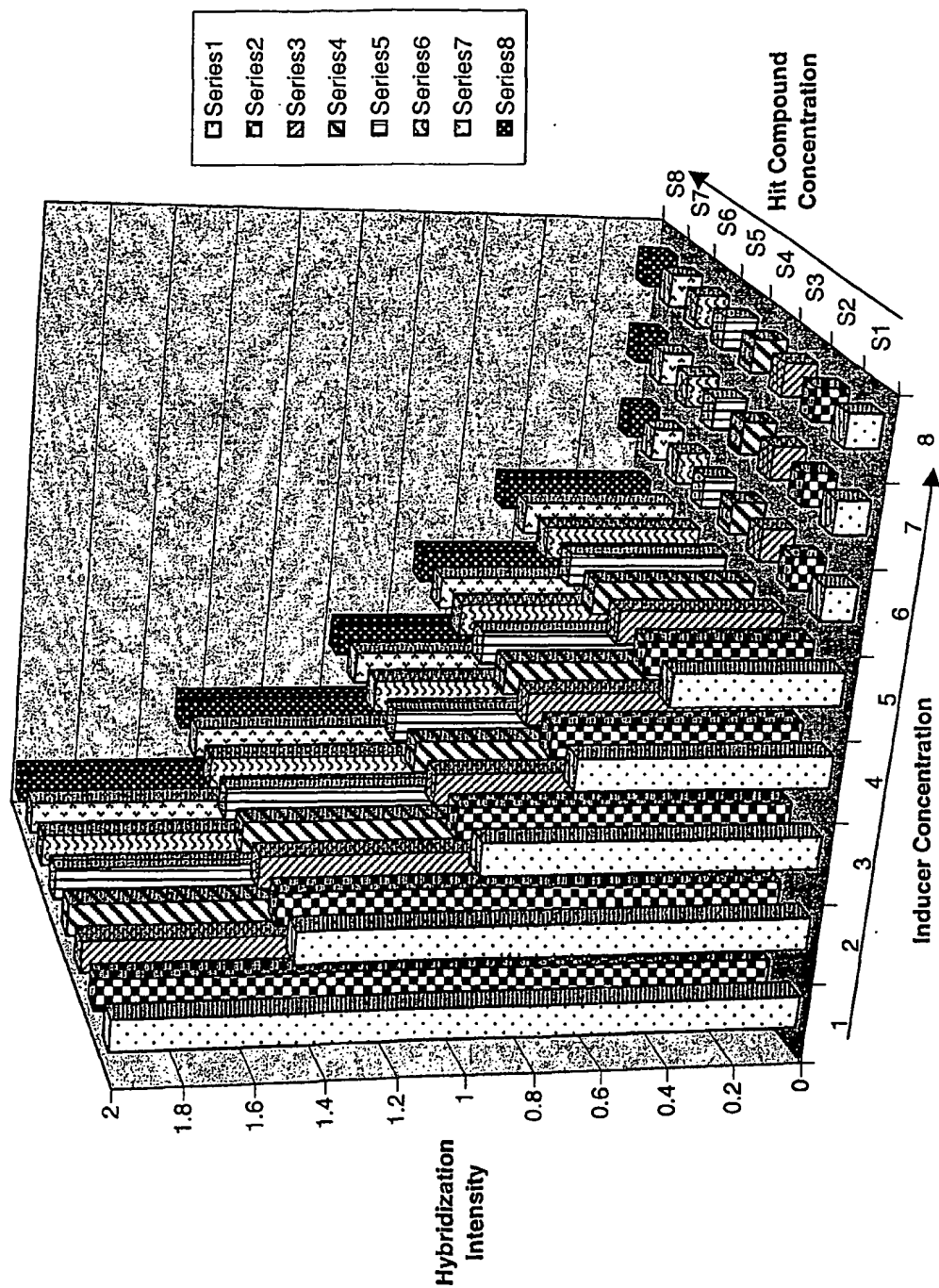
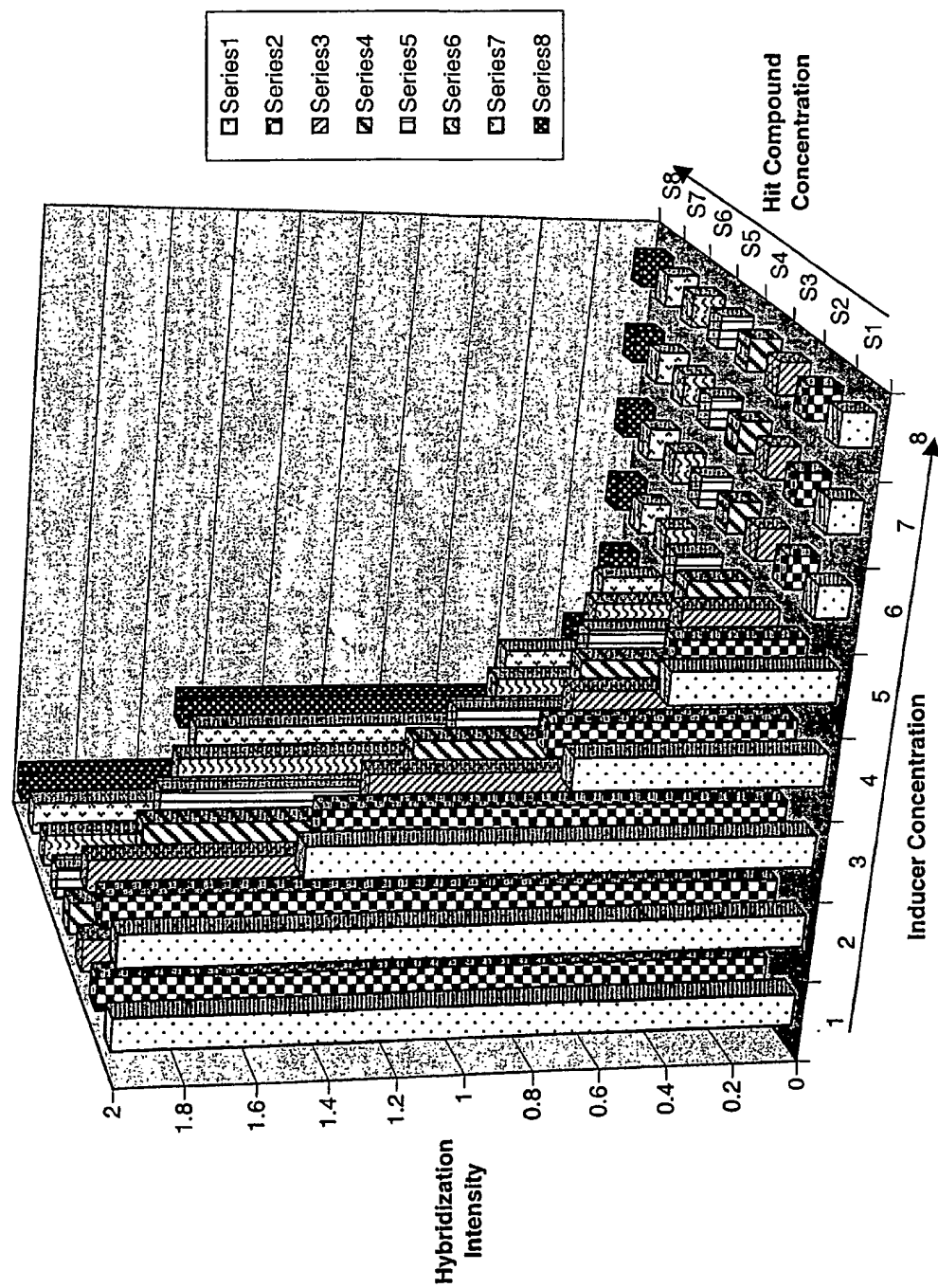



FIG. 4

Hypothetical 3 D Matrix Hybridization Results for A Specific Clone



P_R = Regulatable promoter

 = homology region

P_C = Chromosomal promoter

P_S = Promoter of selectable or identifiable marker

G_S = Gene encoding selectable or identifiable marker

T_T = Transcriptional Terminator

Promoter replacement cassette

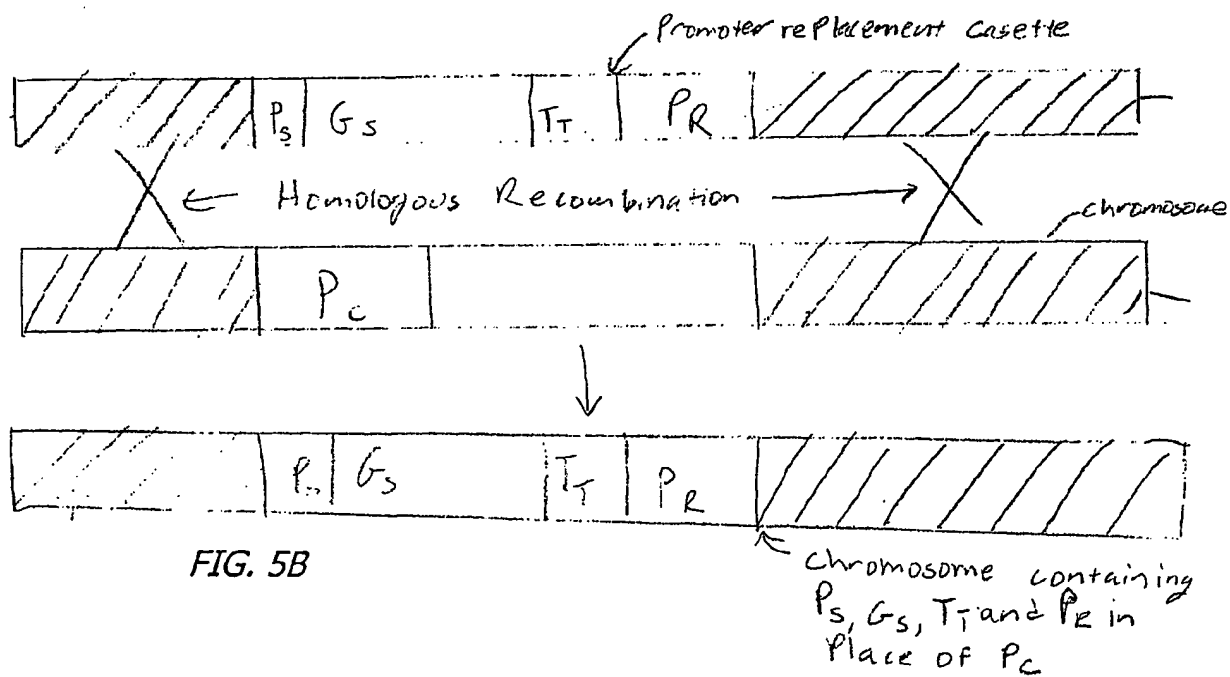
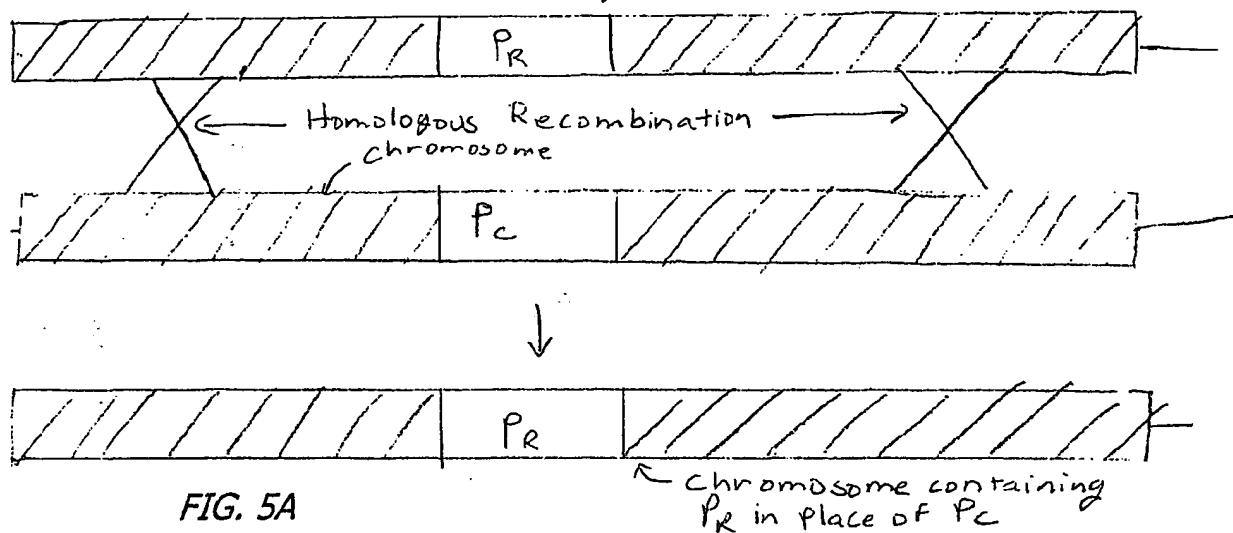
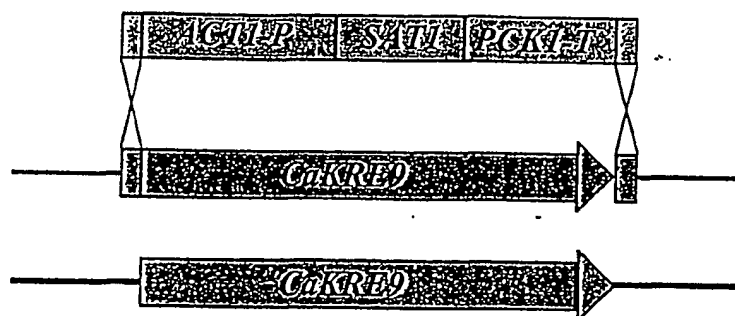


FIG. 6A

- STEP 1: Gene Replacement



- STEP 2: Conditional Expression by Promoter Replacement

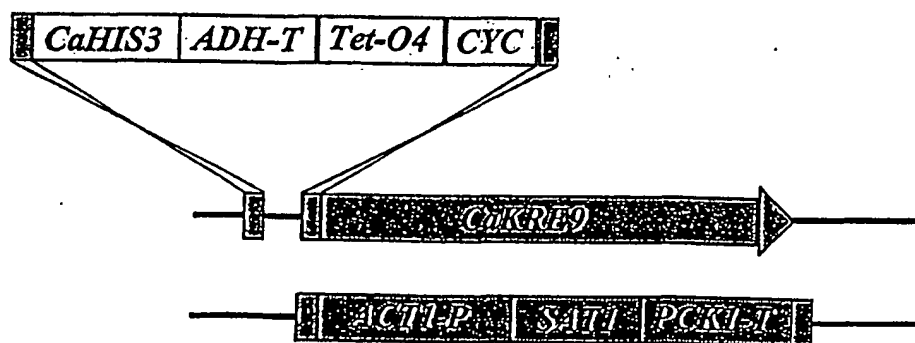
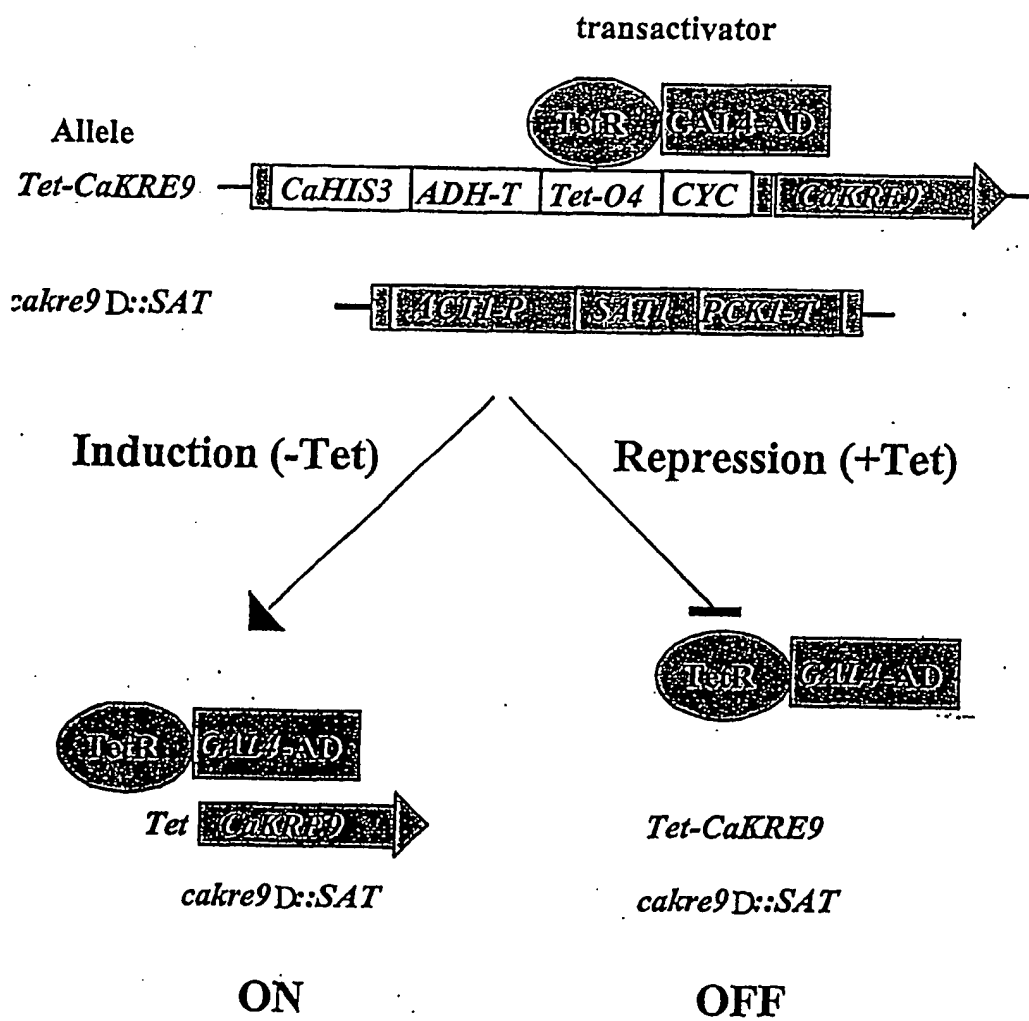


FIG. 6B

C. albicans GRACE Conditional Expression

CaHIS3 expression levels vs 3-AT Sensitivity

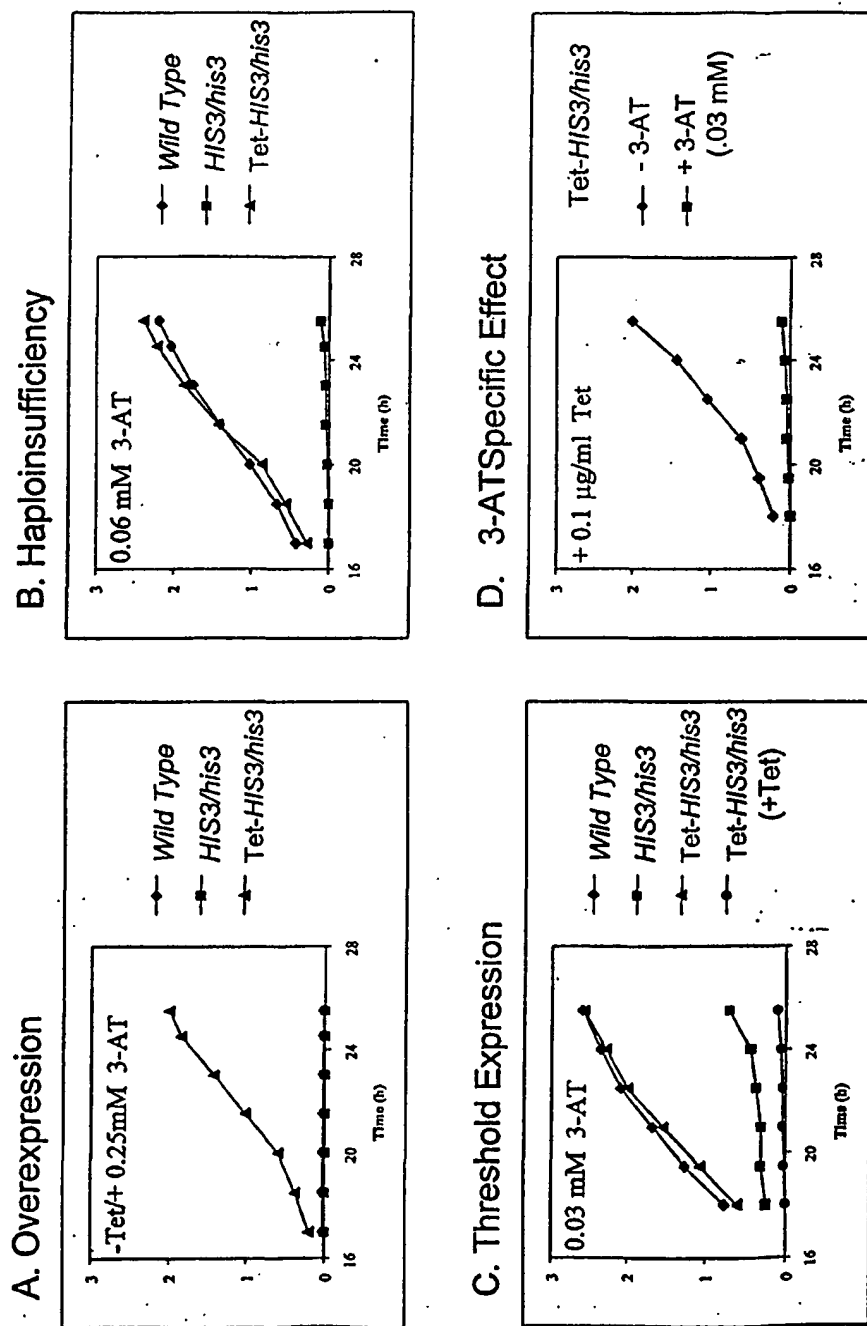


FIG. 7

Constitutive Expression Levels of GRACE Strains

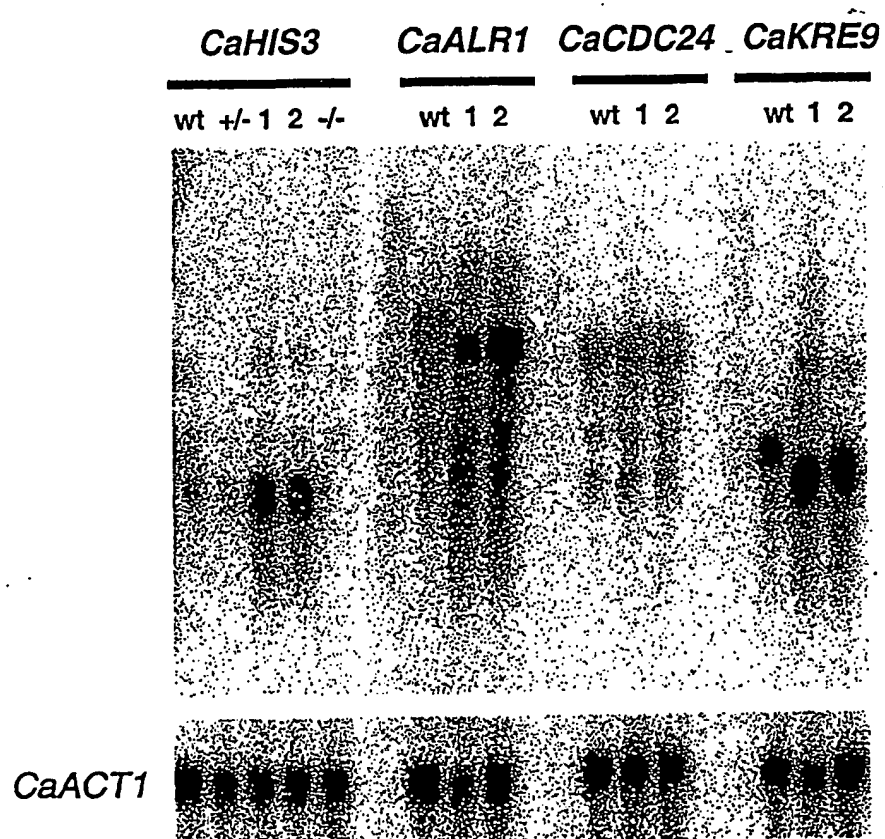
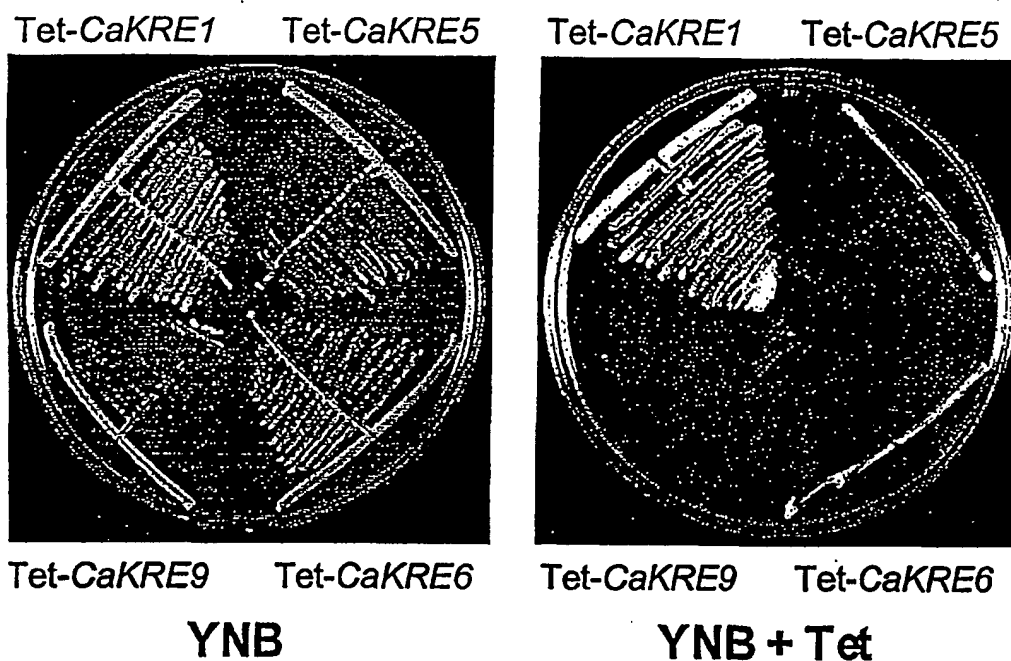


FIG. 8

GRACE Validation of *CaKRE* Targets



Gene	<i>S. cerevisiae</i>	<i>C. albicans</i> URA blaster	<i>C. albicans</i> - GRACE
<i>KRE1</i>	Viable	Viable	Viable
<i>KRE5</i>	Essential	Essential	Essential
<i>KRE6</i>	Essential + <i>skn1Δ</i>	Essential	Essential
<i>KRE9</i>	Essential + <i>knh1Δ</i>	Essential	Essential

FIG. 9

Target Validation by GRACE Method

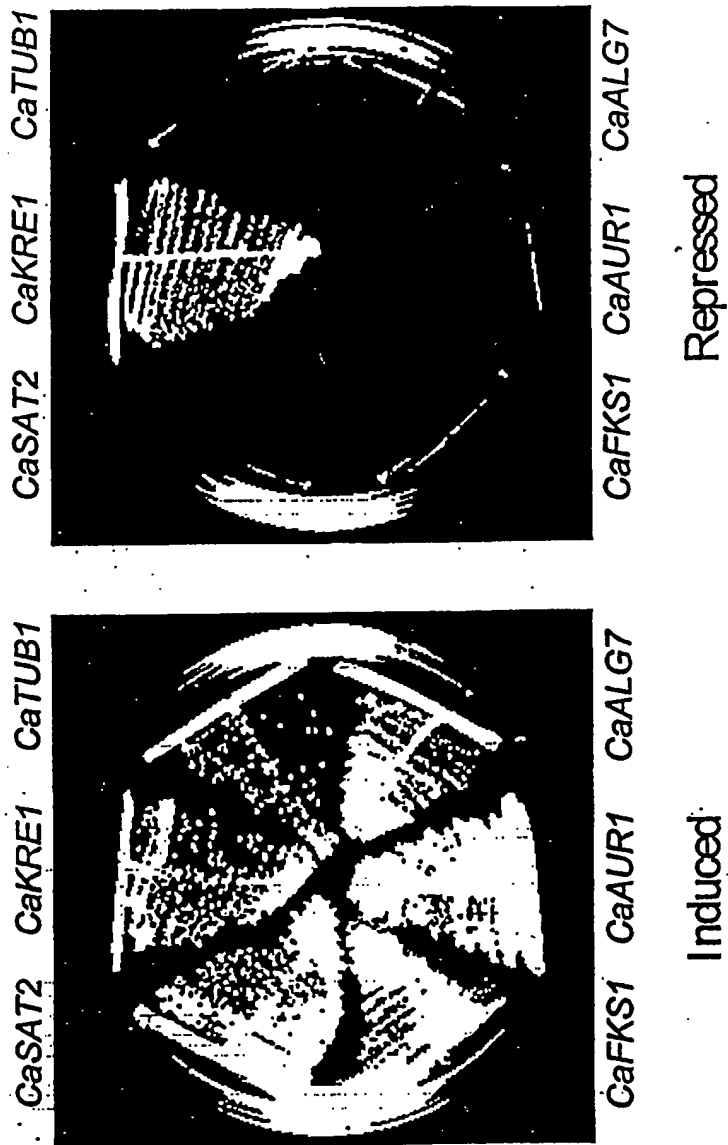
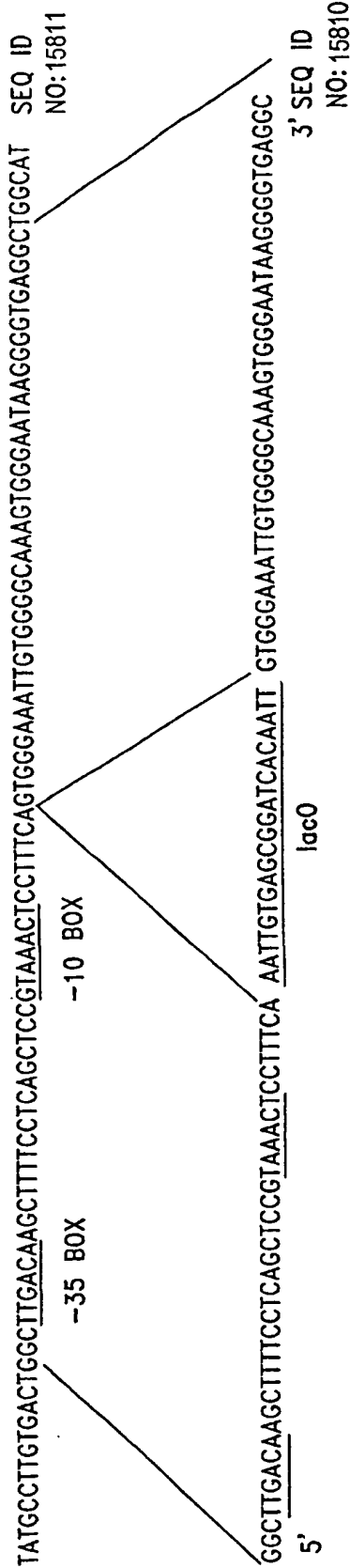


FIG. 10

14/22

PROMOTER FOR yabB yabC ftsL ftsI mure OPERON



OLIGO USED FOR lacO INSERTION

FIG. 11

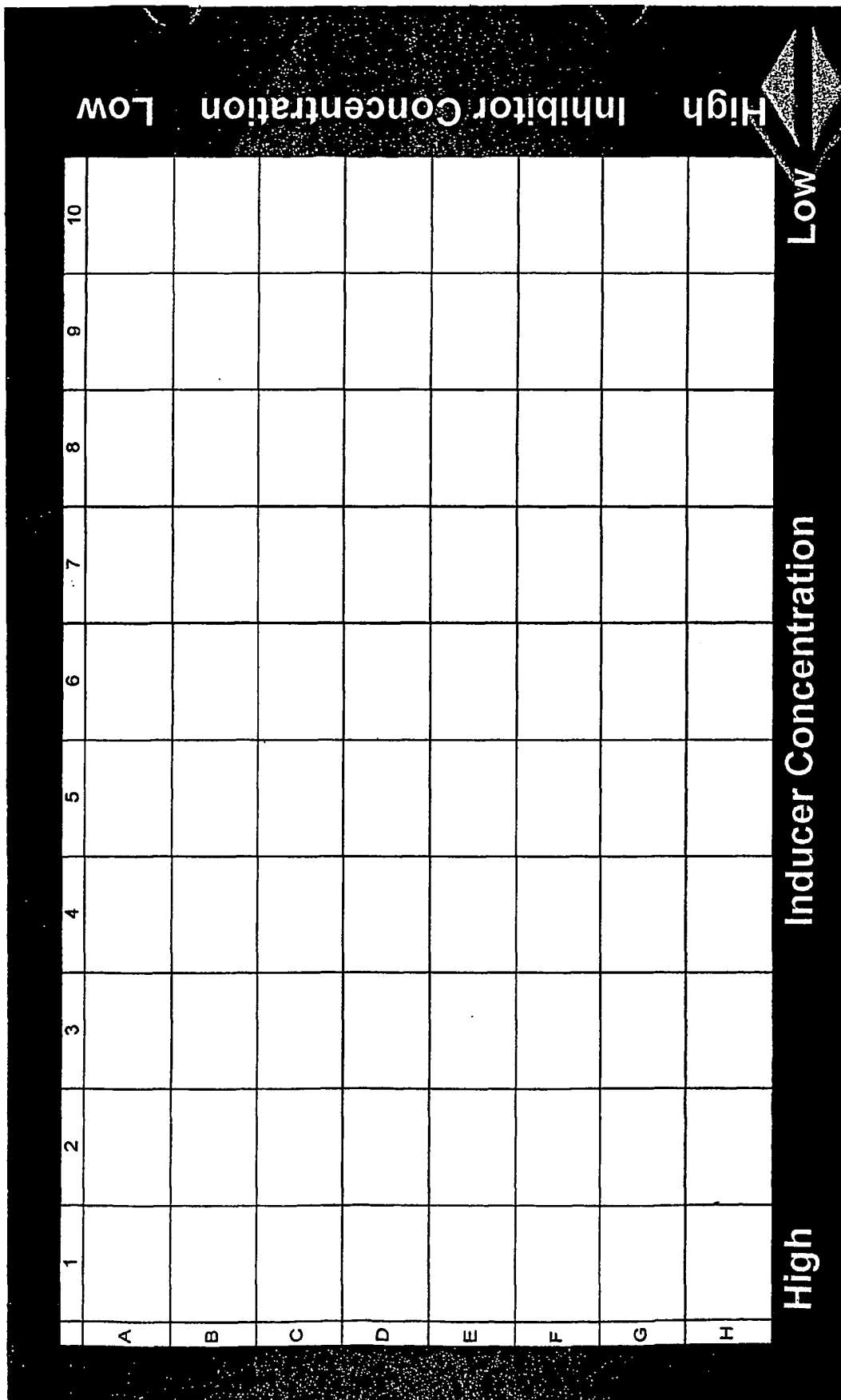
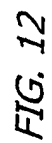


FIG. 13

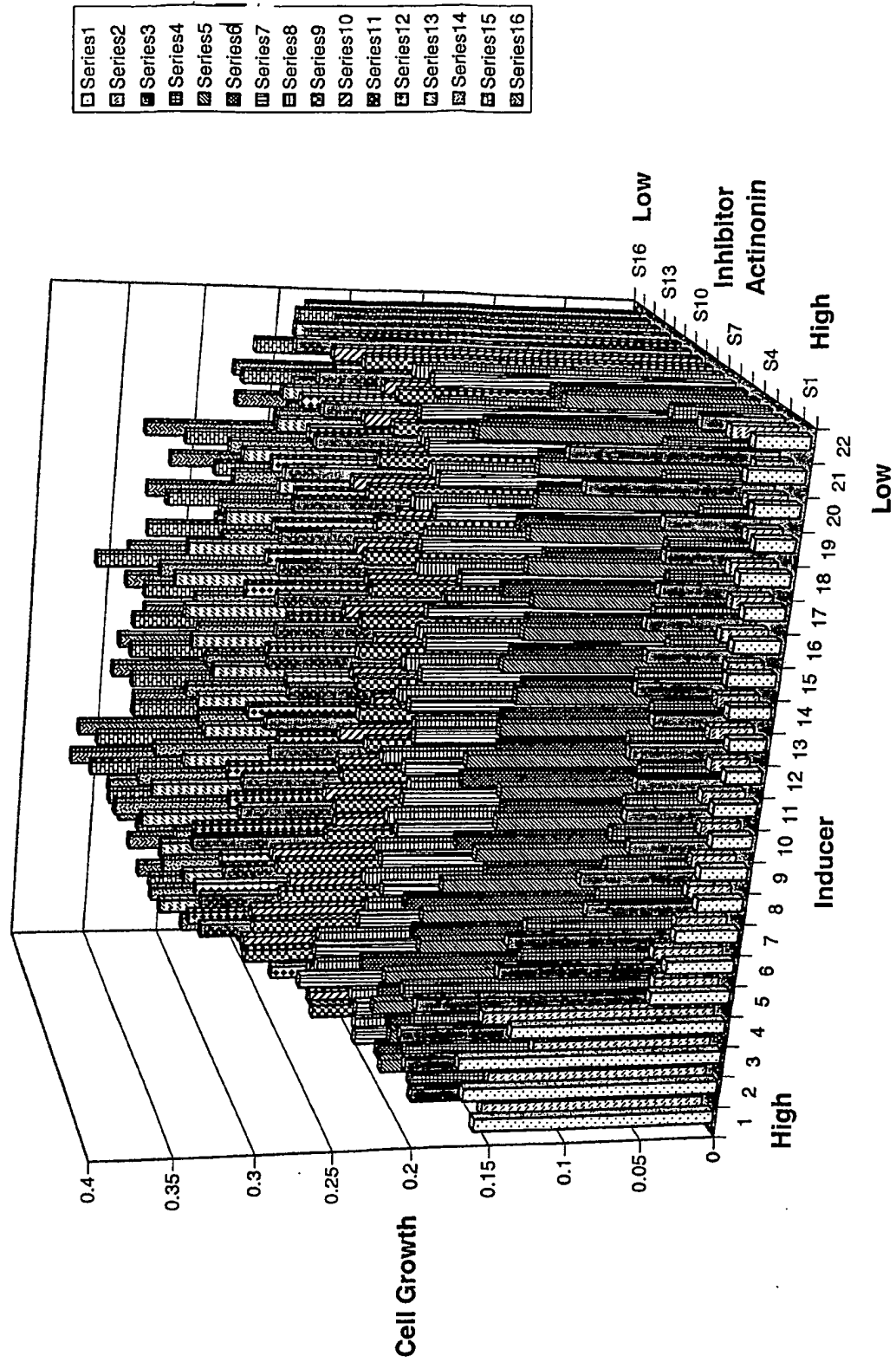


FIG. 14

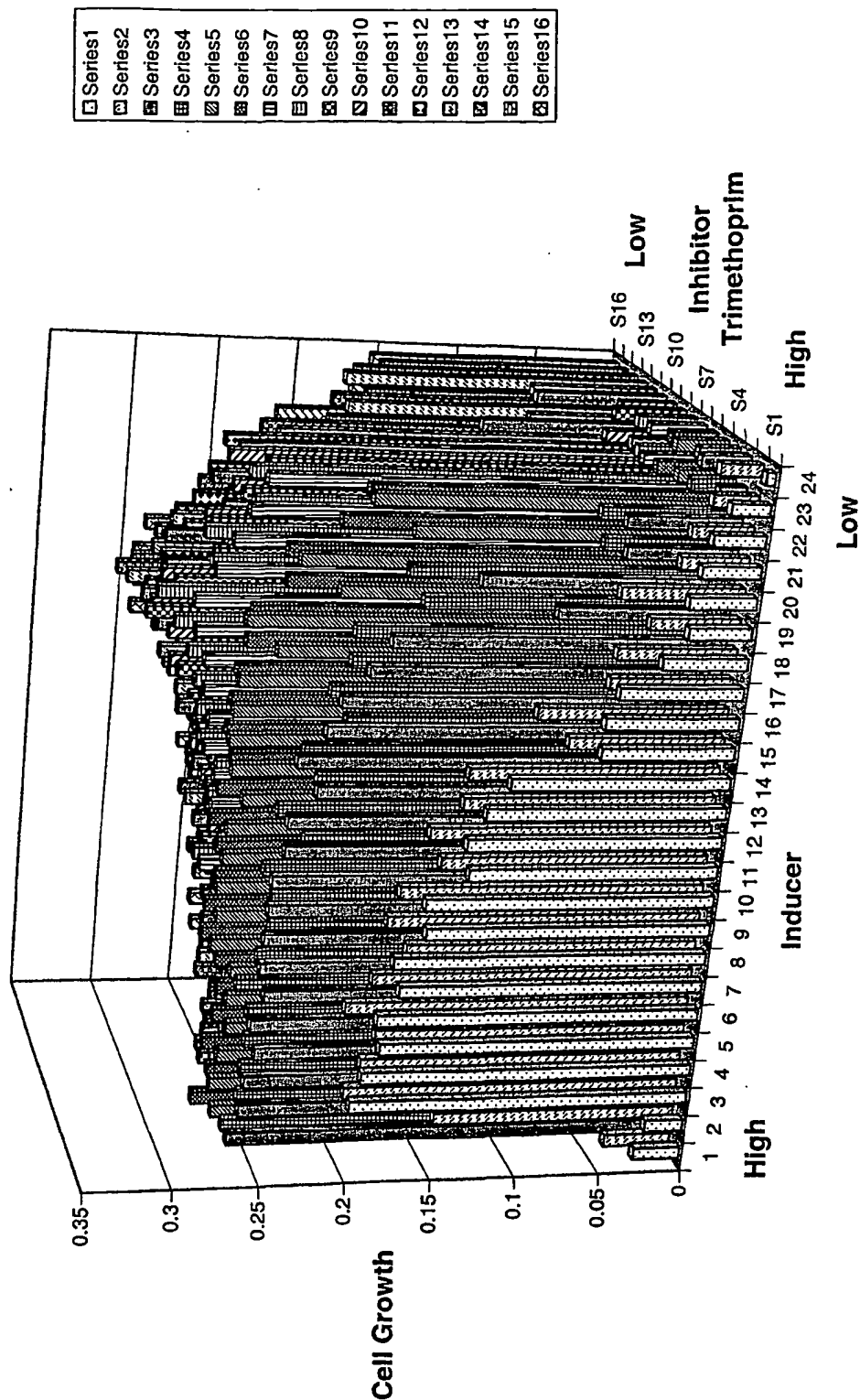


FIG. 15

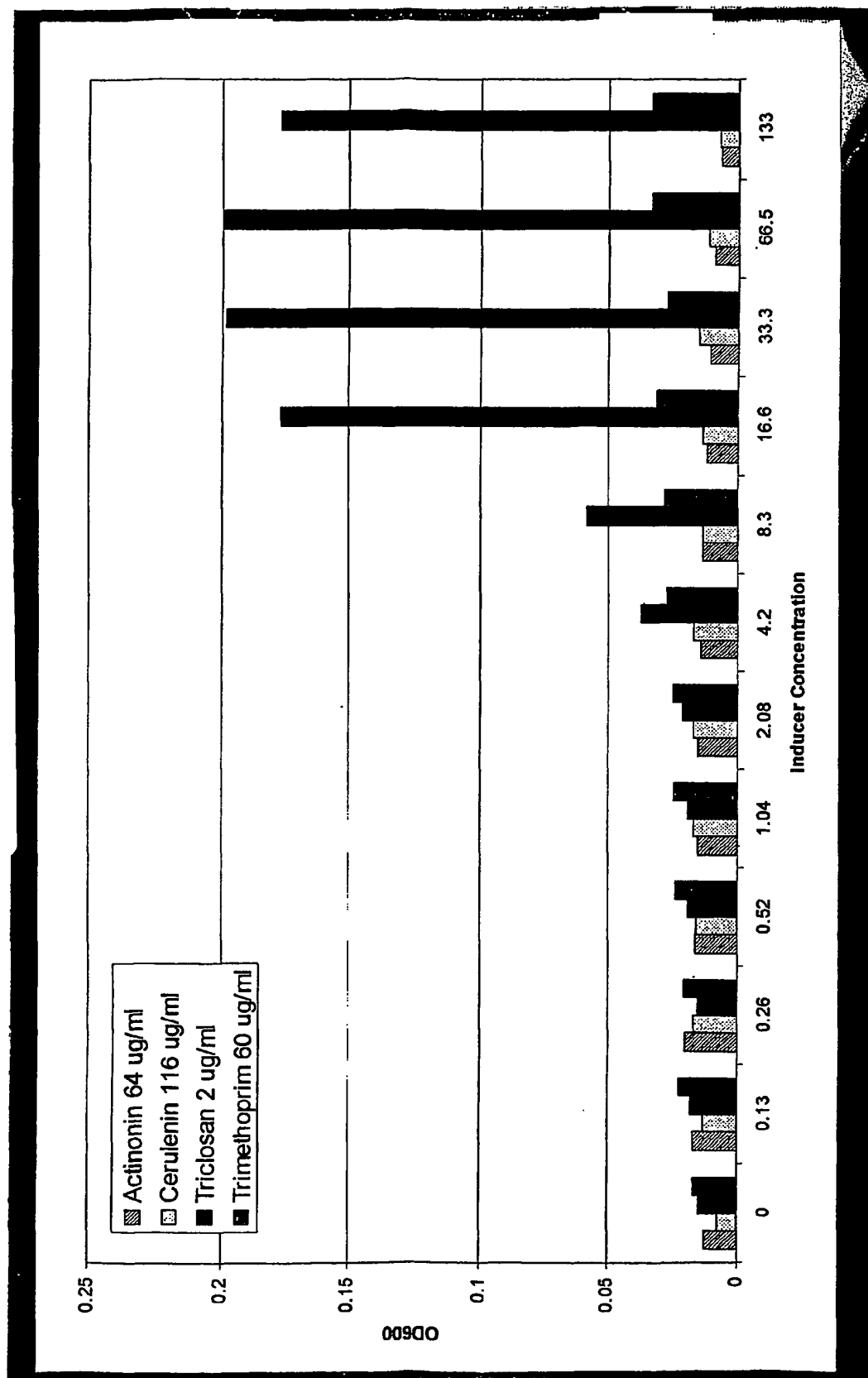


FIG. 16

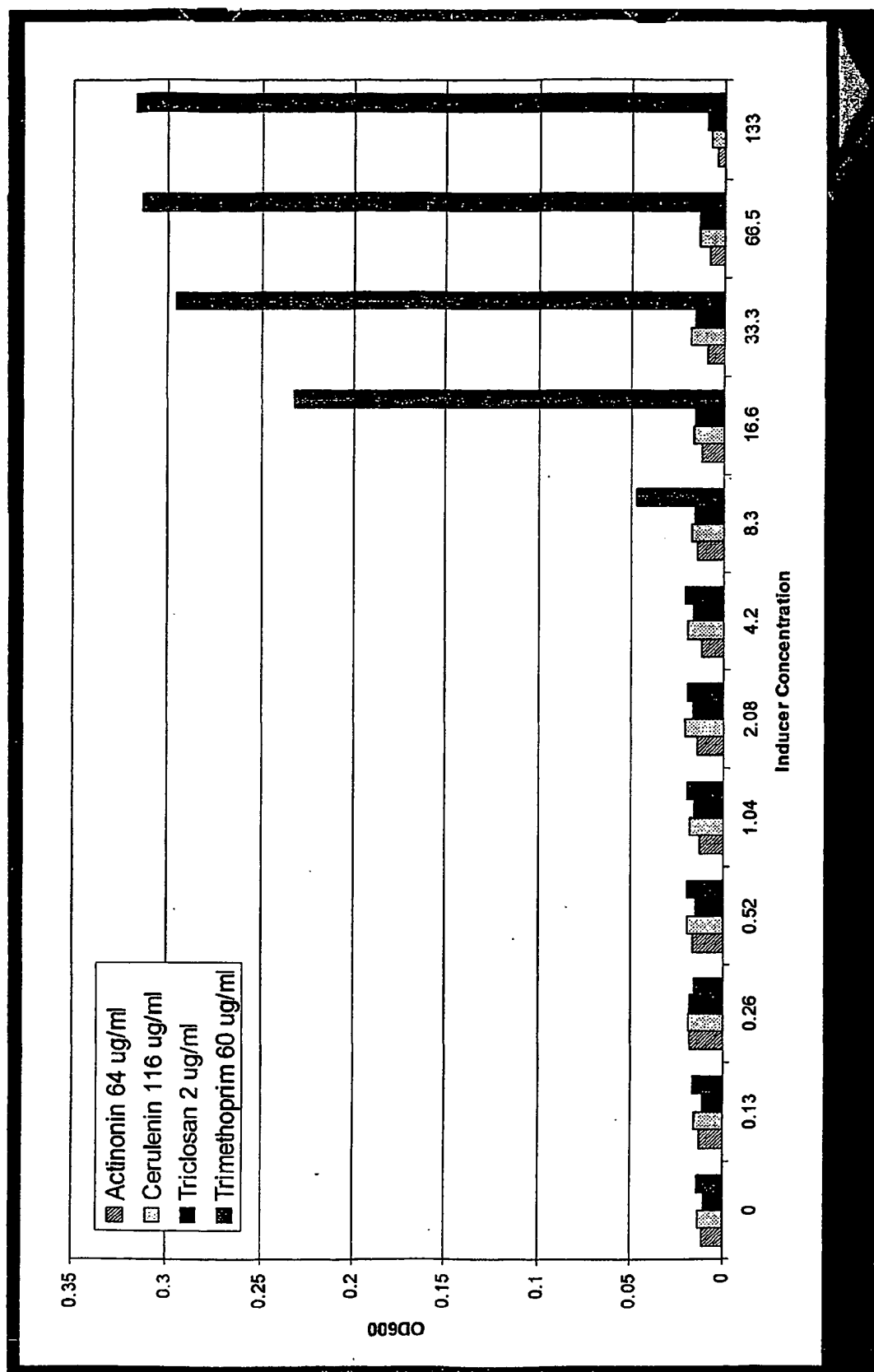


FIG. 17

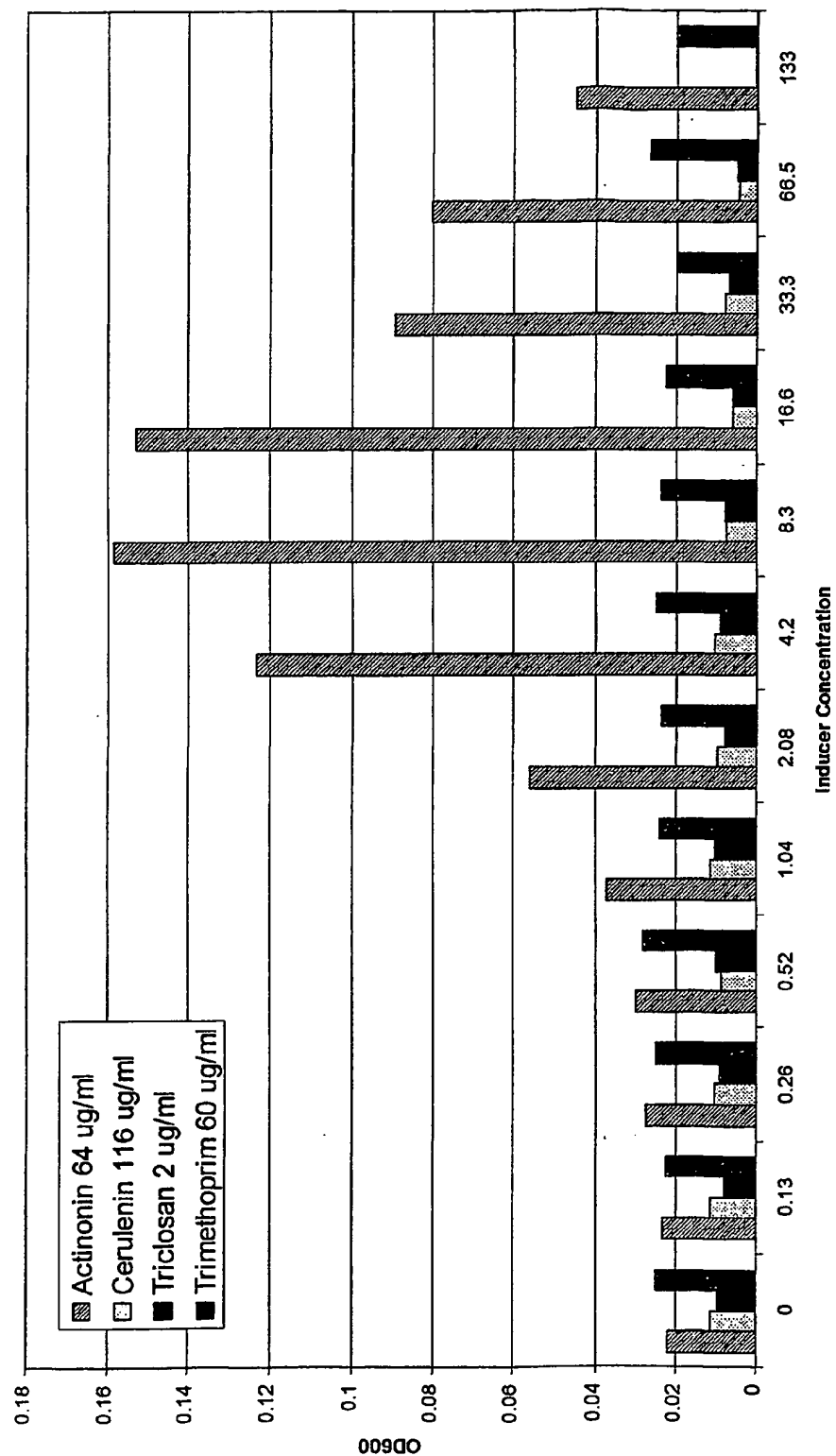
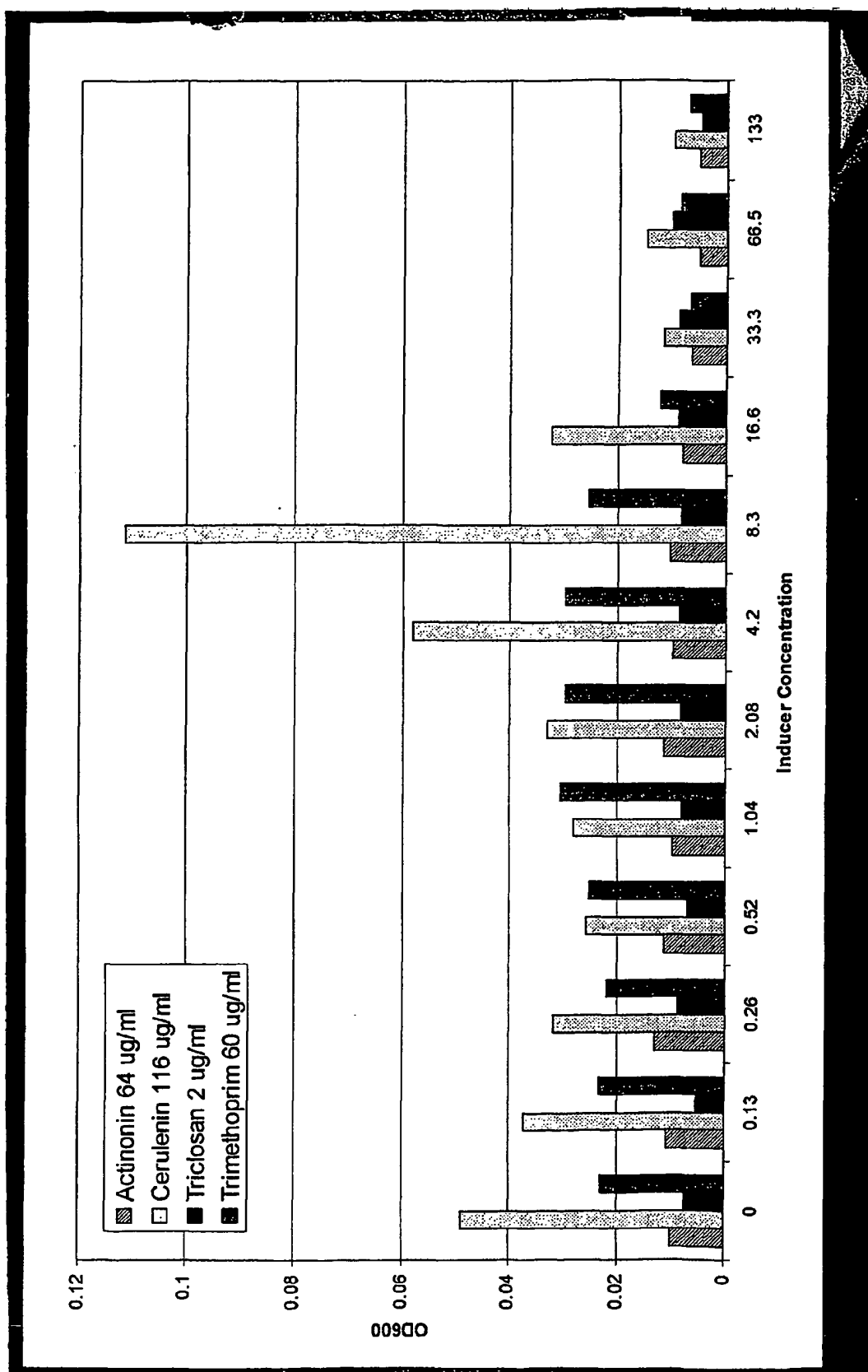


FIG. 18



Target Clone Amplification in a Mixed Culture (Nine Staph Clones)

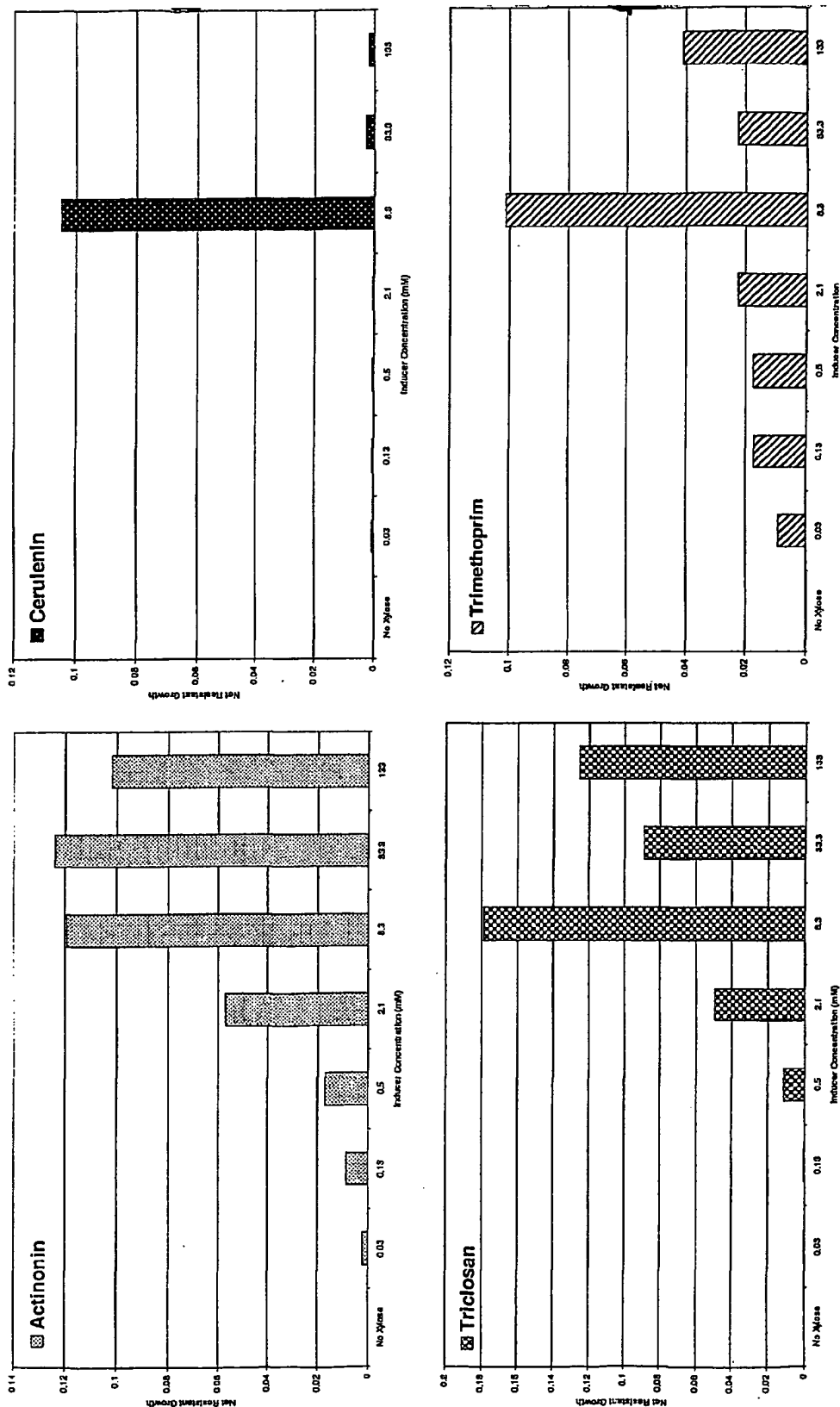


FIG. 19

(19) World Intellectual Property Organization
International Bureau



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(10) International Publication Number
WO 02/086097 A3

(51) International Patent Classification⁷: C12Q 1/68, 1/02,
C12P 19/34, C12N 1/000

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Published:

— with international search report

(88) Date of publication of the international search report:
6 March 2003

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: METHODS FOR IDENTIFYING THE TARGET OF A COMPOUND WHICH INHIBITS CELLULAR PROLIFERATION

(57) Abstract: The present invention relates to cultures or collections of strains which overexpress or underexpress gene products required for the proliferation of an organism. The present invention also includes methods for identifying the target on which a compound which inhibits the proliferation of an organism acts and methods for identifying the extent to which a strain is present in a culture or collection of strains.

WO 02/086097 A3

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/03987

A. CLASSIFICATION OF SUBJECT MATTER

IPC(7) : C12Q 1/68, 1/02; C12P 19/34; C12N 1/000

US CL : 435/6, 91.2, 29, 243

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 435/6, 91.2, 29, 243

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

WEST, STN, antibiotic, resistanc\$, gene\$, identi\$, Compugen, SEQ ID NO: 12600

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DAVIS, B.D. et al. Microbiology, 1968, Hoeber Medical Division, Harper & Row, Publishers, New York, USA, chapter 10, pages 302-328, see entire document.	1-15, 22-28, 49-52, 74, 75, 78-84, 89, 108-114, 121-125, and 142-148
Y	BRAXHAGE, A.A. et al. Use of reporter genes to identify recessive trans-acting mutations specifically involved in the regulation of <i>Aspergillus nidulans</i> penicillin biosynthesis genes. Journal of Bacteriology. May 1995, Vol. 177, No. 10, pages 2781-2788, see entire document.	1-15, 22-28, 49-52, 74, 75, 78-84, 89, 108-114, 121-125, and 142-148

☐ Further documents are listed in the continuation of Box C.☐ See patent family annex.

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document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art

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Date of the actual completion of the international search

28 September 2002 (28.09.2002)

Date of mailing of the international search report

04 NOV 2002

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INTERNATIONAL SEARCH REPORT

PCT/US02/03987

Continuation of Box II Item 4:

1-15, 18, 21-42, 45, 48-53, 60, 63, 70, 73-84, 87, 89-101, 104, 107-114, 117, 120-125, 128, 131-135, 138, 141-148, 151, and 154

INTERNATIONAL SEARCH REPORT

International application No.

PCT/US02/03987

Box I Observations where certain claims were found unsearchable (Continuation of Item 1 of first sheet)

This international report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claim Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claim Nos.:
because they relate to parts of the international application that do not comply with the prescribed requirements to such an extent that no meaningful international search can be carried out, specifically:
3. ☐ Claim Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of Item 2 of first sheet)

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2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this international search report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this international search report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.: Please See Continuation Sheet

Remark on Protest ☐ The additional search fees were accompanied by the applicant's protest.
☐ No protest accompanied the payment of additional search fees.

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